A COMPREHENSIVE PROTEOME ANALYSIS OF HEPATITIS B VIRUS-ASSOCIATED HEPATOCELLULAR CARCINOMA

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SUMMARY

Hepatocellular carcinoma (HCC) is the most common primary liver cancer with more than half of the cases attributed to persistent viral infection by the hepatitis B or C virus. To date, the exact molecular pathogenesis of HCC remains ambiguous. In this study, proteomic based approaches were used to identify protein targets with the aim to unravel the molecular pathogenesis of HCC. Three quantitative approaches, *viz,* 2-D DIGE, cICAT and iTRAQ coupled with 2-D liquid chromatography were used to analyze tumour lysates from moderately- and poorly-differentiated HBV-related HCC. To our knowledge, this is the first study using 3 proteomic techniques to analyse HCC tissues belonging to two different stages of differentiation.

In this study, a total of 163 and 181 proteins were found to be dysregulated in moderately- and poorly-differentiated HCC tissues respectively, among which only 12 proteins were common between all three techniques. Disparity among identified proteins was expected as it is known that each method has its inherent bias and limitation. A subset of these proteins was also verified using western blots to independently confirm the presence of the proteins identified by 2-D DIGE, cICAT and / or iTRAQ. These proteins were further grouped according to their function as annotated by Gene Ontology for the ease of analysis. The majority of affected proteins were those involved in metabolism. Most significantly, we are able to observe increasing abrogation of these metabolic pathways from moderately- to poorly-differentiated HCC. In addition, proteins related to iron homeostasis and defense mechanisms were also shown to be severely impaired. These indicate that the tumourigenic liver had lost its ability to perform its basic metabolic and detoxification functions.

Among the proteins identified, further analysis was conducted on a novel protein family, far upstream binding proteins (FUBPs) that were identified by 2-D DIGE. The over-expression of FUBPs in both stages of HCC are of particular interest due to their transcriptional activity on the oncogene, c-myc. Interestingly, a large number of dysregulated proteins identified were also c-myc associated proteins. In addition, c-myc was also observed to be elevated in the tissues used in this study. It has generally been accepted that c-myc plays an important role in HCC progression, especially in a viral associated carcinogenesis. The exact activators and functions of c-myc, however remain poorly understood. It is possible that FUBPs over-expression is responsible for elevated c-myc levels. Preliminary experiment using FUBP siRNA transfection on Hep3B, a HBV antigen positive liver cell line showed a decrease in cell viability. This effect was however not observed in HepG2, a HCC cell line without HBV in the genome. We therefore propose that the FUBP family of proteins may be one of the possible upstream players that are involved in HBV-related HCC tumourigenesis.

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1-D	One-dimensional
2-DE	Two-dimensional electrophoresis
2-D DIGE	Two-dimensional difference gel electrophoresis
Acc. No.	Accession number
aCGH	Array-based comparative genomic hybridization
ACN	Acetonitrile
AFB1	Aflatoxin B1
cDNA	Complementary DNA
CHCA	α-cyano-4-hydroxy-cinnamic acid
cICAT	cleavable Isotope-coded affinity tag
CyDye	Cyanine fluorescent dye
Da	Dalton
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic acid
DTT	Dithiothreitol
EDTA	Ethylenediaminetetraacetic acid
FAP	Familial adenomatous polyposis
FBS	Fetal bovine serum
FISH	Fluorescence *in situ* hybridization
FUBP	Far upstream binding protein

g	Centrifugal force
GO	Gene Ontology
GRAVY	Grand average of hydropathicity
HBV	Hepatitis B virus
HBsAg	Hepatitis B surface antigen
HCV	Hepatitis C virus
HCC	Hepatocellular Carcinoma
HIF	Hypoxia inducible factor
hr	Hour(s)
HRP	Horse radish peroxidise
IAA	Iodoacetamide
IEF	Isoelectric focusing
iTRAQ	isobaric Tag for Relative and Absolute Quantitation
IPG	Immobilized pH gradient
IPI	International Protein Index
KEGG	Kyoto Encyclopedia of Genes and Genomes
LCC	Large cell change
LC-MS	Liquid chromatography-mass spectrometry
LOH	Loss of heterozygosity
MALDI-TOF/TOF MS	Matrix-assisted laser desorption/ionization-tandem time-of-flight mass spectrometry
min	Minute(s)

miRNA	MicroRNA
M_r	Relative molecular mass
MS/MS	Tandem mass spectrometry
MMTS	Methyl methane-thiosulfonate
MTT	3-4,5-dimethylthiazolyl-2,5-diphenyl-tetrazolium bromide
MW	Molecular weight
NaB	Sodium butyrate
NH_4HCO_3	Ammonium bicarbonate
NNM	N-nitrosomorpholine
PCR	Polymerase chain reaction
PBS	Phosphate buffered saline
pI	Isoelectric point
PTM	Post-translational modification
RNA	Ribonucleic acid
ROS	Reactive oxygen species
rpm	Revolutions per minute
s/n	Signal to noise
SAGE	Serial analysis of gene expression
SCC	Small cell change
SDS-PAGE	Sodium dodecyl sulphate-polyacrylamide gel electrophoresis
SELDI	Surface enhanced laser desorption and ionization
SEREX	Serological analysis of antigens by recombinant expression cloning

SILAC	Stable isotope labeling by amino acid in cell culture
siRNA	Small interfering RNA
TAA	Thioacetemide
TBS-T	Tris buffered saline – Tween
TCEP	Tris-(2-carboxyethyl) phosphine
TFA	Trifluoroacetic acid
TOF	Time of flight
UniProt	Universal Protein Resorce database (http://www.expasy.uniprot.org)
v/v	Volume / Volume
w/v	Weight / Volume

1. LITERATRUE REVIEW

1.1 Hepatocellular Carcinoma (HCC)

1.1.1 Epidemiology

Hepatocellular carcinoma (HCC) is the most common primary liver cancer. Globally HCC ranks fifth amongst the most common cancers but it is the third leading cause of cancer death with an estimated one million death annually (Bosch *et al.,* 2004; Cha and DeMatteo, 2005). It has a high fatality ratio with most patients who develop liver cancer dying within a year (Yuen *et al.,* 2009).

HCC has a wide geographical variability with the highest incidence in developing nations, such as Asia and sub-Saharan Africa, accounting for 80% of new cases (Parkin, 2006; Wong and Ng, 2008). In Southeast Asia, HCC is the second most fatal cancer since the 1970s with a male predominance of 2 to 4 times more than for females (El-Serag and Rudolph, 2007). Over the last 2 decades, there has also been a noticeable increase of HCC in developed countries such as Europe and the United States (El-Serag and Mason, 1999; Zucman-Rossi and Laurent Puig, 2007).

In Singapore, HCC is the fourth most frequently occurring cancer in men with an overall incidence of 18.9 per 100 000 person-year (Singapore Cancer Society). The incidence is highest among the Chinese population compared to the other ethnic groups (Yuen *et al.,* 2009).

1.1.2 Aetiological factors

The risk factors of HCC have been well established. These include persistent hepatitis B or C virus (HBV or HCV) infection, cirrhosis and aflatoxin B1 which accounts for almost 80%

of all HCC cases (Bosch *et al*., 2005; Thorgeirsson *et al.,* 2006). Other aetiological factors include severe alcohol abuse leading to cirrhosis (Stickel *et al.,* 2002; Morgan *et al.,* 2004), smoking, as well as abnormal levels of oestrogen and androgen (Seow *et al.,* 2001). In addition, metabolic abnormalities such as hereditary haemochromatosis (Kowdley, 2004), α-1-antitrypsin defiency, hereditary tyrosinaemia and Wilson's disease can also lead to HCC.

In recent years, diabetes and obesity have also been identified as probable risk factors for HCC (Polesel *et al.,* 2009). HCC, due to obesity, most likely progresses through steatohepatitis disease to cirrhosis and eventually carcinogenesis (Calle *et al.,* 2003). It should also be noted that the risk of HCC increases in the event of multiple risk factors.

1.1.2.1 Hepatitis B virus

Hepatitis B virus (HBV) is a 3.2kb partially double stranded DNA virus which can cause an acute and chronic inflammatory response from the liver. The estimated number of HBV chronic carrier world-wide is 400 million, of which 75% reside in Asia (Lai *et al.,* 2003). This incident level correlates strongly with the incidence of HCC. HBV is the first human virus proven to cause cancer (Parkin, 2001; Beasley, 2009). In Singapore alone, a third of HCC patients are HBV positive (Yuen *et al.,* 1999). Further evidence has shown that patients who are seropositive with chronic HBV infection are about 70-fold more likely to develop HCC (Rabe *et al.,* 2001). Numerous human HCC studies have also shown integrated HBV DNA sequences and expression of viral proteins from these sites (Matsubara and Tokino, 1990; Su *et al.,* 1998).

HBV infection consists of a replicative phase which results in prolonged cycles of liver cell damage followed by regeneration of the hepatocytes and inflammatory processes. This

leads the development of chronic hepatitis, liver fibrosis and cirrhosis that may eventually develop to HCC (Li *et al.,* 2004; Kao *et al.,* 2005). HBV-related HCC has also been observed in non-cirrhotic liver background. In addition the viral genome has also been identified in the early stages of tumourigenesis, suggesting that its integration precedes HCC development (Brechot, 2004). This implies the possibility that the HBV viral genome may have some intrinsic hepatocarcinogenic properties. The genomic alterations that occur as a result of viral integration may therefore be an additional mechanism that causes HCC (Matsubara and Tokino, 1990).

The viral integration is a dynamic process and rearranges as hepatocytes proliferate. This integration can cause cis- or trans-activiation and has been observed to affect a variety of genes involved in proliferation, cell viability and cell signalling (Rabe *et al.,* 2001). Possible transactivators of the virus include truncated preS2/S, hepatitis B spliced protein and HBV-X protein (Caselmann, 1995; Brechot, 2004; Tang *et al.,* 2006). At least one of these sequences has been identified in more than 80% of HBV-related HCC (Schluter *et al.,* 1994).

The most studied candidate, HBV-X protein transactivating function was first hypothesized by Miller and Robinson (1986). *In vivo* studies have shown that HBV-X is able to transactivate a large number of promoters related to inflammation and cell proliferation through protein-protein binding. This thus improves the cellular environment for further viral replication (Tang *et al.,* 2006). HBV-X is also able to increase sensitivity to possible carcinogens or directly affect cellular oncogene levels such as c-myc (Yang *et al.,* 2008) or inactivate tumour suppressors such as p53 (Ueda *et al.,* 1995). It can also modulate protein degradation via proteosome regulation (Brechot, 2004) and stabilization of hypoxia inducible factor (HIF) (Moon *et al.,* 2004). Elevated levels of HIF have been observed during hypoxia conditions

induced by tumourigenesis. Although its direct interactions are not clear, concerted effects of HBV-X and other players such as c-myc and HIF can potentially encourage survival and invasion of tumour cells. HBV is the best investigated aetiological agent with overwhelming evidence in numerous animal models and human samples. However, the exact mechanism of its malignant transformation has yet to be fully understood.

1.1.2.2 Hepatitis C virus

Hepatitis C virus (HCV), a 9.6 kb single stranded RNA virus, with an estimate of 170 million chronically infected individuals worldwide. HCV has increasingly been the major cause of HCC (McGlynn and London, 2005), predominantly in the developed nations such as Europe, United States and Japan (Bosch *et al.,* 1999). Due to its great sequence heterogeneity, HCV is classified according to its various subtype, with 1b having the greatest risk of chronic infections resulting in severe liver damage (Purcell, 1997; Colombo, 1999).

HCV also induces liver inflammation followed by a continuous cycle of hepatocyte death and regeneration. Analogous to HBV infection, this provides a context of genetic mutations and aberrations. Though HCV, made up of RNA, is unable to integrate to its host genomes, it is hypothesized that immune responses against the virus could substantially promote tumourigenesis. Studies have also suggested that the HCV RNA and core proteins are able to impair dendritic cell functions that are important for T-cell activation (Pachiadakis *et al.,* 2005) and evade immune-mediated cell death by interactions with interferon-α and tumour necrosis factor-α (Melen *et al.,* 2004; Gale and Foy, 2005).

HCV core proteins, for example, have been shown to interact with MAPK signalling pathways such as ERK, MEK and Raf, to modulate cell proliferation. Another protein, NS5A of the HCV, is also able to sequester p53 thereby affecting p53-regulated pathways. Studies using mouse models also show that HCV core proteins are able to induce hepatic steatosis as well as reactive oxygen species (ROS) and oxidative stress which may be responsible for HCC development (Moriya *et al.,* 1998; 2001). All these results provide evidence that viral proteins are capable of directly inducing tumourigenesis.

1.1.2.3 Aflatoxins

Aflatoxins are naturally occurring mycotoxins that are produced by many species of *Aspergillus* fungus. Aflatoxin contamination in food remains a serious problem and may account for more than half of the HCC in Africa, China and South-East Asia (Bosch *et al.,* 2005). High levels of exposure to aflatoxins can result in acute hepatic necrosis, and cirrhosis and possibly liver carcinoma. Aflatoxin B1 (AFB1), produced by *Aspergillus flavus and Aspergillus parasiticus*, is the most commonly occurring and potent of the aflatoxins (Mc Lean and Dutton, 1995).

AFB1 is metabolised predominantly in the liver to an AFB1-8,9-exo-epoxide which in turn forms a promutagenic AFB1-N7-guanine DNA adduct. This results in a guanine to thymine transversion mutation (Bressac *et al.*, 1991). Fifty percent of human HCC with high levels of AFB1 exposure has been shown to harbour a specific point mutation in guanine to thymine of codon 249 (AGG to AGT) in the tumour suppressor, p53 (Moradpour and Blum, 2005; Wild and Montesano, 2009). This loss of p53 function may affect apoptosis and eventually promote carcinogenesis.

1.1.2.4 Inherited disorders

Hepatocellular carcinoma may also arise from several inborn errors of metabolism. For example hereditary haemochromatosis results in high iron levels in the liver that leads to increased oxidative stress and probable DNA damage. Approximately 40-60% of patients with hemochromatosis will develop HCC (Niederau *et al.,* 1985). Other autosomal recessive diseases such as α-1 antitrypsin defiency and tyrosinaemia can lead to inflammations and excessive liver necrosis and regeneration. In both cases, about 40% of patients will develop HCC (Eriksson 1985; Cha and DeMatteo, 2005).

It has also been proposed that HCC can be familial, due to occurrences of HCC in children. It has also been shown that HBV infected males with a family background of HCC have 84% chance of getting HCC in comparison to just 9% of individuals without a HCC family history. Similarly, females have 46% chance of HCC compared to 1% in those with no HCC family history (Shen *et al.,* 1991). However, due to confounding environmental factors, the possibility of genetic factors that may contribute to HCC has yet to be defined.

1.1.3 Morphological changes in Hepatocarcinoma

Hepatocarcinogenesis, like other cancers are multistage and multifactorial and involves various genetic alterations that ultimately lead to malignant transformation of normal cells. However unlike other cancers, notably colorectal cancer, no significant progress has been made in elucidating the various molecular players, sequence of events and their interactions in HCC. This is not surprising considering the heterogeneity of numerous aetiological factors that are implicated in HCC.

Despite the complexities presented, the pathogenesis of HCC is believed to develop through a series of possible common events which leads to morphological changes. This consists of a preneoplastic phase that may take about 10 – 30 years to develop, dysplasia and eventually neoplasia (Thorgeirsson and Grisham, 2002). These proposed chronological sequence of events that culminated in the development of HCC are separable and can be studied by well-established histocytological criteria (Fig. 1.1).

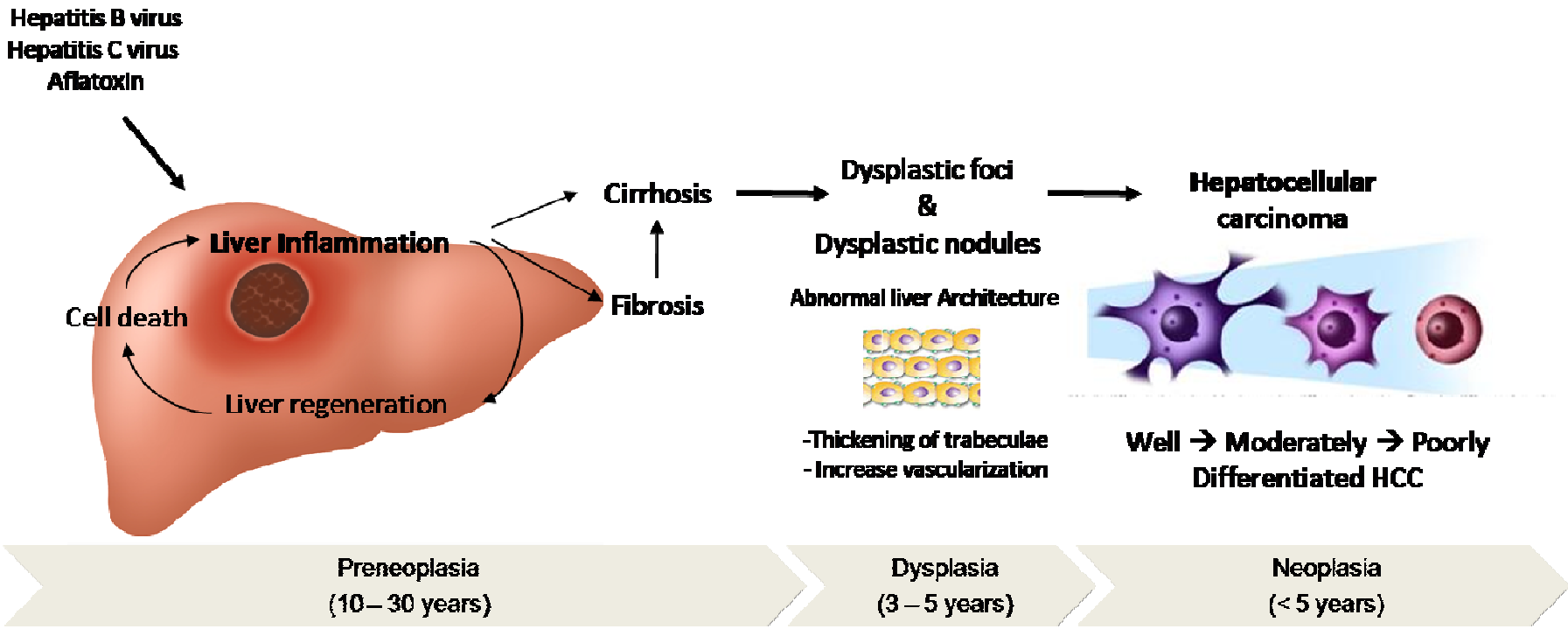


Figure 1.1 : Illustration of the chronological sequence of hepatocellular lesions leading to the development of HCC.

1.1.3.1 Preneoplasia and Dysplasia

Hepatocarcinogenesis is believed to have a long preneoplastic phase. This often begins with chronic hepatitis as a result of various insults that leads to liver inflammation. The liver is hence exposed not just to the aetiological agents, but pronounced levels of inflammatory cytokines, matrix degrading enzymes and mitogenic growth factors (Brechot, 2004). These sustained chronic inflammation and cytokine induced hepatocyte death results in remodelling of liver matrix and rapid liver regeneration.

Formation of excess fibrous connective tissue during its reparative process leads to liver fibrosis. Cirrhotic liver is another common phenomenon which is characterized by replacement of liver tissue by abnormal regenerative nodules surrounded by collagen and scarring. It may occur independently or as a result of fibrosis. It is an irreversible process which leads to progressive loss of liver functions. More than 80% of HCC is formed on a cirrhotic background (Simonetti *et al.,* 1991). Only a small portion of HCC develops from normal looking liver and others display fibrosis or steatosis or liver cell dysplasia.

Rapid cell proliferation without the proper genetic checks and control mechanisms may also lead to a series of lesions such as dysplastic foci or dysplastic nodules. Dysplastic foci consist of abnormal monoclonal hepatocytes that differ from adjacent cells. Microscopic examination of the liver is able to differentiate these cells via cytoplasmic staining, nuclear size or degree of nuclear atypia (Hytiroglou, 2004). Dysplastic foci can be characterized by either small cell change (SCC) or large cell change (LCC) (Watanabe *et al.,* 1983). SCC bears similar cytological similarities to HCC with small cell size and a high nucleus to cytoplasm ratio has been suggested to be precancerous.

Dysplastic nodules, is another characteristic lesions that can be observed in 20-30% of liver biopsies in HCC-virus associated cirrhosis. These nodules, categorized as low or high grade dysplasia, have been established by clinicopatholical studies as precancerous lesions (Takayama *et al.,* 1990). Both grades of dysplasia can be characterized by abnormal cytological lesions, such as clear cell changes and nuclear crowding. High grade dysplastic nodule manifests nuclear hyperchromasia, mild nuclear contour irregularities with 1.3 – 2 times greater in cell density as compared to surrounding hepatic tissues (Theise *et al.,* 2002). Structural changes also include thickening of the trabeculae with up to 3 cells, areas of increased fibrosis and "nodule-in-nodule lesions" which indicates abnormal liver architecture (Hytiroglou, 2004). The subnodules may demonstrate definite features of HCC such as fatty change or iron resistance or higher vascular supply.

1.1.3.2 Neoplasia

Pronounced hepatic lesions, dysplastic nodules and continued genomic alterations may result in changes in the molecular pathways that drive the hepatocytes to evolve into a malignant phenotype, leading to the eventual hepatocarcinoma. Microscopic examination of tumours describes critical increase in cell density or nuclear crowding of at least 2 times compared to the surrounding hepatocytes (Kojiro, 1998). The nucleus may demonstrate further contour irregularities, prominent nuclei or mitotic figures. Tumour cells often arrange in irregular trabeculae forming thicker plates of cells, with clear cell change, fatty accumulation or Mallory bodies and are accompanied by increased vascularisation (Hytiroglou, 2004).

This neoplastic progression of HCC continues to occur in a multi-step histological process that can be broadly classified into well differentiated (where the tumour cells are often

with indistinct margins from the surrounding hepatocytes), followed by moderately differentiated and poorly differentiated. The latter being the most severe stage with high vascular networks and metastatic potential. Although the exact differences in the molecular events is not clear, these stages of HCC can be differentiated by pathological examinations.

1.1.4 Staging of HCC

It is well established that staging systems provide a common language that provides guided patient assessment as well as facilitates the exchange of information in cancer research and clinical trials. A perfect staging system will be advantageous in the prognosis, therapeutic interventions and the overall treatment of the disease.

The vast heterogeneity in risk factors, development and progression HCC has presented a unique challenge in creating a prefect staging system. The most commonly used staging systems for HCC is the Okuda system (see Table 1.1) (Okuda *et al.,* 1985; Gannon and Curley, 2008) and the pathological tumour node metastasis (TMN) staging that was adopted by the International Union Against Cancer (UICC) in 1988 (see Table 1.2) (Sobin and Wittekind, 1997).

Table 1.1 : The Okuda staging system for HCC (adapted from Gannon and Curley, 2008)

Parameters	Value	Points
Tumour size*	>50%	1
	<50%	0
Ascites	Present	1
	Absent	0
Serum Albumin (g/dL)	>3	0
	<3	1
Serum Bilirubin (g/dL)	<3	0
	>3	1
	Stage	
1		0 points
2		1 – 2 points
3		3 – 4 points

* Tumour size is measured in comparison to the largest cross-sectional area of the liver.

Table 1.2 : The UICC TNM staging system (adapted from Gannon and Curley, 2008)

Classification	Morphology
Primary tumours	
TX:	Primary tumour cannot be assessed.
T0:	No evidence of primary tumour.
T1:	Solitary tumour without vascular invasion.
T2:	Solitary tumour 2 cm or less in greatest dimension with vascular invasion, OR multiple tumors limited to one lobe, none greater than 2 cm and without vascular invasion, OR a solitary tumor more than 2 cm in greatest dimension without vascular invasion.
T3:	Solitary tumor more than 2 cm in greatest dimension with vascular invasion, OR multiple tumors limited to one lobe, none more than 2 cm with vascular invasion, OR multiple tumors limited to one lobe, any more than 2 cm in greatest dimension, with or without vascular invasion.
T4:	Multiple tumors in more than one lobe or tumor(s) involve(s) a major branch of the portal or hepatic vein.
Regional Lymph Node	
NX	Regional lymph nodes cannot be assessed.
N0	No regional lymph node metastasis present.
N1	Regional lymph node metastasis present.
Distant Metastasis	
MX	Presence of distant metastasis cannot be assessed
M0	No distant metastasis present
M1	Distant metastasis present.

Stage Grouping			
Stage I	T1	N0	M0
Stage II	T2	N0	M0
Stage III A	T1	N1	M0
Stage III B	T2	N1	M0
Stage III C	T3	N0	M0
Stage III D	T3	N1	M0
Stage IV A	T4	any N	M0
Stage IV B	any T	any N	M1

Both staging systems have their own weaknesses. The Okuda system, for instance, lack sensitivity, while TNM staging on the other hand, relies solely on tumour morphology and does not account for other aspects such as cirrhosis of the liver. Both also lack prognostic value for patients that are diagnosed at an earlier asymptomatic stage (Yan and Yan, 2003). Thus in recent years, numerous other staging systems have been introduced by various countries such as CLIP (Cancer of the Liver Italian Programme) (CLIP investigators, 1998), BCLC (Barcelona Clinic Liver Cancer staging) (Llovet *et al.,* 1999) and China Classification System (Yan and Yan, 2003).

To-date, there has been no consensus as to which staging system should be applied to HCC. This is mainly due to insufficient knowledge in the development and factors involved in predicting its prognosis. These limitations and the lack of proper staging methodology, continues to hamper efforts to not only study HCC but the inability to properly assign the best therapeutic approach to the patients.

1.1.5 Diagnosis and treatment

Due to the asymptomatic features during the course of neoplastic development and the lack of reliable biomarkers, it is not surprising that HCC patients are often diagnosed at very late stages. The disease thus has very poor prognosis with more than 50% of the patients dying within 1 year and less than 6% have a 5 year survival rate (Hoofnagle, 2004).

1.1.5.1 Screening tests

Successful screening and diagnosis of HCC is complicated by the lack of reliable biomarkers. Alpha-fetoprotein (AFP) is the best possible marker today for HCC with sensitivity and specificity that varies in the range of 40 to 60% and 76 to 96% respectively (Spangenberg *et al.,* 2006). In recent years, a fucosylated AFP (AFP-L3) has been found to be a specific indicator of poorly-differentiated and unfavourable diagnosis (Tateishi *et al.,* 2006). Most importantly, AFP levels seem to have a better predictive value in detecting HCC patients without viral hepatitis (94% in non-viral HCC versus 70% in viral-induced HCC) (Spangenberg *et al.,* 2006).

Another commonly used biomarker is an abnormal prothrombin, des-gamma-carboxy prothrombin (DCP) (Liebman, 1989; Aoyagi *et al.,* 1996). It is found to be elevated in 62% of HCC patients and 84% of patients with HCC recurrence (Ikoma *et al.,* 2002). DCP is associated with the risk of portal vein invasion in one of the main end-stage observations (Hamamura *et al.,* 2000). Hence it is more commonly used as a diagnostic marker rather than for surveillance. Though a combination of AFP and DCP would markedly improve its sensitivity, its usefulness for early detection of HCC is controversial. Other promising biomarkers reported include Golgi-protein 73 (Kladney *et al.,* 2000; Marrero *et al.,* 2005), glypican-3 (Nakatsura *et al.,* 2003; Capurro *et al.,* 2003), hepatocyte-growth factor (Yamagamim *et al.,* 2002), insulin growth factor 1 (Mazziotti *et al.,* 2002), vascular endothelial growth factor (Poon *et al.,* 2004; Schoenleber *et al.,* 2009) and transforming growth factor β-1 (Song *et al.,* 2002; Yao *et al.,* 2007). However due to the lack of studies and confounding factors, more work will be needed to confirm their effectiveness.

In addition to tumour markers, other screening strategies used in HCC screening depend on imaging studies. These include ultrasonography, which is reportedly very operator-dependant. It is also biased for detection of large tumour masses, which typically indicates late stages of cancer. Combined use of AFP and ultrasonograpy has been proposed to potentially increase detection rates although this may also increase cost and false-positive rates (Zhang *et al.,* 2004). Furthermore, confirmatory diagnosis often requires computed tomography (CT) or magnetic resonance imaging (MRI) which may also be costly.

1.1.5.2 Treatment

To date, the only curative treatments for HCC are surgical resection or liver transplantation (Poon *et al.,* 2000). However, even for the patients who undergo resection, the recurrence rate can be as high as 50% at 2 years, especially in cirrhotic patients (Belghiti *et al.,* 1991; Figueras *et al.,* 1999). The main cause of recurrence is the development of new tumours in the remnant liver which are often in a preneoplastic state (Imamura *et al.,* 2003). Hence for such cases, a liver transplantation is often a better option. The scarcity of donor liver continues to be a universal problem and many succumb to death while waiting due to tumour advancement.

In some cases when HCC lesions are unresectable, there is a need for non-surgical treatment. Radiofrequency ablation (RFA), for example, utilises a needle with an electrode is placed percutaneously into targeted tumour using ultrasound guidance and tumour tissues are heated to cause necrosis (Gough-Palmer and Gedroyc, 2008). Other treatments include conventional or molecular targeted chemotherapy and radiotherapy.

1.1.5.3 Prevention

Since chronic HBV and HCV are amongst the predominant cause of HCC, infection control is a priority in primary prevention of HCC. The first nationwide HBV vaccination at birth programme was launched in Taiwan in 1984 (Beasley, 2009). Twenty years after its launch, the number of chronic HBV infections dropped from 10 – 17% before the vaccination programme to 0.7 – 1.7% after its launch. This corresponded to a lowered childhood HCC incidence rate (Chang, 1998; Chang, 2009). The study also reported cases of vaccine failure, due to vaccine escape mutants, genetic hyporesponsiveness and poor compliance.

Nevertheless, universal vaccination has since been implemented by the World Health Organisation (WHO), especially for high risk population groups such as healthcare workers, neonates of HBV carrier mothers and patients with immuncompromised states (Zanetti *et al.,* 2008). HBV vaccination success in preventing HCC will however be better evaluated in several years to come. On the other hand, development of an effective vaccination against HCV has been severely hampered by the high genetic variability of the virus. HCV spread can however be better managed through awareness of blood-borne infection and better screening in blood banks (Lavanchy, 2009).

Secondary prevention includes interferon therapy and anti-HBV drugs (oral nucleotides analogs) to prevent deterioration of liver damage by suppressing hepatitis. Although interferon effects are still debatable, anti-HBV nucleotides analogs suppresses viral duplication and viral DNA integration into the host genome (Patterson and Angus, 2009). Secondary prevention is also necessary for patients following successful resection to reduce the probability of recurrence.

1.1.6 Common molecular themes in HCC

Biological research on HCC to-date had focused on deciphering the various aetiologies of HCC and the common pathological pathways that preceded tumourigenesis. Inflammatory processes and oxidative stress are in particular a common occurring event in viral-induced hepatocarcinogenesis. This often is a consequence of the continuous cycle of liver necrosis and regeneration (Farazi and DePinho, 2006).

This continued uncontrolled growth also led to numerous genetic and epigenetic alterations (Thorgeirsson and Grisham, 2002) resulting in numerous chromosomal aberrations such as loss of heterozygosity and aberrant DNA methylation patterns (Saito *et al.,* 2001; Lin *et al.,* 2001). p53 mutations and inactivation is another event observed in the molecular pathogenesis of viral- and AFB1-induced HCC (Feitelson *et al.,* 2002; Zhang *et al.,* 2006; Farazi and DePinho, 2006). Other molecular targets of specific pathways such as cyclin dependent kinase, oncogenes (cyclin D1, c-myc and c-met) (Fietelson *et. al.,* 2002) and several signalling molecules (MAPK) have also been described in HCC. Ability to identify of these common molecular targets holds great importance in understanding the molecular processes involved in HCC and the promise of creating better drugs or preventive measures.

1.1.6.1 Challenges in understanding HCC

Despite the continued success of identifying numerous affected genes in tumourigenesis, no “true specific” genetic changes have been identified in HCC (Tannapfe and Wittekind, 2002). The heterogeneity of genetic aberrations as documented by numerous independent HCC studies suggested that distinct molecular players but related genetic pathways are likely to be affected during hepatocarcinogenesis (Thorgeirsson and Grisham, 2002). Thus,

proposing that neoplastic morphological / pathological changes that are observable in HCC are contributed by a variety of possible combinations of molecular alterations.

The on-going aim to elucidate the development and progression of HCC is currently dedicated to identify and characterize new molecular players along with their interactions using large scale profiling and comparative technologies. Hypothesis free approaches using “omics” based studies are non-biased and have the ability to compare and identify novel molecular players. Most importantly, “omics” approaches will provide the opportunity to simultaneously highlight groups of aberrant molecules in a sample set. These analyses may shed some light on the specific regulatory pathways that are involved in the pathogenesis of HCC. In addition, the dysregulated proteins that are identified may assist in identifiying potential biomarkers and to elucidate therapeutic targets.

1.2 "Omics" based biology in Hepatocarcinogenesis

The traditional scientific study to solving problems often relies on a "one-gene at a time" approach. "Omics" based biology, on the other hand refers to the study of entities in aggregate (Weinstein, 1998; Evans, 2000). With the success of genomics in Human Genome Project in the late 1990s, coupled with major advancement in high-throughput techniques and computational tools, new "omics" disciplines are being developed. These include transcriptomics, proteomics, metabolomics, pharmacogenomics and numerous other large scale techniques (Weinstein, 2002).

The promises of "omics" have since led to an explosive number of applications in evolutionary analysis, metabolic diseases, drug studies as well as cancer research. The emphasis have thus shifted from a linear method of investigating known genes, proteins or mechanism towards a hypothesis-free, discovery driven approach with the hope of identifying novel players and their interactions. Although, discovery-driven research is different from the traditional hypothesis-driven research, it has slowly been accepted to be complementary and synergistic (Hieter and Boguski, 1997).

Current efforts in HCC are also geared towards revealing global expression profiles of proteins with the aim to understand the mechanisms involved in hepatocarcinogenesis. The following sections describe the "omics" based studies that have been employed for identification of molecular alterations and the discovery of various prognostic or diagnostic biomarkers.

1.2.1 Functional genomics in HCC

Genomics is one of the major "omics" research directions to date. Genomics, coined by Thomas Roderick (1986), described the "scientific discipline of mapping, sequencing and analyzing genomes". The current emphasis is on functional genomics which refers to "genome-wide or system-wide approaches to assess gene functions using information provided by structural genomics" (Hieter and Boguski, 1997). In addition to cytogenetics and interphase fluorescence *in situ* hybridization (FISH), systematic genomic analysis using array-based comparative genomic hybridization (aCGH) and genome-wide allelotyping have been routinely used to search for genetic aberrations in various diseases including HCC.

1.2.1.1 Chromosomal instabilities

Genomic alterations such as aberrant patterns of chromosomal instability, CpG methylation and DNA arrangements due to HBV integration are often observed in HCC. In an attempt to systematically identify these chromosomal rearrangements, aCGH was used on a total of 158 HBV-associated HCC cases. In this study, Poon *et al.,* (2006) revealed a tumour progression model that associated gains in the chromosomal arm 1q21-23 and 8q22-24 as an early event. Additional chromosomal gains in the 3q22-24 arm were described as late genomic events that were associated with poor prognosis and tumour recurrence. These results were also consistent with previous findings which showed 21% and 17% gains of 1q and 8q in preneoplastic lesions of HCC (Zondervan *et al.,* 2000; Marchio *et al.,* 2001).

Several other frequently reported chromosomal loci aberrations are summarized in Table 1.3. These regions have also been reported to contain essential genes that are potentially important players in carcinogenesis. Among the chromosomal regions listed in Table 1.3, loss

of heterozygosity (LOH) in 17p, 13q, 9p and 6q can be related to reported loss of function in p53, retinoblastoma (Rb), p16 and IGF2R respectively. Over-expression of proto-oncogene, c-myc often observed in HCC may also be attributed to the chromosomal gain in 8q arm.

Table 1.3 : Common chromosomal alterations in HCC

Chromosomal loss	1p, 4q, 5q, 8p, 9q,13q, 16p, 16q, 17p	Nagai *et al.,* 1997 Kusano *et al., 1999* Nishida *et al.,* 2003 Herath *et al.,* 2006	Poon *et al.,* 2006 Hertz *et al.,* 2008 Saelee *et al.,* 2008
Chromosomal gain	1q, 3q, 6p, 8q, 17q, 20q		

1.2.1.2 Epigenetic alterations

In addition to chromosomal alterations, malignant transformations due to epigenetic alterations such as DNA methylation and histone modifications have also been reported in HCC (Herath *et al.,* 2006). Chromatin immunopercipitation assays (ChIP-on-chip) coupled with polymerase chain reactions (PCR) or microarray for quick detections is one of the most widely used techniques.

One such study by Kondo *et al.,* (2007) evaluated multiple DNA methylation sites quantitatively in 23 paired HCC tissue sample. They identified increase hypermethylation in $p16^{INK4a}$ promoter sites with reduced levels of $p16^{INK4a}$ expression as tumour progresses. Other frequent promoter methylation in HCC had also been described in $p15^{INK4b}$ (Wong *et al.,* 2000), E-cadherin (Kanai *et al.,* 1997) and 14-3-3 sigma (Kondo *et al.,* 2000).

1.2.2 Transcriptomics: gene expression profiling in HCC

HCC progression can also be determined by changes in expression levels of cancer-related genes. With the use of genome wide mRNA expression studies, we are able to obtain a comprehensive view of the alteration of gene expression patterns in a disease state. Genomic analysis can be conducted with the use of oligonucleotide chips, serial analysis of gene expression (SAGE) and complementary DNA (cDNA) microarrays.

The first cDNA microarray analysis for HCC was reported by Lau *et al.,* (2000) using 10 pairs of HCC and non-tumourous tissues. Since then, more than 300 microarray studies coupled with statistical analysis and bioinformatics had since been applied on HCC studies to identify dysregulated genes based on clinicopathological features such as cancer staging, progression (Anders *et al.,* 2003; Shao *et al.,* 2005), viral infection (Okabe *et al.,* 2001; Iizuka *et al.,* 2002), prediction of metastasis (Chen *et al.,* 2002) and tumour recurrence (Iizuka *et al.,* 2003).

Deregulation of the Wnt/β-catenin pathway, cyclins, cyclin-dependent kinases and metabolic proteins, as described earlier in hypothesis driven studies, were also observed in microarray analysis (Xu *et al.,* 2001; Thorgeirsson *et al.,* 2006). This thus has increased the level of confidence in large scale profiling techniques. Aside from merely identifying molecular aberrations, such genome wide studies also enables one to draw insights based on all regulated genes as a whole. Iizuka *et al.,* (2005) for example, described that many of the regulated genes identified in their HBV-associated HCC analysis were all downstream of c-myc. Although, over-expression of c-myc identified was not statistically significant in the study due to large heterogeneity in the samples, the data obtained strongly suggested the oncogene as a central molecule in HCC progression particularly in genotype-C HBV.

DNA microarray has also been used to identify new biomarkers to improve HCC detection. Using 218 HCC tissue specimens from patients with either low or high serum AFP, Jia *et al.,* (2007) proposed 5 new candidate genes. These include known serum proteins, GPC3, midkine (MDK) and SERPINI1 as well as 2 additional genes, PEG10 and QP-C with diagnostic potential on patients with normal AFP levels or small HCC. Some of these genes have also been observed via other molecular techniques to be up-regulated in tumour tissues (Midorikawa *et al.,* 2003; Hippo *et al.,* 2004).

Collectively, these microarray analyses identified diverse up- and down-regulated genes which suggest that a variety of cellular processes are affected in HCC progression. These differences could be the result of multiple aetiologies involved in HCC and its mutifactorial tumour development (Iizuka *et al.,* 2008). Choi *et al.,* (2004) also cautioned that although results from each microarray analysis maybe promising, a single-set analysis may lead to false findings. The use of data integrations in meta-analysis was suggested to help identify molecular alterations and pathways in uncovering the processes involved in HCC.

1.2.3 MicroRNAs involvement in HCC

Identification of small non-coding RNAs such as small nucleolar RNA (snRNA), small interfering RNAs (siRNA) and microRNAs (miRNA), capable of regulating gene expression has since led to the study of RNomics (Filipowicz, 2000; Huttenhofer *et al.,* 2001). miRNA, endogenous non-coding RNAs of 20 ± 2 nucleotides, had taken centre-stage due to its ability to alter gene expression through mRNA degradation and translational inhibition (Zhang, 2008). Consequently, dysregulation of miRNA have been identified in several diseases including

cancer (Visone and Croce, 2009). Its expression signatures in tumours can be studied efficiently with commercially available microarray with miRNA probes.

One of the earliest work comparing HCC tumours and non-tumour tissues using miRNA by Murakami *et al.,* (2006) identified 8 dysregulated miRNA. Most significantly, using support vector machines (SVM) these miRNAs had a prediction accuracy of 97.8 % of HCC versus non-tumours classification. Similar analysis had since been used to identify important signatures of miRNA clusters in determining metastatic potential (Budhu *et al.,* 2008), HBV and HCV specific alterations (Ura *et al.,* 2009) and prognosis of HCC (Li *et al.,* 2008). Other studies using miRNA as a new strategy to understand HCC were summarized by Gramantieri *et al.,* (2008).

1.2.4 Proteomics

Proteomics is another key area of research in the post-genomic era which has been utilized extensively in numerous cancer studies (Godovac-Zimmermann and Brown, 2001). High throughput analysis of the total proteome has been suggested to provide a better representation of biological processes as proteins are dynamic and constantly changing in response to both external and internal stimuli (Anderson and Anderson, 1998). Proteome analysis hence provides data which is not readily apparent from DNA aberrations or expression levels of mRNA transcripts. These are of critical importance for the description of the state of a biological system such as quantity of protein expression, the subcellular location, the state of modification, association with ligands as well as the rate of change with time.

The proteome of any cell consists of normally thousands to tens thousands of complex mixture of proteins present in different organelles (Haynes and Yates, 2000). Proteins also have diverse physicochemical properties such as molecular weight, isoelectric point and hydrophobicity which make it impossible to analyse the global expression levels with just a single technique. In addition to total protein profiling, studies have also developed sub-cellular proteome analysis to focus on protein regulation levels in organelles and post-translational modifications. Such prefractionation strategies however involve additional pre-processing steps which may cause variations in sample preparations and costs. These extra steps will also require higher amounts of proteins which may be limiting for clinical samples.

Most significantly, proteome analysis can be effectively applied to cell lines, tissues and biological fluids such as serum, cerebrospinal fluid and urine. The availability of a wide range of samples enables a more encompassing study of a particular organism or disease. The use of biological fluids also makes proteomics a more apt technique in biomarker discovery. As technology improved, different proteomic platforms have emerged to improve global profiling as well as comparative studies. The widely used proteomic platforms are summarized in Figure 1.2. Most of these platforms are coupled to mass spectrometry (MS) such as matrix assisted laser desorption / ionization (MALDI) or electrospray ionization (ESI) and bioinformatics software to enable identification of proteins at a high level of automation and sensitivity.

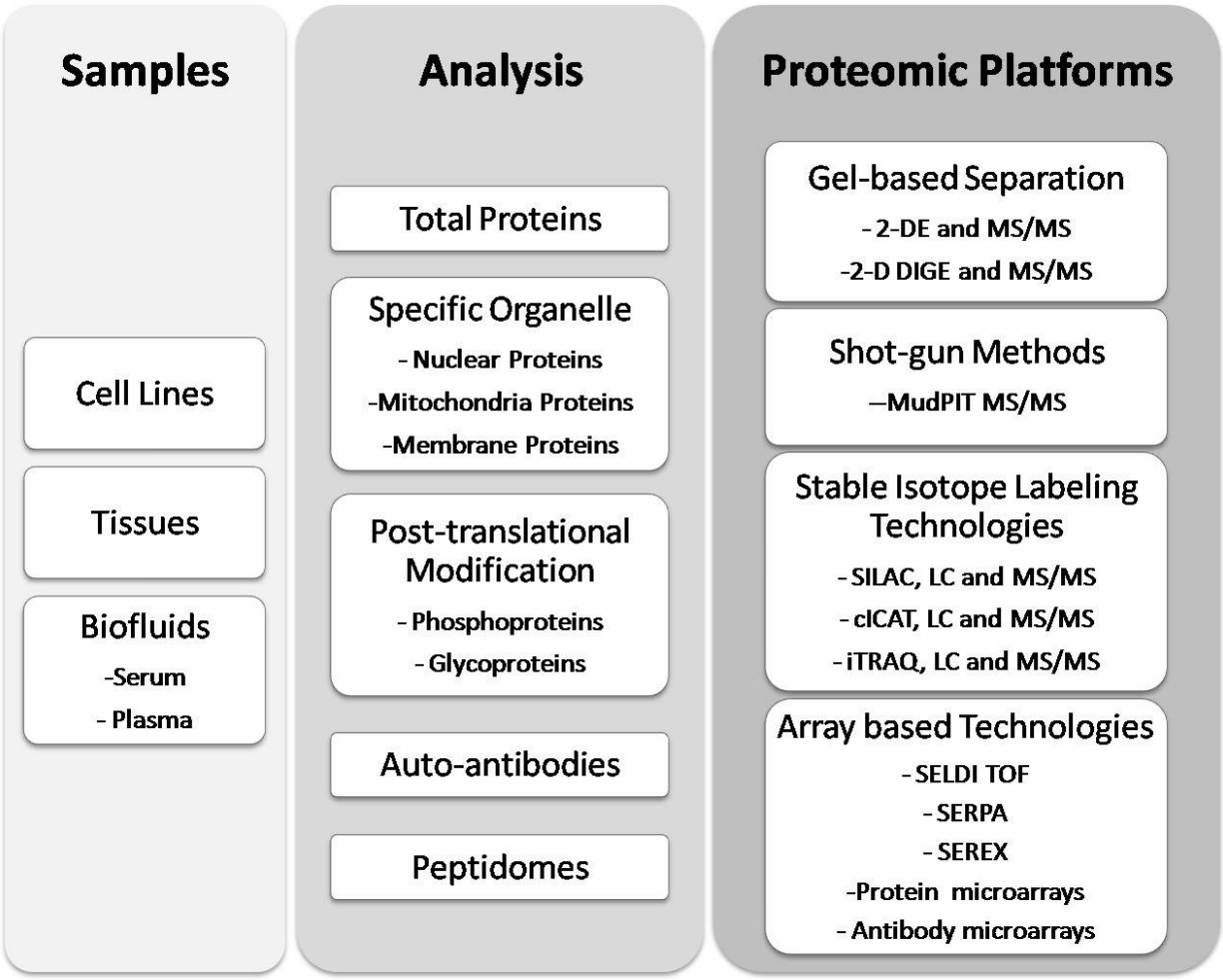


Figure 1.2 : Summary of the various sample, analysis and platforms available in a proteomic study. 2-DE; 2-dimensional electrophoresis, 2-D DIGE; 2-dimensional Difference Gel electrophoresis, LC; liquid chromatography, MudPIT; Multidimensional Protein Identification Technology, SILAC; Stable-isotope labelling by amino acids in cell culture, cICAT; cleavable Isotope Coded Affinity Tag; iTRAQ; isobaric tags for relative and absolute quantitation; SELDI; surface enhance laser desorption and ionization, SERPA; serological proteome analysis, SEREX; serologic analysis of recombinant cDNA expression, MS; mass spectrometry.

1.2.4.1 Proteome analysis of HCC cell lines

Early proteomic studies on hepatocarcinogenesis were dedicated on large scale profiling using 2-dimensional gel electrophoresis (2-DE) on various HCC cell lines such as Chang, WRL-68 (Wirth *et al.,* 1995) and HCC-M (Seow *et al.,* 2000). 2-DE can also be used in comparative analysis to investigate differences between hepatoma (BEL-7404) and normal liver cell line (L2) (Yu *et al.,* 2000). These studies also initiated uploading of 2-D gel images and data-mining software as a useful resource for other HCC groups (Hochstrasser *et al.,* 1992; Liang *et al.,* 2002; Cho *et al.,* 2002).

HCC cell lines were also used as *in vitro* models to understand the mechanisms of viral induced tumourigenesis. Studies investigating HCV interacting proteins (Choi *et al.,* 2004; Kang *et al.,* 2005) and HCV induced liver cell lines (Mannova *et al.,* 2006) identified dysregulation in a myriad of factors such as HSP 27, HSP 90, cytokeratins and vesicle formation in lipid rafts suggesting direct roles of HCV in inducing tumourigenesis. Similar study, using Chang liver cells transfected with HBV-X gene selected 16 regulated protein spots but failed to identify them (Tan and Chen, 2005). Without protein identification, no probable mechanistic role of HBV-X can be established.

HCC cell lines with different metastatic capacities were also evaluated using 2-DE by comparing cell clones, MHC97-H and MHC97-L (Ding *et al.,* 2004; Cui *et al.,* 2004). It was proposed that cytokeratin 19 (Ding *et al.,* 2004) and S100A4 (Cui *et al.,* 2007) might be capable in strengthening motility and invasive mechanisms. The same cell lines were also used in a recent study using stable-isotope labelling by amino acids in cell culture (SILAC) to identify differentially regulated proteins (Chen *et al.,* 2008). A total of 152 proteins were identified, several were common to proteins identified in earlier studies. Solute carrier family 12 member

2 (SLC 12A2) significantly showed higher levels in MHC97-H and was able to distinguish patients' sera that had high metastasis. Another protein disulfide-isomerase A4 (PDIA4) was also able to identify patients' sera with metastasized lesions. This study described confidently that the results from *in vitro* models can potentially be translated to clinical settings.

1.2.4.2 Proteomic approaches using animal models

Animal models have also been used extensively to study the physiological and molecular mechanisms of HCC. Various genetic alterations (HBV or HCV induction, HBV-X gene, p53 knockouts, c-myc transfections, β-catenin) and chemical induction using thioacetamide (TAA), N-nitrosomorpholine (NNM) and ciprofibrate are just some examples that have been used to induce cirrhosis and HCC in rodents (reviewed by Newell *et al.,* 2008). These models have been instrumental in understanding the various pathway involved in initiation and progression of HCC.

Some of these studies have also utilized proteomics as a global wide approach in identifying the potential molecular players upon drug treatment. Using 2-DE gels, Low *et al.,* (2004) proposed the involvement of 4 major metabolic clusters (energy, iron and heme, carbonyl compound and gluthathione related proteins) as primary players in the development of TAA induced cirrhosis in rat livers. Similar approach was also conducted to study the effects of another drug, NNM, and to identify early players in the carcinogenesis process (Fella *et al.,* 2005). This study also described changes in metabolism and anti-oxidative activities. In another study, 2-DE analysis was conducted on an anti-cancer drug, cell differentiated agent II (CDA-II), to analyse its effects in a metastatic HCC nude mice model (LCI-D20) (Shen *et al.,* 2006; Fan *et al.,* 2009). The study successfully showed a 41.8% inhibition of tumour growth and

identified 27 differentially expressed proteins (HSP 27, HSP 60, alpha-enolase, cytokeratin 8, etc). The study also showed that CDA-II drug reduced the levels of cancer related genes (c-myc, N-ras, MMP-9).

Another well established animal model for HBV-associated HCC, is the woodchuck (*Marmota monax*) which has been shown to develop hepatocellular adenomas upon infection of another hepadnaviridae, woodchuck hepatitis virus (WHV) (Tennant *et al.,* 2004). Similar to HBV, WHV can also cause chronic hepatitis and HCC. The woodchuck infected by WHV had hence been a useful model to understand HBV progression and evaluation of antiviral drugs.

Among the numerous studies using the woodchuck model, a glycoprotein serum profile of WHV infected woodchucks was conducted using 2-DE (Block *et al.,* 2005). This study showed higher levels of α-1,6-linked fucosylation in the serum of HCC woodchucks compared to those non-HCC. HCC associated proteins such as AFP and α-1-antitrypsin were identified to be hyperfucosylated. Additionally, Golgi Protein 73 (GP73) was identified to be elevated and hyperfucosylated in woodchucks with HCC. Elevated levels of GP73 were verified in human sera infected by HBV with or without tumourigenesis but it was specifically hyperfucosylated in viral induced HCC (Mehta and Block, 2008).

Though further validations of GP73 on a larger human sample size are necessary, this study provides evidence of the significance of animal models. Identification of differentially expressed proteins in these animal studies enables understanding of the effects of drug treatments or genetic alterations as well as novel tumour markers. As it is usually difficult to obtain tissues of early stages of tumour in human samples, animal models can help bridge this gap and facilitate the understanding of HCC progression.

1.2.4.2 Proteome analysis of HCC tissues

The identification of dysregulated proteins were also extended to comparing proteome profiles of human HCC tumour versus non-tumour tissues as well as cirrhotic livers (Kim *et al.,* 2002; Lim *et al.,* 2002; Park *et al.,* 2002). As summarised in Table 1.4, the most extensively used method in HCC analyses had been 2-DE. It was a popular choice because of its ability to provide a global view of protein expression and its high resolving power to identify protein isoforms and post-translational modifications. The use of fluorescence CyDye labelled samples in 2-dimensional Difference Gel electrophoresis (2-D DIGE) (Liang *et al.,* 2005; Lee *et al.,* 2005) had further improved the conventional 2-DE by minimizing technical limitations such as inter-gel non-reproducibility. This had also greatly enhanced the statistical confidence in detecting and quantifying true biological changes.

With the use of gel based comparative analysis, different protein levels in HBV induced HCC (Li *et al.,* 2005; Liang *et al.,* 2005; Song *et al.,* 2006; Sun *et al.,* 2007; Zhang *et al.,* 2007) and HCV associated HCC (Takashima *et al.,* 2003; Yokoyama *et al.,* 2004; Blanc *et al.,* 2005) were evaluated. Comparisons between these 2 viral induced HCC were also described by Kim *et al.,* (2003). There were also other works which focused on identifying differences between tumour and non-tumour tissues by disregarding the different aetiological factors (Kim *et al.,* 2002; Zeindl-Eberhart *et al.,* 2004; Lee *et al.,* 2005). In general, these studies revealed frequent alterations in enzymes involved in glycolysis, fatty acid metabolism and S-adenosylmethionine (AdoMet) cycle. Down-regulation in antioxidation proteins such as catalase and glutathione synthetase along with over-expression of heat shock proteins were also common phenomenon.

High levels of HSP 27, first identified in metastatic tumour tissues by 2-DE, were confirmed by western blots and immunohistochemistry (IHC) (Song *et al.,* 2006). This over-

expression was however not observed in RT-PCR thus illustrating the poor correlation efficiency between mRNA and proteins. Phosphorylation levels of HSP 27 were also shown to decrease as tumour progresses (Yasuda *et al.,* 2005), suggesting that phosphorylated HSP 27 has protective mechanisms against tumourigenesis. Luk *et al.,* (2006) further implicated over-expression of 2 HSP members (HSP 70 and GRP 78) along with HSP27 in determining poor prognosis of HBV-associated HCC. Up-regulation of other proteins such as proliferating cell nuclear antigen (PCNA) and isoforms of stathmin were also proposed as tumour markers in HBV-associated HCC (Li *et al.,* 2005).

In addition to comparing tumour versus non-tumour tissues, Yokoo *et al.,* (2007), elegantly conducted the first proteomic study analysing HCC intrahepatic recurrence. The group conducted a comparative proteomics study using 2-D DIGE on tissue samples from patients with or without HCC recurrence over a 2 year period after corrective surgery. Twenty-three differentially expressed proteins involved in signal transduction, glucose metabolism, cytoskeletal and chaperone proteins were selected. These were proposed to identify patients with a high risk of recurrence that will require further therapeutic strategies.

A major drawback in 2-DE based studies is the inability to detect low abundant proteins. In view of this, Codarin *et al.,* (2009) analysed only nuclear enriched proteins from the tumour and its corresponding non-tumour samples. This was the first study to analyse subfractionated HCC liver samples. The group identified 52 proteins including HSPs and metabolic proteins that have been well described in earlier studies and 7 proteins not previously studied in HCC. Though the proteins identified also included non-nuclear proteins possibly due to contaminations during enrichments, the identification of these proteins will shed light on their functional roles in tumourigenesis.

Although the majority of the work conducted thus far were dominated by 2-DE, the limitations of gel based method had became gradually apparent. Its inability to identify low copy number proteins, hydrophobic proteins and proteins with extreme size and isoelectric point has often been raised. Therefore, in recent years alternative proteomic platforms have been progressively introduced in numerous cancer researches. To date, there have only been 5 HCC proteomic studies using protein microarray, SELDI-TOF MS and non-isotope labels coupled with liquid chromatography (Table 1.4).

Protein microarrays made up of 83 different antibodies were used to analyse 30 HCC and the non-tumour tissues. This technique enabled high-throughput analysis of a specific list of proteins of interest. Thus Tannapfel *et al.,* (2003) were able to successfully identified 32 significantly regulated proteins. These proteins were confirmed with western blots and 2 of which (cyclin D1 and suppressor of cytokine signalling 1) were further investigated using tissue microarray on 210 HCC samples. By using parallel methods, these studies were able to convincingly prove the dysregulation of the proteins identified.

Using another array based technique, SELDI, Melle *et al.,* (2004) were able to successfully identify 2 distinct peptide sequences but were however, unable to identify the proteins. SELDI coupled with 2-DE was later used by the same group (Melle *et al.,* 2007) and they identified 53 proteins, 3 of these (ferritin light subunit, adenylate kinase 3 and bliverdin reductase B) were further confirmed by IHC. Since SELDI technique required small amount of samples for analysis, it was proposed to be an ideal method for HCC studies.

In addition, stable isotope labelling techniques using, isotope-coded affinity tags (ICAT) and isobaric tags for relative and absolute quantitation (iTRAQ) have also been used in recent HCC analysis. These methods allow the multiplexing of different samples that have been pre-

labelled with the respective isotopes before undergoing liquid chromatography and mass spectrometry (MS). The difference in expression levels can be determined by the relative peak intensities from the MS spectrum. Li *et al.,* (2004) used cICAT to compare the expression profile of one pair of HCC tumour and non-tumour tissue. Although the work identified 149 regulated proteins, the use of only 1 pair of tissues rendered it statistically insignificant and would require further anlaysis.

Similarly, in a recent iTRAQ study, only one pair of HCC tumour and non-tumour tissues were used and identified 141 regulated proteins (Chaerkady *et al.,* 2008). This study however used 174 tissue microarrays (TMAs) to validate a subset of proteins. These include enzymes in the urea cycle, which were described for the first time as being down-regulated in HCC tumours. The significance of urea cycle aberration is however not clear from their studies. Despite the use of only one pair of HCC tissue and the lack of in depth analysis, the use of liquid chromatography separation coupled to cICAT or iTRAQ labels greatly enhanced the number of proteins being identified. This may enable us to better understand the molecular prognosis of HCC.

Table 1.4 : Summary of the work thus far that employed proteomic techniques on HCC tissues

Year Published	Authors' Name	Source of tissues	No. of HCC tissues	Viral Status	Control used	Background of tissues*	Proteomic technique used	No. of Proteins identified	Comments
2002	Kim J *et al.,*	Korea	11	4 HBV postive 11 HCV positive	adjacent non-tumour	-	2-DE MALDI TOF MS	16	7 tissues were cirrhotic 2 tissues were from females and 8 tissues were from males
2002	Lim SO *et al.,*	Korea	6	All HBV positive	Not clear	All Grade II	2-DE MALDI TOF MS	21	-
2002	Park KS et al.,	Korea	10	7 HBV positive	adjacent non-tumour	4 well- / 6 moderately-differentiated	2-DE MALDI TOF MS	26	4 tissues were cirrhotic 3 tissues were from females and 7 tissues were from males
2002	Park KS et al.,	Korea	19	-	adjacent non-tumour	-	2-DE MALDI TOF MS	1	Only tissue ferritin light chain protein levels were analysed
2003	Kim W *et al.,*	Korea	21	7 HBV postive 7 HCV positive 7 non-viral	adjacent non-tumour	3 --> grade I 3 --> grade I>II 4 --> grade I<II 11 --> grade II	2-DE MALDI TOF MS	60	Study was comparing HBV versus HCV viral induced HCC
2003	Tannapfel A *et al.,*	Germany	30	-	15 normal livers	-	Protein microarrays	32	210 paired HCC tissues were subsequently used for validations using tissue microarray
2003	Takashima M *et al.,*	Japan	21	All HCV positive	adjacent non-tumour	-	2-DE MALDI TOF MS	11	-
2004	Yokoyama Y *et al.,*	Japan	20	All HCV positive	adjacent non-tumour	4 well- / 15 moderately- / 1 poorly-differentiated	2-DE MALDI TOF MS	11	12 out of 20 tissues showed indications of cirrhosis
2004	Melle C et al.,	Germany	9	-	adjacent non-tumour	3 --> pT2N0 3 --> pT3N0 1 --> pT3N+ 1 --> pT4N0 1 --> pT4N+	SELDI TOF	2 distinct peptide sequences	SELDI only provides protein signatures and not identification
2004	Li C et al.,	China	1	All HBV positive	adjacent non-tumour	Grade II	ICAT 2D LC MS/MS	261	Only 1 patient was used, lack statistical confidence

2004	Zeindl-Eberhart *et al.,*	Germany	10	4 HBV postive 5 HCV positive 1 HCV positive + alcohol anamnesis	2 male, 1 female and 1 fetal liver	1 --> grade I-II 2 --> grade II 5 --> grade II-III 2 --> grade III	2-DE MALDI TOF MS	90	6 patients were positive for cirrhosis
		Hong Kong	6	All HBV positive	adjacent non-tumour	-			-
2005	Liang CR *et al.,*	Singapore	7	All HBV positive	adjacent non-tumour	3 well differentiated 4 poorly differentiated	2-D DIGE MALDI TOF MS/MS	6 42	-
2005	Lee IN *et al.,*	Taiwan	8	4 HBV positive 3 HCV positive 1 HBV & HCV	adjacent non-tumour	1 --> grade I-II 4 --> grade II 2 --> grade II-III 1 --> grade III	2-D DIGE nanoLC MS/MS	34	2 tissues were HCV positive, 1 was both HBV and HCV 4 tissues were cirrhotic background
2005	Li C *et al.,*	China	10	All HBV positive	adjacent non-tumour	All Grade III	2-DE MALDI TOF MS	45	-
2005	Takashima M *et al.,*	Japan	26	All HCV positive	adjacent non-tumour	6 well - / 15 moderately - 5 poorly differentiated	2-DE MALDI TOF MS	1	Only alpha enolase level was analysed in this study
2005	Blanc JF *et al.,*	France	4	All HCV positive	adjacent non-tumour	1 --> F2 stage 3 --> F3 stage (Metavir Classification)	2-DE MALDI TOF MS / LC MS-MS	155	Additional 10 paired tissues were used fro validation
2006	Kuramitsu Y *et al.,*	Japan	21	All HCV positive	adjacent non-tumour	-	2-DE MALDI TOF MS	18	Focused on regulation on glutamine synthetase
2006	Song HY *et al.,*	China	12	All HBV positive	-	All Grade II & III	2-DE MALDI TOF MS/MS	16	The study focuses on metastasis 6 tissues were non-metastasis and 6 were metastasis
2006	Ai J *et al.,*	China	10	-	adjacent non-tumour	All Grade III	2-DE ESI MS/MS	20	-
2006	Luk JM *et al.,*	China	67	-	adjacent non-tumour	-	2-DE MALDI TOF MS	90	-
2006	Lee TH *et al.,*	Taiwan	9	4 HBV positive 4 HCV positive 1 HBV & HCV	adjacent non-tumour	4 --> grade I 5 --> grade II	2-DE MALDI TOF MS	20	The study was focused on effects of NFkB on viral induced HCC. EMSA assays were also conducted

2007	Melle C *et al.,*	Germany	25	-	adjacent non-tumour	pT2 & pT3 the exact details were not stated	SELDI TOF 2-DE MALDI TOF MS/MS	53	-
2007	Sun W *et al.,*	China	12	All HBV positive	adjacent non-tumour	6 --> grade II 6 --> grade III	2-D DIGE MALDI TOF MS/MS	71	2 tissues were females (Grade II), all others were males
2007	Zhang D *et al.,*	Singapore	6	All HBV positive	adjacent non-tumour	All well differentiated	2-DE MALDI TOF MS	15	-
2007	Luk JM et al.,	China	63	57 HBV positive 9 negative	adjacent non-tumour	41 --> stage I-II 25 --> stage III-IV	2-DE MALDI TOF MS/MS	-	Proteins identified were used for aritificial neural network (ANN)
2007	Yokoo H *et al.,*	Japan	37	4 HBV postive 17 HCV positive 1 HBV and HCV 5 unknown	-	12 --> Early recurrance 15 --> Non recurrance	2-D DIGE MALDI TOF MS	23	The only study analysing post-operative recurrance of HCC
2008	Orimo T *et al.,*	Japan	45	-	7 normal 11 adjacent non-tumour	6 well - / 14 moderately - 7 poorly differentiated	2-D DIGE MALDI TOF MS/MS	26	-
2008	Zubaidah RM *et al.,*	Singapore	12	All HBV positive	adjacent non-tumour	5 moderately differentiated 7 poorly differentiated	2-D DIGE MALDI TOF MS/MS	78	All males
2008	Minagawa H *et al.,*	Japan	1	All HBV positive	adjacent non-tumour	Moderately differentiated	2-D DIGE MALDI TOF MS/MS	66	Only 1 patient was used. Gene expression study (SAGE) was conducted simultaneously
2008	Seimiya M *et al.,*	Japan	10	7 HCV positive 3 unknown	adjacent non-tumour	1 --> grade I 5 --> grade II 4 --> grade III	2-D DIGE MALDI TOF MS/MS	83	-
2008	Teramoto R *et al.,*	Japan	18	17 HCV positive 1 unknown	adjacent non-tumour	8 well- / 9 moderately-differentiated	2-D DIGE MALDI TOF MS/MS	125	-
2008	Chaerkady R *et al.,*	India	1	-	adjacent non-tumour	-	iTRAQ LC MS/MS	151	Only 1 patient was used. Proteins of interest were
2009	Codarin E *et al.,*	Italy	20	7 HBV postive 5 HCV positive 5 non-viral 3 unknown	adjacent non-tumour	-	2-DE MALDI TOF MS	52	Nuclear enriched 19 tissues were from males and 1 tissue was female

1.2.4.3 Proteome analysis of serological markers for HCC

Identification of biomarkers using biological fluids has been especially attractive due to the non-invasive nature of sample collection. Serum proteomics were traditionally conducted on 2-DE comparing disease patients' sera against normal sera. Steel *et al.,* (2003) identified decrease of carboxy terminal fragment of complement C3 and an isoform of apolipoprotein A1in HBV-associated HCC patients. However lowered levels were also observed in HBV carriers without HCC which suggest that the changes were not cancer specific.

A common problem in serum 2-DE profiles (Steel *et al.,* 2003) is the inherent high abundant serum proteins such as albumin and immunoglobulin that often masks other proteins in the region. This also limits the dynamic range of proteins that can be identified. This can be overcome by immunodepletion of abundant proteins (Kawakami *et al.,* 2005; Feng *et al.,* 2005). Alternative strategies using surface enhance laser desorption and ionization-time of flight mass spectrometry (SELDI-TOF MS) have also been used extensively (Schwegler *et al.,* 2005; Paradis *et al.,* 2005; He *et al.,* 2008). This technique was however only able to identify differential peaks without protein identification. Other drawbacks also included limited dynamic range and reproducibility (Anderson and Anderson, 2002).

There is also increasing evidence that there is a human immune system response to tumours, hence indicating the presence of tumour derived auto-antibodies. Taking advantage of this, several studies aimed at elucidating auto-antibodies in serum were reported. This was accomplished by serologic analysis of recombinant cDNA expression libraries (SEREX) (Wang *et al.,* 2002), screening serum auto-antibodies against protein antigens on microarrays and 2-DE western blots (serological proteome analysis; SERPA).

Using SEREX and SERPA, Takashima *et al.,* (2006) successfully identified 4 proteins which elicited immunoreactivity against HCC sera. The pathological significance of heat shock 70 kDa protein 1 (HSP70), glyceraldehyde 3-phosphate dehydrogenase, peroxiredoxin and manganese superoxide dismutase (Mn-SOD) remained to be elucidated. A similar study identified 28 immunoreactive proteins, 17 of which also showed response using sera from cirrhosis or chronic hepatitis patients (Looi *et al.,* 2008). The eleven HCC specific proteins include HSP70, peroxiredoxin as identified earlier and several others such as aconitate dehydrogenase and fumarate hydratase. Whilst the potential of these tumour associated auto-antibodies is great, studies have cautioned of the lack of cancer specific auto-antibody. There is thus, a need to validate these makers against other malignancies (Wright *et al.,* 2007).

1.3 Current perspective in HCC studies

The pioneer HCC proteomic studies reported earlier highlighted the enormous potential of proteomics in understanding HCC. A large number of studies described aberrations in metabolic pathways, dysregulations of antioxidation proteins, heat-shock protein members and various transport proteins. These common alterations have also been summarized in several recent reviews (Sun *et al.,* 2007; Santamaria *et al.,* 2007; Sun *et al.,* 2009).

The increasing number of differentially regulated proteins obtained thus far has no doubt extended the current knowledge of HCC molecular pathogenesis. There is however increasing concerns in the heterogeneity of protein repertoires identified by the different proteomic analyses (Santamaria *et al.,* 2007). This disparity in protein data observed may be attributed by the concept that tumours are often heterogeneous and are capable of progressing through diverse molecular pathways. Additionally, these variations are also likely contributed by the use of non-standardized tissues samples (as observed in Table 1.4). This included analyses using different stages of HCC tissues and various aetiologies such as HBV- , HCV- or alcohol-induced HCC. Other confounding factors include the use of different controls or reference samples. Therefore, these variations in the choice of biological samples used, hinders our ability to constructively integrate the molecular data obtained from the different HCC studies. This thus hampers the ability to fully understand the disease and create hurdles in identification of biomarkers.

1.3.1 Advantages and limitations of proteomic platforms

Another possible contributing factor that results in the variation of proteins identified could be due to the techniques utilized. As described earlier, most of the studies to date had employed gel based (2-DE and 2-D DIGE) separation coupled with mass spectrometry analyses (Table 1.4). This technique aimed to identify differentially regulated proteins by visualization of thousands of proteins on a 2-D gel. It is commonly used because of its ability to identify protein isoforms and post-translational modifications. In addition to merely eye-balling the differences, softwares are currently available to aid in improving the accuracy in selecting regulated protein spots. Despite these improvements, and the utility of CyDye in 2-D DIGE, this technique still has its inherent limitations. Identification of HCC dysregulated proteins are hence constrained by protein resolution in the 2-D gel. For example, low abundant proteins as well as proteins with extreme molecular weight, isoelectric point, or hydrophobicity are often missed in HCC analysis utilizing 2-D DIGE.

As an alternative to gel based separation, liquid chromatography techniques directly coupled to mass spectrometers had also been used in HCC proteome profiling. These techniques are capable of identifying complex samples via separation of peptides in one or more consecutive chromatographic steps such as strong cation exchange followed by reverse-phase column to increase resolution (*e.g.* MudPIT). Liquid chromatographic techniques overcome the major limitation that 2-DE faced, by separating peptides instead of proteins. The other advantages of LC-MS include automation and high processing speed.

This approach can also be used for comparative proteomics with the use of stable isotope labelling. Peptide mixtures can be pre-labelled with cleavable Isotope Coded Affinity Tags (cICAT) (Li *et al.,* 2004) and isobaric tags for relative and absolute quantitation (iTRAQ)

(Chaerkady *et al.,* 2008). Differential protein expression between HCC tumours and non-tumours can then be determined by the relative abundance of the various peptides as determined by the mass spectrometers. Despite the successes in using this technique, it does have its limitations. For example, it requires strong computational capabilities to manage the large data generated and accurately and significantly identify differentially regulated proteins. Most significantly, is the loss information for post-translational modifications and / or protein isoforms that are not able to be discern by peptide sequences that are identified by mass spectrometry.

Therefore in recent years it is apparent that due to the inherent bias and limitations of each methodology, each approach results in limited targets with lack of depth and coverage. It is thus accepted that no single technique in protein separation is complete when attempting to profile proteome changes.

1.3.1.1 Proposed multiple proteomic approaches

In an effort to overcome the limitations and to harvest the advantages of the different platforms discussed, new strategies to combine these approaches had been gaining popularity. Several comparative studies had since employed two different techniques to increase the ability of identifying dysregulated proteins effectively. These included HCC analysis using SELDI-TOF and 2-DE (Melle *et al.,* 2007), brain ischemia using 2-DE and ICAT approaches (Khwaja *et al.,* 2007; Haqqani *et al.,* 2007) and endometrial cancer tissues using ICAT and iTRAQ (DeSouza *et al.,* 2005).

The possibility of using 3 different proteomic approaches was also explored by Wu *et al.,* (2006). They used a 6-protein mix standard and optimization on colorectal cancer cell line (HCT-116) and observed that there was limited overlap of proteins identified by the different methods. These preliminary studies suggest that these techniques are complementary and the strategy of using multiple approaches will increase the depth and extend the coverage in protein identification.

2. AIMS OF THE STUDY

Carcinogenesis of the liver represents a complex and multi-factorial disease. It entails a myriad of aetiologies and molecular mechanisms that may not be justifiably elucidated by single-candidate studies. Despite numerous functional genomics researches thus far, the challenges of understanding HCC are continuously fuelled by the inconsistencies in targets identified by the different groups. This is most commonly due to maverick choices of samples and differing identification methods. Henceforth, even with the most computationally-advanced analytical platforms, we are unable to comprehend the changes that occur during the development and progression of the disease.

In this project, we utilize 3 quantitative proteomic strategies to comprehensively identify the differentially expressed proteins involved in hepatocarcinogenesis. This effort aims to reconcile the library of data by restricting technology-specific limitations and technical discrepancies. Additionally the panel of tissue samples, carefully selected to reflect local demographics, were matched for gender, presence of liver cirrhosis and HBsAG positivity. The end point of this project concomitantly seeks to identify new targets that may narrow gaps of missing links involved in the progression of HBV-associated hepatocarcinogenesis.

The main aims of this project can be summarized as following:

1. Identify differentially expressed proteins in tumour tissues against their adjacent non-tumour tissues using three quantitative proteomic analyses. These techniques are (i) 2-D DIGE using CyDye labels followed by gel-based separation as well as stable isotope labels (ii) cICAT and (iii) iTRAQ followed by 2-dimensional liquid chromatography (2-D LC).

2. Ascertain the proteins that are involved in the progression of HCC by profiling two stages of the cancer, moderately- and poorly-differentiated tissues, separately.

3. Verify the selected proteins identified from this study using western blots. This will confirm the observations made by the proteomics approaches.

4. Characterize a novel protein family, far upstream binding proteins (FUBPs), identified as over-expressed in both stages of HCC analysed in this study. In order to understand FUBPs role in cancer progression *in vitro* transfections were also conducted on two different HCC cell lines, Hep3B and HepG2.

This is the first single effort to apply three quantitative techniques to achieve a comprehensive snapshot of proteomic changes in HCC tumourigenesis. The proteins identified serve as a basis of future investigative work to extend better understanding in the molecular pathogenesis of HCC. Studies as such opens up novel avenues towards understanding the biology of liver cancer, and in turn advance areas in disease preventive, treatment and diagnostics, especially via unravelling of novel biomarkers or therapeutic targets.

3. MATERIALS AND METHODS

3.1 Materials

3.1.1 Hepatocellular Carcinoma Tissues

The liver tissues used in this study were obtained from twelve patients diagnosed with either moderately differentiated HCC or poorly differentiated HCC. All patients were male and suffered from cirrhosis with chronic HBV infection. There was also no metastasis at the point of surgery. Tissues collected were grouped according to histology report; 5 had moderately differentiated HCC; and 7 had poorly differentiated HCC. The clinical data of the patients are presented in Table 3.1. Paired tissues were obtained from each patient, one from the adjacent non-tumour (normal) region and the other from the tumour region of the resected liver. The tissues were immediately snap-frozen in liquid nitrogen and stored at -151^{o}C before use. Usage of these samples was approved by the Ethics committee.

Table 3.1 : Clinical characteristics of patient samples used in this study.

Patient No.	TNM	Tumour size (cm)	Serum ALB (g/L)	Age at operation	Ehinicity
Moderately differentiated HCC					
131	T3N0M0	8.00	42	32	Chinese
196	T3N0M0	2.50	44	40	Chinese
199	T3NXMX	7.80	31	63	Chinese
200	T4N0M0	4.50	39	42	Chinese
203	T3NXMX	4.50	39	69	Chinese
Poorly differentiated HCC					
120	T3NXMX	6.00	25	66	Indian
126	T3N0M0	5.00	37	53	Chinese
155	T4NXMX	9.00	38	63	Chinese
157	T3N0M0	8.00	17	66	Chinese
187	T3N0M0	13.10	38	61	Chinese
207	T3N0MX	6.00	40	61	Javanese
215	T4NXMX	3.80	42	83	Chinese

3.1.2 Cell lines

Liver cell lines, HepG2 and Hep3B were provided by Dr Theresa Tan (Department of Biochemistry, NUS) and Bioprocessing Technology Institute respectively. All cells were maintained at 37^{o}C in a 5% CO_2 humidified atmosphere.

3.1.2.1 Cell culture media and reagents

Cell Culture Reagents	**Source**
Dulbecco's Modified Eagles' Medium (DMEM)	Sigma Aldrich (St. Louis, MO, USA)
Fetal Bovine Serum (FBS)	Gibco, Invitrogen Corporation (Carlsbad, CA, USA).
Sodium Bicarbonate	Sigma Aldrich
Trypsin (+ EDTA)	GIBCO BRL (Gaithersburg, MD, USA)
10X PBS	NUMI

3.1.3 Instruments and Equipments

3.1.3.1 Isoelectric Focusing (IEF)

Pre-cast non-linear (NL) 7 cm or 18 cm Immobilized pH Gradient (IPG) strips, pH 3-10 (GE Healthcare Bio-Sciences, Sunnyvale, CA, USA)

Ettan IPGphor / IPGphor II IEF unit (GE Healthcare Bio-Sciences)

3.1.3.2 SDS-PAGE

PROTEAN-II XL electrophoresis cell (Bio-Rad Laboratories, Hercules, CA, USA)

Mini PROTEAN-III electrophoresis module (Bio-Rad Laboratories)

3.1.3.3 Liquid Chromatography

Ultimate™ dual-gradient LC system equipped with a Probot™ MALDI (Dionex-LC Packings, Sunnyvale, CA, USA)

Strong cation-exchange (SCX) column (FUS-15-CP, Poros 10S) (Dionex-LC Packings)

C18 PepMap™, 0.3 × 1-mm trap column (3 –μm, 100 Å) (Dionex-LC Packings)

Monolithic PS-DVB, 0.2 × 50-mm reverse-phase column (Dionex-LC Packings).

3.1.3.4 Mass Spectrometry

Applied Biosystems 4700 and Applied Biosystems 4800, Proteomics Analyzer [Matrix-assisted laser desorption/ ionization time-of-flight/time-of-flight mass spectrometer (MALDI-TOF/TOF-MS)] (Applied Biosystems Inc., Framingham, MA, USA)

3.1.3.5 Transblotter

Trans-Blot Cell (Bio-Rad Laboratories)

3.1.3.6 Centrifuges

Beckman TL-100 Ultracentrifuge (Beckman Coulter Inc., Fullerton, CA, USA)

Eppendorf Centrifuge 5810R (Hamburg, Germany)

3.1.3.7 Spectrophotometer

Infinite M200 Tecan (Männedorf, Switzerland)

3.1.3.8 Scanners

UMAX ImageScanner (UMAX Technologies Inc.) (Fremont, CA, USA)

Molecular Dynamics TYPHOON 9410 variable mode Imager (GE Healthcare Bio-Sciences)

3.1.4 General Chemicals and Reagents

Chemicals & Reagents	Source
2D Cleanup Kit	GE Healthcare Bio-Sciences
α-cyano-4-hydroxycinnamic acid (CHCA)	Sigma Aldrich (St. Louis, MO, USA)
Acetic acid	Merck (Darmstadt, Germany)
Acetonitrile	EM Science (Gibbstown, NJ, USA)
Ammonium bicarbonate	Sigma Aldrich
Ammonium Persulfate (APS)	Bio-Rad Laboratories
Bromophenol blue	USB (Cleveland, OH, USA)
3-(3-cholamidopropyl)dimethyammonio-1-propane (CHAPS)	USB

Cleavable Isotope Coded Affinity Tags (cICAT) labels and reagents	Applied Biosystems Inc.
Coomassie® Plus Protein Assay Reagent Kit	Pierce (Rockford, IL, USA)
Cover Fluid	GE Healthcare Bio-Sciences
Cy3 N-hydroxysuccinamide ester DIGE dyes (Cy3) Cy5 N-hydroxysuccinamide ester DIGE dyes (Cy5) Cy2 N-hydroxysuccinamide ester DIGE dyes (Cy2)	GE Healthcare Bio-Sciences
Dimethyl sulphoxide (DMSO)	Sigma Aldrich
Dithiothreitol (DTT)	Bio-Rad Laboratories
DNase I	Roche Diagnostic (Mannheim, Germany)
EDTA disodium dihydrate	Bio-Rad Laboratories
Formaldehyde	Merck
Glycerol	BDH laboratory Supplies (Poole, England)
Glycine	Merck
Glycine, ultrapure, MB Grade	USB
HALT™ protease inhibitor cocktail (100X)	Pierce
Iodoacetamide (IAA)	Sigma Aldrich
IPG buffer	GE Healthcare Bio-Sciences
isobaric Tags for Relative and Absolute Quantification (iTRAQ) labels and reagents Kit	Applied Biosystems Inc.
Lipofectamine™ RNAiMAX	Invitrogen
Methanol	Merck
RNase A	Roche Diagnostic
Seaplaque® GTG® Agarose, Low melting temperature	BMA (Rockland, ME, USA)
Silver Nitrate	Merck

siRNA ON-TARGETplus™ SMARTpool FUBP1, L-011548-00-0005 FUBP2, L-009490-00-0005 FUBP3, L-029452-00-0005 Non-Targetting Pool Control, D-001810-10-05	Dharmacon RNAi Technologies (Thermo Scientific, IL, USA)
Skimmed Milk	Anlene
Sodium carbonate	Merck
Sodium dodecylsulfate (SDS)	Bio-Rad
Sodium thiosulfate	Merck
Thiourea	Fluka Chemie (Buchs, Switzerland)
Tris(hydroxymethyl)-aminomethane (Tris)	J.T. Baker (Phillipsburg, NJ, USA)
Tris(hydroxymethyl)-aminomethane (Tris) ultrapure, MB Grade	USB
Trifluoroacetic acid (TFA)	Sigma Aldrich
Trypsin (sequencing grade)	Promega Corporation (Madison, WI, USA)
Trypsin (+ $CaCl_2$)	Applied Biosystems Inc.
Urea	Bio-Rad Laboratories
Urea, ultrapure, MB Grade	USB

3.1.5 Western Blot reagents

3.1.5.1 Antibodies

Antibodies	Source
Mouse anti-Fumarate Hydratase (H00002271-M01)	Abnova (Taipei City, Taiwan)
Mouse anti-Triosephosphate isomerase (H00007167-M01)	Abnova
Rabbit anti-Alpha enolase (sc15343)	Santa Cruz Biotechnology Inc. (Santa Cruz, CA, USA).
Rabbit anti-Superoxide dismutase (Cu-Zn) (ab20926)	Abcam PLC (Cambridge, UK)
Rabbit anti-Catalase (AB1212)	Millipore (Billerica, MA, USA)
Mouse anti-DJ1 (sc70964)	Santa Cruz Biotechnology Inc.
Rabbit anti-Regucalcin (SML-RO1001-EX)	CosmoBio Ltd. (Tokyo, Japan
Mouse anti-ES1 (H00008209-M01)	Abnova
Mouse anti-GRP75 (SPS825)	Stressgen (Victoria, BC Canada, USA)
Rabbit anti-Ezrin (ab40839)	Abcam
Mouse anti-Nucleophosmin (ab10530)	Abcam
Rabbit anti-Periostin (ab14041)	Abcam
Rabbit anti-Lupus LA (sc33593)	Santa Cruz
Mouse anti- Nucleotide diphosphate kinase A / NDKA (ab27719)	Abcam
Mouse aniti-FUSE Binding Protein 1/2 (FUBP1/2) (ab56418)	Abcam

Mouse anti-FUSE Binding Protein 3 (FUBP3) (ab53438)	Abcam
Rabbit anti- c-myc (sc764)	Santa Cruz
Rabbit anti-actin (A2066)	Sigma
Rabbit anti-glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (sc25778)	Santa Cruz Biotechnology Inc.
Goat anti-rabbit IgG, HRP conjugated	Pierce
Sheep anti-mouse IgG, HRP conjugated	GE Healthcare Bio-Sciences

3.1.5.2 Detection System

Enhance Chemiluminescence (ECL) Western blotting detection system (GE Healthcare Bio-Sciences).

Advanced- ECL (AECL) Western blotting detection system (GE Healthcare Bio-Sciences).

Super Signal West Dura substrate (Pierce)

Kodak Biomax MR Film (Eastman Kodak Company, Rochester NY, USA)

Konica Minolta Processing Machine SRX-101A (Germany)

3.1.6 Softwares and Databases

3.1.6.1 Image Analysis

ImageQuant software (GE Healthcare Bio-Sciences)

DeCyder image analysis software (Ver. 6.5): Differential In-gel Analysis (DIA) and Biological Variation Analysis (BVA) software (GE Healthcare Bio-Sciences)

3.1.6.2 MS Data Analysis

GPS Explorer™ software Version 3.6 (Applied Biosystems Inc.)

MASCOT search engine (version 2.1; Matrix Science)

International Protein Index (IPI) human database Version 3.31 (European Bioinformatics Institute, Hinxton, UK)

3.2 Sample preparation

3.2.1 Tissue sample preparation

Human liver tissues were ground into a fine powder in liquid nitrogen and subsequently solubilized in a cocktail of 7 M urea, 2 M thiourea, 4% (w/v) CHAPS, 10 mM Tris supplemented with 1x HALT protease inhibitor cocktail, 50 µg/ml DNase I and 50 µg/ml RNase A. The lysates were then centrifuged at 50 000 *g* (Beckman TL-100 Ultracentrifuge) for 2hr at 15^{o}C to remove any insoluble cell debris. The supernatant was stored at -80^{o}C. All protein estimations were carried out using the Coomassie Plus Protein Assay Reagent kit with minor modifications. Bovine serum albumin provided in the kit was used as the standard.

3.2.2 Cell line sample preparation

3.2.2.1 Cell culture

HepG2 and Hep3B cells were cultured in Dulbecco's Modified Eagles' Medium (DMEM) in 10% MEM non-essential amino acid, 10% sodium pyruvate and 10% FBS. Media were changed every 3-4 days and cells were split by trypsinization with 0.5% (w/v) trypsin and 0.2% (w/v) ethylenediaminetetraacetic acid disodium salt (EDTA) when they reached confluence.

3.2.2.2 Cell lysate preparation

At the appropriate time point and confluence, cells were rinsed with 1X PBS and trypsinized. After 5 min, media containing FBS were added to terminate the action of trypsin. The resulting suspension was centrifuged at 100*g* for 10 min at 4 ^{o}C. After discarding the

supernatant, the cells were resuspended in ice-cold 1X PBS. The cells were washed thrice before centrifuging at 8000*g* for 5 min at 4 ^{o}C and the supernatant was removed. The final cell pellet was incubated for 30 min in a cocktail of 7 M urea, 2 M thiourea, 4% (w/v) CHAPS, 10 mM Tris supplemented with 1x HALT protease inhibitor cocktail, 50 µg/ml DNase I and 50 µg/ml RNase A. This solution was centrifuged at 20 817 *g* (Eppendorf Centrifuge 5810R), 15^{o}C for 1 hr to remove any insoluble cell debris. The supernatant was stored at -80^{o}C and protein concentration was determined using Coomassie Plus Protein Assay Reagent kit with some modifications.

3.3 2-dimensional gel electrophoresis (2-DE)

3.3.1 Isoelectric Focusing on IPG (Immobilized pH gradient) Strips

Pre-cast 7 cm or 18 cm, pH 3-10 nonlinear immobilized pH gradient (IPG) strips were rehydrated passively for 16 hr with 150 µl or 350 µl of rehydration buffer respectively. The rehydration buffer consisted of 7 M urea, 2 M thiourea, 4% (w/v) CHAPS, 20 mM dithiothreitol (DTT), 0.2% (w/v) IPG buffer and trace amounts of bromophenol blue. The IPG strips were overlaid with a low viscosity Immobiline DryStrip Cover Fluid to minimize evaporation and urea crystallization.

Rehydrated IPG strips were transferred onto a flatbed Ettan IPGphor Electrophoretic Unit for isoelectric focusing. The samples were then loaded using the cup loading method on Ettan IPGphor Strip Holders. First dimensional IEF was performed at a maximum current setting of 50 µA per strip at 20 ^{o}C. The protocol for 7 cm IPG strip was as follows : (i) 100 V, 50 Vhr; (ii) 200 V, 100 Vhr; (iii) 500 V, 250 Vhr; (iv) 1000 V, 500 Vhr; (v) 1000 V-8000 V,

4500 Vhr; (vi) 8000 V, 12000 Vhr achieving a total of 17400 Vhr for 4.5 hr. Isoelectric focusing for the 18 cm strip was performed with the following parameters: (i) 200 V, 500 Vhr; (ii) 500 V, 750 Vhr: (iii) 1000 V, 500 Vhr; (iv) 1000-8000 V, 2250 Vhr; and (v) 8000V, 40 000 Vhr; achieving a total of 44 000 Vhr for 10 hr.

3.3.2 Second Dimension Sodium Dodecyl Sulphate – Polyacrylamide Gel Electrophoresis (SDS – PAGE)

A two-step equilibration procedure using SDS-containing buffer was performed on the focused IPG strip prior to the second dimensional separation in SDS-PAGE. In the reducing step the strip was saturated with solution containing 6M urea, 30% (v/v) glycerol, 50mM Tris-HCl (pH 6.8), 1% (w/v) DTT, 2% (w/v) SDS and trace amounts of bromophenol blue dye for 15 min with constant mixing on a shaker. This was followed by an alkylating reaction using a similar buffer with DTT being replaced by 2.5% (w/v) iodoacetamide (IAA) buffered at pH 8.8 for 15 min.

IPG strips were then loaded onto 1.0-mm thick, 10 % polyacrylamide gels and sealed in place with 0.75% (w/v) agarose dissolved in Tris/Glycine/SDS electrophoresis buffer with trace amount of bromophenol blue. SDS-PAGE was performed at a constant current of 15 mA/gel for the small gels and 15 mA/gel for 20 min followed by 30 mA/gel for the large format gels. MINI-PROTEAN III was used for the small gels and PROTEAN II xi cell electrophoresis unit was used at 10^{o}C for the large gels. Tris/Glycine/SDS electrophoresis buffer used was 25 mM Tris, 192 mM glycine and 0.1% (w/v) SDS. SDS-PAGE was carried out until the tracking dye had migrated to within 3 mm from the end of the gel. Broad range or dual-colour molecular weight standards applied on sample application strips were electrophoresed concurrently.

3.3.3 Vorum Silver Staining

After SDS-PAGE, the gels were removed from the glass plates for silver staining. The gels were fixed in 50% methanol, 12% acetic acid and 0.05% formalin for at least 2 hr. They were washed in 35% ethanol thrice for 20 min. The gels were then sensitized in 0.02% sodium thiosulphate for 2 min. After each gel was rinsed thrice with water for 5 min, they were incubated in 0.2% silver nitrate and 0.076% formalin for 20 min. The silver nitrate solution was then discarded and each gel was washed twice for 1 min with water.

The gels were then developed in 6% sodium carbonate, 0.004% sodium thiosulphate and 0.05% formalin. The developer was removed upon attaining the desired intensity and 1.46% sodium EDTA was added for 20 min to stop the reaction. Finally, each gel was washed thrice with water for 5 min. Every step was carried out under constant shaking. The images of silver stained gels were captured using the Image Master Lab Scan v3.01 software.

3.3.4 Difference Gel Electrophoresis

3.3.4.1 Labeling with CyDye Flours

Liver tissue lysates were labelled with Cy2, Cy3 and Cy5 following the protocols in the Ettan DIGE User Manual (GE Healthcare Biosciences) with minor modifications. Briefly, 40 μg of protein from either the non-tumour or tumour lysates were labelled with of 320 pmol of Cy3 or Cy5. For each pair of tissue, triplicate gels were run. A dye-swap was performed on one out of the three gels. The pooled standard which contained all the samples was labelled with

320 pmol of Cy2 to serve as an internal standard for image matching and cross-gel statistical analysis.

The amount of dye added ensured that only 3% of the available proteins and only a single lysine residue per protein molecule was labelled (minimal labelling) so that the molecular weight and solubility of labelled proteins were not affected. These were incubated on ice in the dark for 30 min before 1 µl of 10 mM free lysine was added to quench the reaction.

An equal volume of sample buffer consisting of 7 M urea, 2 M thiourea, 4% CHAPS and 10 mM Tris was added to each labelled sample and allowed to stand on ice for 10 min. These labelled samples were then pooled accordingly for 2-D DIGE analysis. IEF and SDS-PAGE was conducted as stated above. The DIGE experimental design for moderately and poorly differentiated HCC liver tissues are shown in Table 3.2 and 3.3 respectively.

Table 3.2 : DIGE experimental design for moderately-differentiated HCC liver tissues. A total of five paired samples were used. For each sample pair triplicate gels were run, and which are represented by A, B and C.

Gel No.	Cy 2 Standard	Cy 3	Cy 5
01	Pooled sample from all 5 patients – 131 , 196 , 199 , 200 , 203	Non-Tumorous 131A	Tumorous 131A
02		Non-Tumorous 131B	Tumorous 131B
03		Tumorous 131C	Non-Tumorous 131C
04		Non-Tumorous 196A	Tumorous 196A
05		Non-Tumorous 196B	Tumorous 196B
06		Tumorous 196C	Non-Tumorous 196C
07		Non-Tumorous 199A	Tumorous 199A
08		Non-Tumorous 199B	Tumorous 199B
09		Tumorous 199C	Non-Tumorous 199C
10		Non-Tumorous 200A	Tumorous 200A
11		Non-Tumorous 200B	Tumorous 200B
12		Tumorous 200C	Non-Tumorous 200C
13		Non-Tumorous 203A	Tumorous 203A
14		Non-Tumorous 203B	Tumorous 203B
15		Tumorous 203C	Non-Tumorous 203C

Table 3.3 : DIGE experimental design for poorly-differentiated HCC liver tissues. A total of seven paired samples were used. For each sample pair triplicate gels were run, and which are represented by A, B and C.

Gel No.	Cy 2 Standard	Cy 3	Cy 5
01	Pooled sample from all 7 patients – 120 , 126 , 155 , 157 , 187 , 207 , 215	Non-Tumorous 120A	Tumorous 120A
02		Non-Tumorous 120B	Tumorous 120B
03		Tumorous 120C	Non-Tumorous 120C
04		Non-Tumorous 126A	Tumorous 126A
05		Non-Tumorous 126B	Tumorous 126B
06		Tumorous 126C	Non-Tumorous 126C
07		Non-Tumorous 155A	Tumorous 155A
08		Non-Tumorous 155B	Tumorous 155B
09		Tumorous 155C	Non-Tumorous 155C
10		Non-Tumorous 157A	Tumorous 157A
11		Non-Tumorous 157B	Tumorous 157B
12		Tumorous 157C	Non-Tumorous 157C
13		Non-Tumorous 187A	Tumorous 187A
14		Non-Tumorous 187B	Tumorous 187B
15		Tumorous 187C	Non-Tumorous 187C
16		Non-Tumorous 207A	Tumorous 207A
17		Non-Tumorous 207B	Tumorous 207B
18		Tumorous 207C	Non-Tumorous 207C
19		Non-Tumorous 215A	Tumorous 215A
20		Non-Tumorous 215B	Tumorous 215B
21		Tumorous 215C	Non-Tumorous 215C

3.3.4.2 Protein visualization

Each of the fluorescent tagged samples in a gel was visualized independently by the Typhoon Variable Mode Imager 9410 using optimal excitation/emission wavelength for each DIGE fluor: Cy2 (488/520 nm), Cy3 (532/580 nm), and Cy5 (633/670 nm). The images were previewed and checked by ImageQuant v5.0. By overlapping Cy3 and Cy5 images, the spots that were up- or down- regulated could be visualized. Protein spots stained mainly by Cy5 had red hues, while those stained by Cy3 appeared greenish in colour. An equal representation of both dyes in the protein spots appeared yellow. Following fluorescence scanning, the CyDye labeled gels were post stained with silver stain to detect protein spots for excision. Silver staining was carried out as stated in Section 3.3.3.

3.3.4.3 Decyder image analysis

Computerized evaluations of the highly complex DIGE gels patterns were performed using a specially designed DeCyder image analysis software (Ver. 6.5): Differential In-gel Analysis (DIA) and Biological Variation Analysis (BVA). The DIA software was used to co-detect the Cy2, Cy3 and Cy5 images for each gel. It also helped to detect protein spots for the calculation of the normalized protein abundance difference between samples relative to the internal standard. BVA was used to match multiple images from different gels and provide statistical data on differential protein expression levels for comparative cross-gel statistical analysis.

A threshold limit of 1.5-fold difference was selected as the statistically significant quantitative change and student's *t*-test at 95% statistical confidence (significance level, $p < 0.05$) was set. Spots were also manually confirmed to be significantly regulated when viewed

using the 3-D simulation of the protein spot intensity. In addition, the spots must be present in at least 3 out of 5 gels for the moderately differentiated and 4 out of 7 for the poorly differentiated HCC tissues.

3.3.5 In-gel tryptic digestion

Spots that satisfied the above criteria were selected for excision and in-gel tryptic digestion. Briefly, differentially expressed proteins were manually excised using a self made plunger from the silver stained DIGE labeled gels and transferred to a 96-well polymer microtitre plate. Each gel spot was incubated in 150µl of washing buffer (2.5mM ammonium bicarbonate, 50% (v/v) ACN) at 4°C for at least 24 h. A fresh aliquot of washing solution was replaced and each spot was incubated for 15 min at 37°C, followed by drying in a centrifugal concentrator. The spots were then subjected to reduction with 20 µl of 10 mM DTT in 100 mM ammonium bicarbonate and incubated at 56 °C for 1 h with constant shaking. Each spot was then alkylated with 20 µl of 55 mM IAA in 100 mM ammonium bicarbonate and incubated in the dark at ambient temperature for 45 min. After washing each spot with 100 µl of 100 mM ammonium bicarbonate for 10 min, the gel spots were dehydrated with 100 µl of ACN for 10 min. The washing and dehydration steps were repeated before the spots were dried in a centrifugal concentrator.

Enzymatic digestion was performed with the addition of 10 µl of 0.01 µg/µl sequencing grade modified trypsin in 25 mM ammonium bicarbonate to each gel spot. To reduce the number of trypsin peaks in mass spectrometry analysis, the plugs are first left in the 4°C fridge for 30 min to maximize trypsin uptake. Following this the excess trypsin was removed and 10 µl of 25mM ammonium bicarbonate was added to hydrate each gel spot and incubated at 37 °C

for 16 hr. Upon removing the tryptic digested peptides from each gel spot, 10 µl of 0.1% (w/v) trifluoroacetic acid (TFA) in 50% (w/v) aqueous acetonitrile (ACN) was added to each spot to enhance peptide extraction and sonicated for 20 min.

3.3.6 Mass Spectrometry Analysis and Database Search

Peptide digest from each gel spot were mixed with 1.2 µl CHCA matrix solution (5 mg/mL α-cyano-4-hydroxy-cinnamic acid in 0.1% (v/v) TFA, 50% (v/v) ACN) and spotted onto a MALDI target plate. Peptide mass spectra were obtained using the ABI 4800 Proteomics Analyzer MALDI-TOF/TOF Mass Spectrometer. For MS analysis, typically 1000 shots were accumulated for each sample. MS data were automatically obtained with the five most intense ions selected for MS/MS. The peptides were subsequently subjected to MS/MS analyses using air with a collision energy of 2kV and a collision gas pressure ~1 x10 $^{-6}$ Torr. Stop conditions were implemented so that 2000 to 3000 shots were accumulated depending on the quality of the spectra.

MASCOT search engine (version 2.1; Matrix Science) was used to search all of the tandem mass spectra. GPS Explorer^{TM} software Version 3.6 was used to create and search files with MASCOT search engine for peptide and protein identification. International Protein Index (IPI) human database Version 3.31 was used for the search which was restricted to tryptic peptides. The search parameters allowed for N-terminal acetylation, cysteine C-terminal carbamidomethylation and methionine oxidation. Peptide mass tolerance and fragment mass tolerance were set to 150 ppm and ± 0.4 Da respectively.

3.4 Quantitative Proteomics using stable-isotope labeling technologies

Protein lysates from either the non-tumour or tumour were first precipitated using the 2-D Clean-Up kit. The protein pellets were subsequently resuspended in either

(i) denaturing buffer (50mM Tris and 1.0% (w/v) SDS, pH 8.5) for cleavable Isotope Coded Affinity Tag (cICAT) labeling or

(ii) dissolution buffer (500mM triethylammonium bicarbonate and 0.1% (w/v) SDS) for isobaric Tag for Relative and Absolute Quantification (iTRAQ) labeling.

3.4.1 cleavable Isotope Coded Affinity Tag (cICAT) labeling

cICAT labeling and processing of the samples were carried out according to manufacturer's protocol using the reagents provided (Applied Biosystems Incorporation). Briefly, a total of 100 μg of proteins from the non-tumour and tumour lysates were reduced with 1.25 mM Triscarboxyethylphosphine (TCEP). Non-tumour and tumour lysates were subsequently labeled with cICAT light and heavy reagents respectively for 2 hr at 37^{o}C in the dark. They were subsequently combined and trypsinized at 37^{o}C for 16 hr. Upon completion of *in-situ* digestion, the digested peptide mixture was passed through a strong-cation exchange cartridge before being enriched with an avidin affinity cartridge. Next, the cICAT-labeled peptides were dried by lyophilization and re-dissolved in cleaving reagents and incubated at 37^{o}C for 2 hr. After the removal of biotin, peptides were lyophilized again before reconstituted for 2-Dimensional liquid chromatography (2-D LC).

3.4.2 isobaric Tag for Relative and Absolute Quantification (iTRAQ) labeling.

iTRAQ labeling and processing of the samples were carried out as described by the protocol with minor modifications and using the reagents provided from Applied Biosystems. 100μg of protein from each sample was reduced with 5mM of TCEP at 60°C for 1 hr, followed with alkylation step for 10 min using 10mM of methyl methanethiosulfonate (MMTS) in room temperature. Each sample was subsequently diluted to achieve a final concentration of 0.05% (w/v) SDS prior to trypsinization at 37°C for 16 hr. Each tryptic digest was then labeled for 1 hr with one of the four isobaric amine-reactive tags. The labeling was carried out at random ensuring that 2 pairs of patient tissues were labeled as follows: Tag_{114} – non-tumour; Tag_{115} – tumour; Tag_{116} – non-tumour; and Tag_{117} – tumour samples.

These four iTRAQ-labeled samples were then combined and passed through a strong cation exchange cartridge as recommended by Applied Biosystems. The eluate obtained was further desalted using a Sep-Pak cartridge (Millipore), lypholised and reconstituted in appropriate buffers for 2-D LC.

3.4.3 Two-Dimensional Liquid Chromatography separation of labeled peptides.

Each of the lypholised cICAT and iTRAQ-labeled peptide mixtures were then dissolved in 2% (v/v) acetonitrile (ACN) containing 0.05% (v/v) TFA and further separated using an Ultimate™ dual-gradient LC system (Dionex-LC Packings) with a Probot™ MALDI spotting device. A two-dimensional LC separation was performed as follows: for the first dimensional separation, the labeled peptide mixture was injected into a 0.3 × 150-mm strong cation-exchange (SCX) column (FUS-15-CP, Poros 10S; Dionex-LC Packings). The mobile phase A used was 5mM KH_2PO_4 buffer, pH 3, 5% ACN and mobile phase B was 5mM KH_2PO_4 buffer,

pH 3, 5% ACN + 500 mM KCl respectively. The flow rate was 6µl/min. A total of 9 fractions were obtained using step gradients of mobile phase B: unbound, 0-5, 5-10, 10-15, 15-20, 20-30, 30-40, 40-50, 50-100% of B. The eluting fractions were captured alternatively onto two 0.3 × 1-mm trap column (3-µm C18 PepMap™, 100 Å; Dionex-LC Packings), washed with 0.05% TFA and followed by gradient elution in a 0.2 × 50-mm reverse-phase column (Monolithic PS-DVB; Dionex-LC Packings). In the second-dimensional separation, mobile phase A was 2% ACN with 0.05% TFA and mobile phase B was 80% ACN with 0.04% TFA. The gradient elution step was 0-60% B in 15 min at a flow rate of 2.7µl/min. The LC fractions were mixed directly with MALDI matrix solution (7mg/ml CHCA and 130µg/ml ammonium citrate in 75% ACN) at a flow rate of 5.4µl/min via a 25-nl mixing tee (Upchurch Scientific) before they were spotted onto a 192-well MALDI target plate (Applied Biosystems) using a Probot Micro Precision Fraction collector (Dionex-LC Packings), at a speed of 5 sec per well. An internal standard consist of 50 fmol of ACTH (18-39) peptide (*m/z* = 2465.199) was also spiked into each well.

3.4.4 Mass spectrometry analysis and Database search

The samples on the MALDI target plates were analyzed using a 4700 Proteomics Analyzer mass spectrometer (Applied Biosystems Incorporation) with MALDI source and TOF/TOF™ optics. MS/MS analyses were performed using nitrogen at collision energy of 1 kV and a collision gas pressure of ~1×10^{-6} Torr.

The GPS Explorer™ software Ver. 3.6 (Applied Biosystems Incorporation) was used to create and search files with the MASCOT search engine (version 2.1; Matrix Science) for peptide and protein identifications in both the cICAT and iTRAQ-labeled samples. The

International Protein Index (IPI) human database (Version 3.31) was used for the search and this was restricted to tryptic peptides.

3.4.4.1 cICAT-labeled samples

For MS analysis, an average of 1000 shots was accumulated for each sample well. In MS/MS fragmentation only cICAT pairs with normalized ratio (normalized against median ratio of all the cICAT pairs detected) greater than 40% were selected. These also include singletons. The resolution used for parent ion selection was 200. Variable modifications such as heavy and light cICAT-labeled cysteine, N-terminal acetylation and pyroglutamation (E & Q), and methionine oxidation were selected. One missed cleavage was allowed, with precursor error tolerance set to 150 ppm and MS/MS fragment error tolerance to 0.4 Da.

cICAT quantification was performed using GPS Explorer^{TM} software (Ver. 3.6) and normalized against median ratio obtained from all the cICAT peptide pairs detected in one sample. The ratios were calculated by comparison of the cluster area of the heavy-ICAT labeled peptide with that of the light-ICAT labeled peptide.

3.4.4.2 iTRAQ-labeled samples

For each MS spectrum, 1000 shots were accumulated. In MS/MS fragmentation, 6 000 shots were combined for each precursor ion with signal to noise (S/N) ratio greater or equal to 100. For precursors with S/N ratio between 50 and 100, 10 000 shots were acquired. The resolution used to select the parent ion was 200. For both MS and MS/MS, peaks were deisotoped and no smoothing was applied before peak detection. In MS/MS, only the peaks

from 60 Da to 20 Da below each precursor mass with S/N ≥ 10 were selected. Peak density was also limited to 30 peaks per 200 Da and the maximum number of peaks was set at 125. Fixed modification such as cysteine methanethiolation, N-terminal iTRAQ labeling, and iTRAQ labeled-lysine were selected while methionine oxidation was considered as variable modification. One missed cleavage was allowed and precursor error tolerance was set to 150 ppm while MS/MS fragment error tolerance was set to 0.4 Da.

iTRAQ quantification was performed using the GPS Explorer™ software (Ver. 3.6) and normalized among samples. iTRAQ ratios were calculated based on the areas of the iTRAQ reporter fragment peaks (114, 115, 116 and 117), and included only peptides identified with C.I. % above cutoff thresholds as described in 3.4.4.4. The average iTRAQ ratio and standard deviation (S.D.) were determined using the GPS Explorer™ software.

3.4.4.3 Determination of cut-off threshold for fold change

To determine cut-off threshold for cICAT and iTRAQ fold changes, 2 equal amounts of bovine serum albumin (BSA) or 6-protein mix were labeled with the cICAT or iTRAQ reagents respectively (Tan *et al.,* 2008). The significant cut-off threshold proposed was based on the standard deviation (S.D.) of all the ratios of the respective labeled peptides. The respective ratios determined were as follows: cICAT labeled peptides 1.36 based on 1 + 3 S.D and iTRAQ labeled peptides 1.3 based on 1 + 2 S.D.

A more stringent ratio of 1.4 was used in this study for up-regulated proteins and reciprocally 0.71 was the cut-off threshold for down-regulated proteins. These values were selected to ensure the similar stringency as the proteins selected for 2-D DIGE. In addition,

regulated proteins will only be selected if it is consistently regulated in 3 out of 5 patients or 4 out of 7 patients in moderately- and poorly-differentiated HCC.

3.4.4.4 Estimation of false positive rate to determine cut-off score.

A randomized database generated using IPI human database Version 3.31, via a Pearl script downloaded from http://www.matrixscience.com/help/decoy_help.html, was also used to search for both the cICAT and iTRAQ labeled samples. The false positive rate was calculated by comparing the peptide hits obtained from these 2 databases at different ion score C.I. % in the peptide level. The minimum ion score C.I. % was determined to ensure that no more than 5% false positive rate was achieved. Based on this cut-off threshold, all the proteins identified from the random database search were matched to a single-peptide. Proteins identified that were matched to at least 2 peptides were thus statistically confident. For single-peptide matched proteins, only those with ion score C.I. % greater than the highest C.I. % obtained from the random database search were selected as significant.

3.5 Bioinformatics annotation tools

Proteins annotations obtained from the IPI database (http://www.ebi.ac.uk/IPI/) were converted to Swiss-Prot accession numbers as derived from the IPI database. Theoretical M_r and pI values were derived from Swiss-Prot database (http://au.expasy.org/tools/pi_tool.html). An in-house program, Click-Me, was used to estimate the experimental M_r and pI of the protein spots identified from 2-D DIGE.

The GRAVY scores were determined using the ProtParam tool (http://au.expasy.org/cgi-bin/protparam). Data obtained were tabulated and summarized using a PHP script developed in-house. The proteins' sub-cellular localization and biological functions were obtained from Gene Ontology consortium (http://www.geneontolgy.org/) and further verified by Swiss-Prot database annotations. Protein pathways and interactions were determined by the Kyoto Encyclopedia of Genes and Genomes (KEGG) (http://www.genome.jp/kegg/).

Venn diagrams were drawn proportionally using 3Venn applet (http://www.cs.kent.ac.uk/people/staff/pjr/EulerVennCircles/EulerVennApplet.html) (Chow and Rodgers, 2005). Ingenuity Pathway Analysis (IPA) (Ingenuity Systems, Mountain View, CA, USA, www.ingenuity.com) was used to further analyse the proteins identified. Direct relationships between proteins are displayed graphically as nodes (individual proteins) and edges (biological relationship between nodes).

3.6 FUBP siRNA transfection

Both cell lines, HepG2 and Hep3B, were seeded in 24-well plates one day prior to transfection. Each well consists of 1.25 x 10^4 cells in 500µl of DMEM media with 10% (v/v) FBS. Cells at 60% density were then transfected with non-targetting control siRNA or FUBP1, FUBP2, FUBP3 or mixture of all 3 FUBP siRNA (ON-TARGET*plus*™, Dharmacon RNAi Technologies, Thermo Scientific, IL, USA).

The transfection mixture was prepared by first mixing 50 µl of DMEM containing varying concentration of siRNA with 50 µl of DMEM containing 0.5 µl of Lipofectamine™ RNAiMAX (Invitrogen) reagent followed by an addition of 400 µl of DMEM with 10% (v/v) FBS. This mixture was incubated at room temperature for 30 min. The seeding media from each well was then replaced with the respective media with siRNA. The transfected cells were returned to the CO_2 incubator. At appropriate time points, the cells were either treated with 3-(4,5-dimethylthiazolyl-2,5-diphenyl-tetrazolium bromide (MTT) reagent for cell proliferation assays or lysed as mentioned earlier for western blot analysis.

3.6.1 Cell proliferation assay

At the 72 hr time point, 250 µl of MTT at 5mg/ml were added to each well and incubated at 37^{o}C for 2 hrs. In this assay, MTT was used as a colorimetric substrate for measuring cell viability. Non-viable cells, with altered cellular redox activity were unable to reduce the dye. The media was aspirated and formazan precipitates were dissolved in 500 µl of DMSO. Wells containing all mixtures except cells were used as blanks. The absorbance in each well was measured at 550 nm using a spectrophotometer. All experiments were conducted in 4 sets of wells and was repeated using 3 separate batches of cells.

3.7 Immunoblotting

Equal aliquots of whole cell lysate from the HCC tissues were either resolved on 1-DE or 2-DE gels using 7cm, pH 3-10, nonlinear IEF strips. IEF and SDS-PAGE were carried out as described earlier. Upon completion of electrophoresis, the gels were equilibrated in Towbin transfer buffer (25 mM Tris, 192 mM glycine, 0.1 % SDS, 20 % methanol). Proteins were then electro-blotted onto PVDF membranes. After transfer, blots were blocked with 2% (w/v) BSA dissolved in TBS-T (20 mM Tris-HCl, 150 mM NaCl, 0.1 % (v/v) Tween 20, pH 7.5) overnight.

Table 3.4 summarised all the various antibody concentrations and respective blocking solutions used. In general, all primary antibodies were diluted (as recommended) in 1% (w/v) blocking solution in TBS-T and incubated for 2 hrs. Three 15 min washes with TBS-T were performed which were followed by 1 hr of secondary antibody incubation with 1% (w/v) blocking solution in TBS-T. The blots were again rinsed with TBS-T to remove any non-specific binding. Subsequent visualization was performed using Enhance Chemiluminescence (ECL), Advance Enhance Chemiluminescence (AECL) or Super Signal West Dura substrate. The image was exposed to Kodak Biomax MR Film and developed by the KONICA MINOLTA Processing Machine SRX-101A.

Table 3.4 : Concentration of primary and secondary antibody used

Primary antibody (Ratio)	Secondary antibody (Ratio)	Developing reagent (Time)
Fumarate Hydratase (1: 1000)	Sheep anti-mouse (1 : 5000)	ECL (8 min)
Triosephosphate isomerase (1:1000)	Sheep anti-mouse (1 : 5000)	ECL Advance (2 min)
Alpha-enolase (1:1000)	Goat anti-rabbit (1 : 5000)	Dura (3 min)
Superoxide dismutase (Cu-Zn) (1:1000)	Goat anti-rabbit (1 : 5000)	ECL (3 min)
Catalase (1: 10 000)	Goat anti-rabbit (1 : 5000)	ECL Advance (3 sec)
DJ-1 (1:1000)	Sheep anti-mouse (1 : 5000)	Dura (3 min)
Regucalcin (1: 1000)	Goat anti-rabbit (1 : 5000)	Dura (10 sec)
ES1 (1:1000)	Sheep anti-mouse (1 : 5000)	ECL (8 min)
Stress-70 / GRP75 (1:1000)	Sheep anti-mouse (1 : 5000)	ECL Advance (10 sec)
Ezrin (1 : 1000)	Goat anti-rabbit (1 : 5000)	ECL Advance (1 min)
Nucleophosmin (1 : 1000)	Sheep anti-mouse (1 : 5000)	Dura (30 sec)
Lupus LA (1 : 1000)	Goat anti-rabbit (1 : 5000)	Dura (30 sec)
Nucleotide diphosphate kinase A NDKA (1 : 1000)	Sheep anti-mouse (1 : 5000)	Dura (3 min)
FUSE Binding Protein 1/2 (FUBP1/2) 1 : 1000	Sheep anti-mouse (1 : 5000)	Dura (8 min)
FUSE Binding Protein 3 (FUBP3) (1 : 1000)	Sheep anti-mouse (1 : 5000)	Dura (1 min)
c-myc (1 : 1000)	Goat anti-rabbit (1 : 5000)	ECL Advance (1 min)
Actin (1 : 1000)	Goat anti-rabbit (1 : 5000)	ECL Advance (15 min)
GAPDH (1 : 1000)	Goat anti-rabbit (1 : 5000)	Dura (5 min)

4. RESULTS

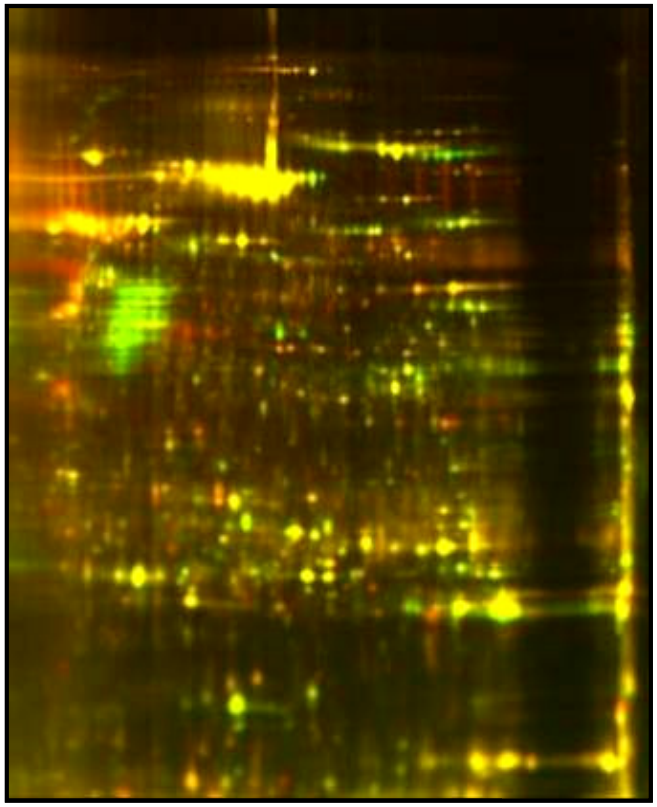
4.1 Differential proteome analysis of HCC tissues

4.1.1 Difference gel electrophoresis (2-D DIGE)

In 2-D DIGE, three spectrally distinct CyDye probes (Cy2, Cy3 and Cy5) were used to pre-label the proteins before separation by 2-DE gel for analysis. Their non-overlapping excitation/emission spectra enabled multiplexing of different samples on the same gel. Three different fluorescent images can thus be derived from a single gel. By overlaying Cy3 and Cy5 images, which represent the control and treated fractions respectively, differentially expressed protein spots could be detected visually in a differential display image.

Proteins that were up-regulated in HCC tumour tissues would show progressively higher red hues while those that are down-regulated would be greenish in colour. Unaffected proteins would be represented by yellow spots. A representative 2-D DIGE image of proteins from moderately and poorly differentiated HCC is illustrated in Figure 4.1 A and B respectively.

A



B

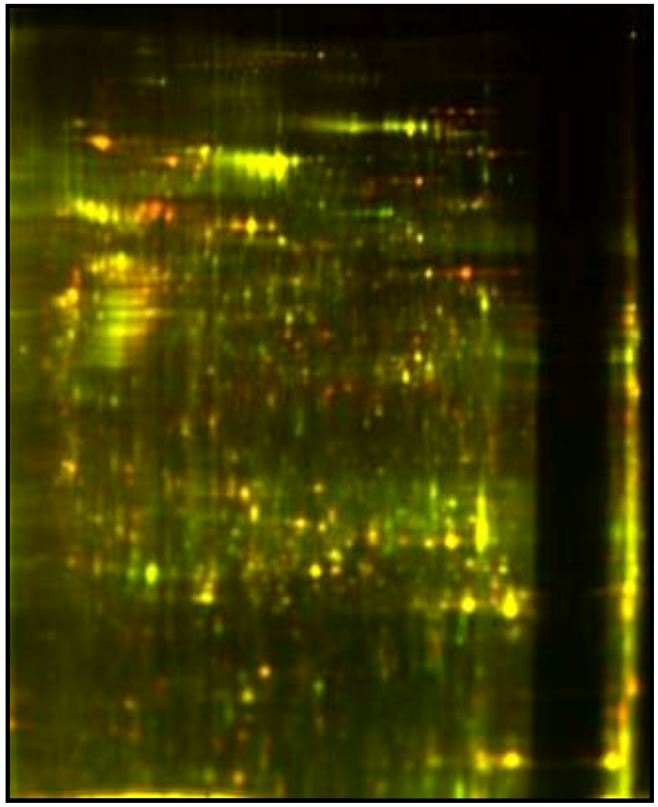


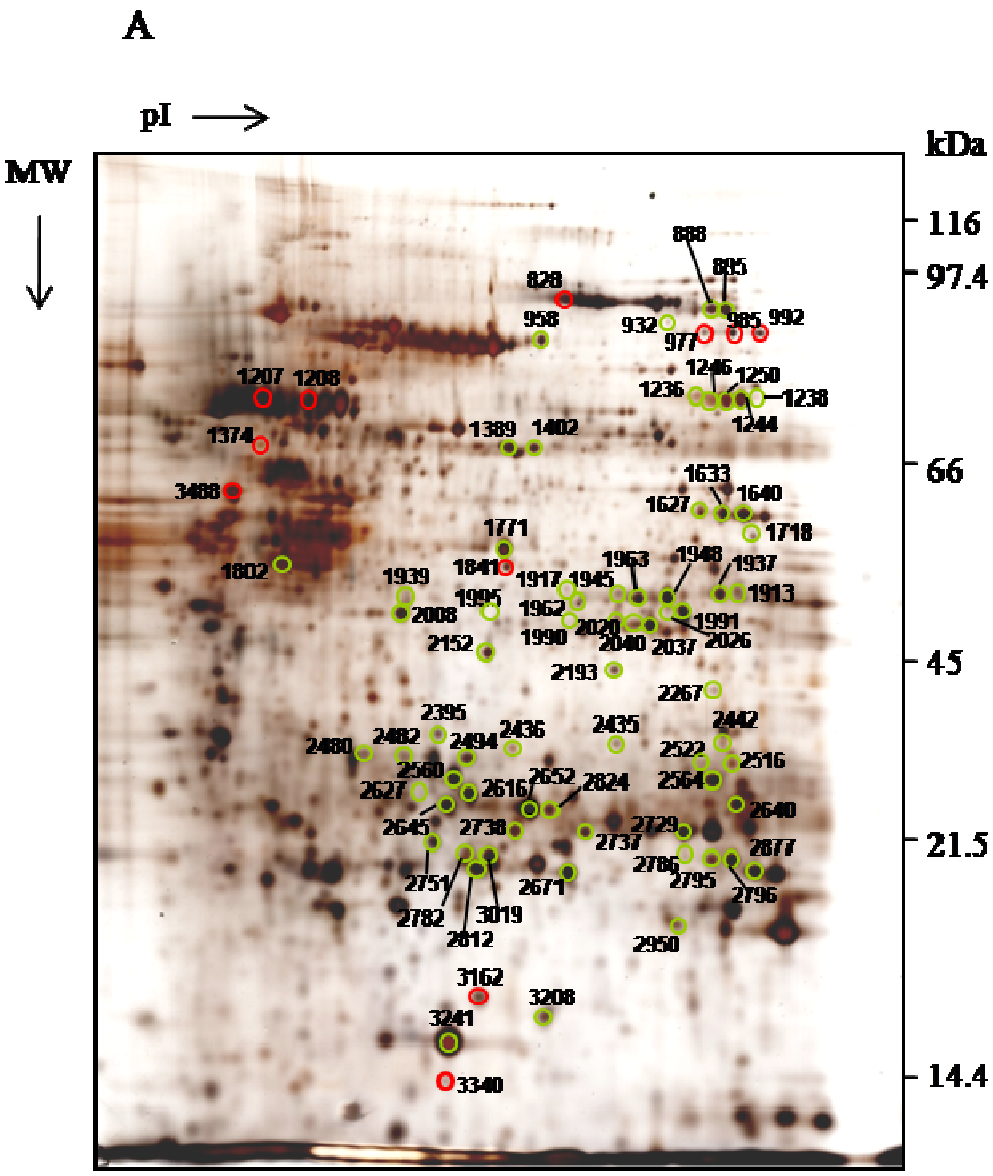
Figure 4.1 : Representative images of 2-D DIGE analysis (A) moderately differentiated HCC and (B) poorly differentiated HCC tissues.

4.1.2 Decyder Analysis and MALDI TOF/TOF MS

DeCyder-DIA and DeCyder-BVA software were subsequently used to perform automated intra-gel co-detection of labeled samples, background removal and inter-gel matching for differential expression analysis. The protein abundance (a measure of the spot intensity) of each experimental sample is directly normalized to the internal standard (Cy2 label of control and treated sample). An average of 2500 spots was detected in each 2-D DIGE gel.

A total of 148 protein spots that exhibited more than 1.5-fold difference in intensity and with a statistical confidence of $p<0.05$ were excised for mass spectrometry. In addition these protein spots were also manually checked to ensure each were present with similar regulation in at least 3 out of 5 or 4 out of 7 of the paired samples in moderately differentiated and poorly differentiated HCC respectively.

With these criteria, a total of 54 and 26 proteins (excluding isoforms) were successfully identified by mass spectrometry for the moderately- and poorly-differentiated HCC tissues respectively. These protein spots are highlighted on the representative silver stained gel images using the master numbers generated by the DeCyder software (Figs. 4.2 A and B). A significant number of the proteins identified were isoforms arising from post-translational modifications. The complete lists of these proteins are shown in Appendix I.


A
pI
MW
kDa
116
97.4
66
45
21.5
14.4
888
885
828
958
932
977
985
992
1246
1250
1236
1238
1244
1207
1208
1374
1389
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3340

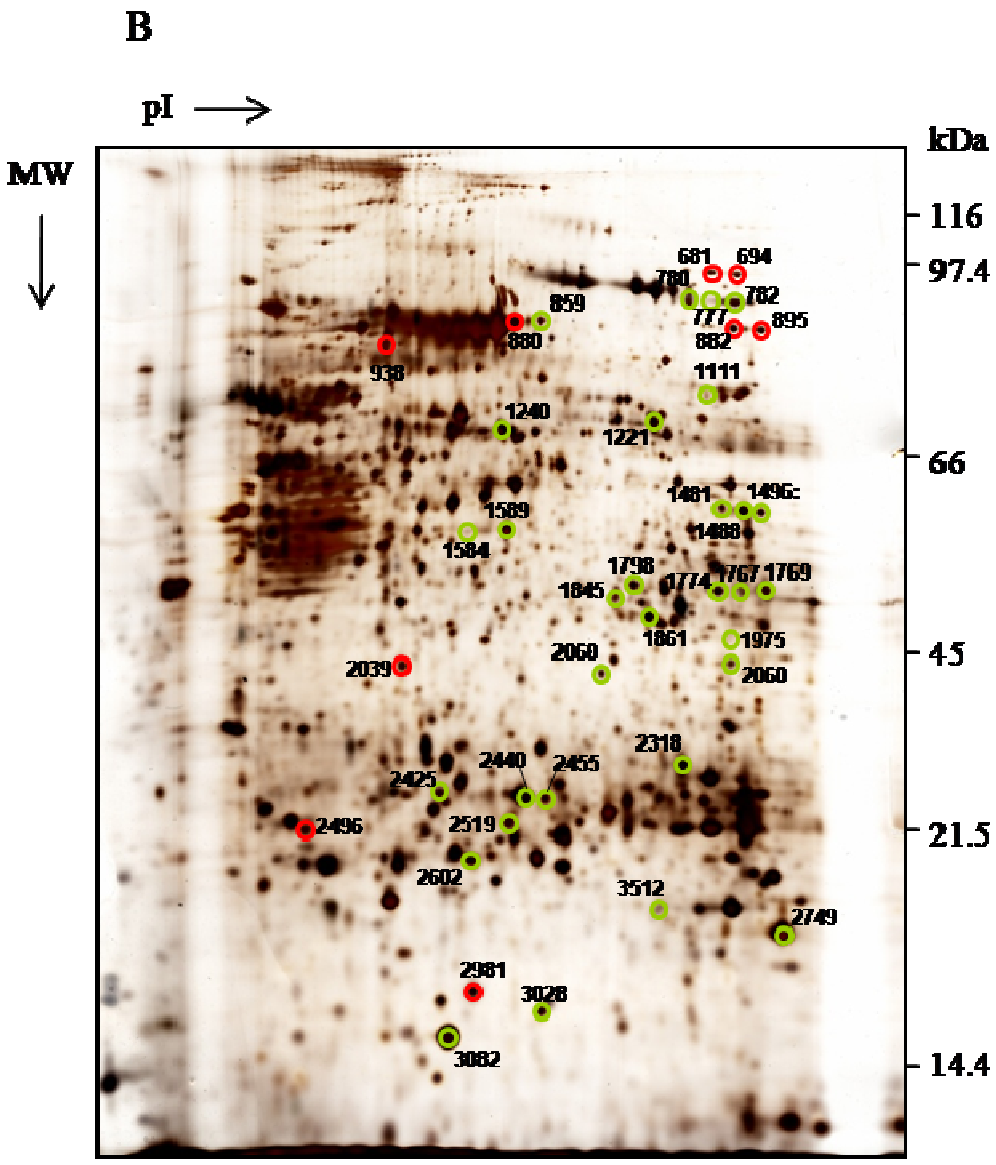


Figure 4.2 : Differentially expressed protein spots in the 2D gels are marked with master numbers in (A) moderately-differentiated tumour tissues and (B) poorly-differentiated tumour tissues. *Protein spots that are down-regulated are in green and up-regulated proteins are in red.

4.1.2 Stable-isotope labeling techniques

4.1.2.1 cICAT coupled to 2-D LC and MALDI TOF/TOF MS

Affinity-purified cICAT labeled peptides were separated by two-dimensional chromatography and analysed by mass spectrometry. With the aid of GPS Explorer™ software and manual checks, an average of 100 statistically significant proteins with confidence interval greater than 95% was typically identified from each sample set.

cICAT ratio of each protein were determined by comparison of the cluster area of the heavy-ICAT labelled peptide (tumour) with that of the light-ICAT labelled peptide (non-tumour) from each mass spectrometry runs. Figure 4.3A depicts an enlarge image of the MS spectrum image of a peptide from 60kDa heat shock protein (HSP60) labelled with the light and heavy cICAT reagents. The ratio can thus be obtained by comparing the relative abundance of the 2 peaks. MS/MS spectrum from the precursor ion at m/z 1864.035 (Fig. 4.3B) illustrates the identification of the sequence of the peptide.

In this study, the criterion for protein identification includes an average cICAT ratio of each protein by more than 1.4 or less than 0.71. In addition, these proteins must be consistently regulated in at least 3 out of 5 and 4 out of 7 in each moderately- and poorly-differentiated HCC tissues respectively. A total of 57 and 24 proteins from moderately and poorly differentiated proteins respectively were identified as significantly regulated (Appendix II).

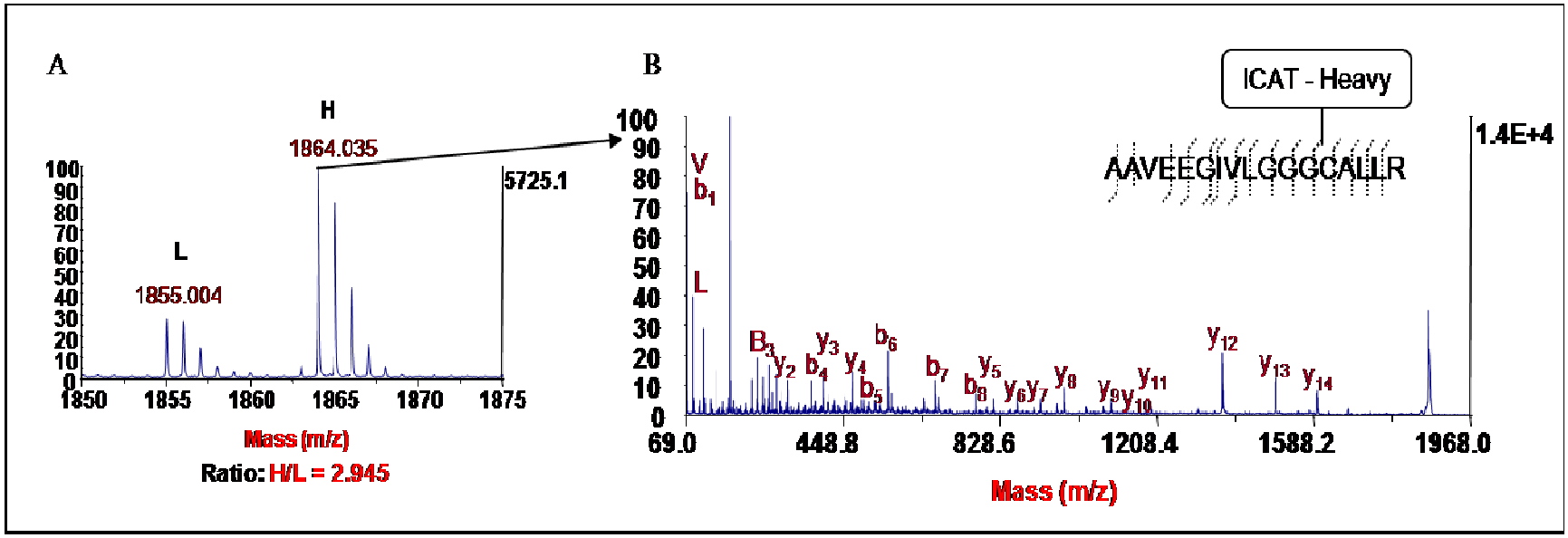


Figure 4.3: Representative mass spectra of 60kDa heat shock protein (HSP60) analyzed by MALDI-TOF/TOF MS upon tryptic digestion. (A) MS spectrum with tryptic peptides of HSP60 labelled by the cICAT heavy and light reagents; arrow indicates ion at *m/z* = 1864.035 selected for MS/MS (B) MS/MS spectrum of the peptide AAVEEHIVLGGGCALLR (m/z = 1864.035), where y- and b-ions are denoted along with immonium ions (V, valine; L, leucine); y- and b-fragmentations are also indicated with tilted dotted lines above and below the sequence, respectively.

4.1.2.2 iTRAQ coupled to 2-D LC and MALDI TOF/TOF MS

iTRAQ labeled peptides were also fractionated by two-dimensional chromatography and analysed by mass spectrometry. With the aid of GPS Explorer™ software, using statistical stringencies as described earlier, an average of 500 proteins with quantitative information were typically identified from each sample set.

iTRAQ ratios were calculated based on the cluster areas of the iTRAQ reporter fragment peaks (114, 115, 116 and 117) obtained from MS/MS fragmentation. Figure 4.4A depicts an enlarged image of the MS spectrum containing the precursor ion NAGVEGSLIVEK (m/z 1503.8) from the protein HSP60. The MS/MS spectrum of this peptide is shown in Figure 4.4B. The relative abundance of this peptide can be calculated using the reported ion peaks at m/z 114, 115, 116 and 117 (Fig. 4.4C).

Proteins from each sample sets that were over-expressed by 1.4 or down-regulated by 0.71 folds were accepted. These proteins must also be consistently regulated in at least 3 out of 5 and 4 out of 7 in each moderately- and poorly-differentiated HCC tissues respectively. In moderately differentiated HCC samples a total of 90 proteins were significantly regulated, whilst in the poorly differentiated HCC samples, a total of 151 differentially expressed proteins were selected (Appendix III).

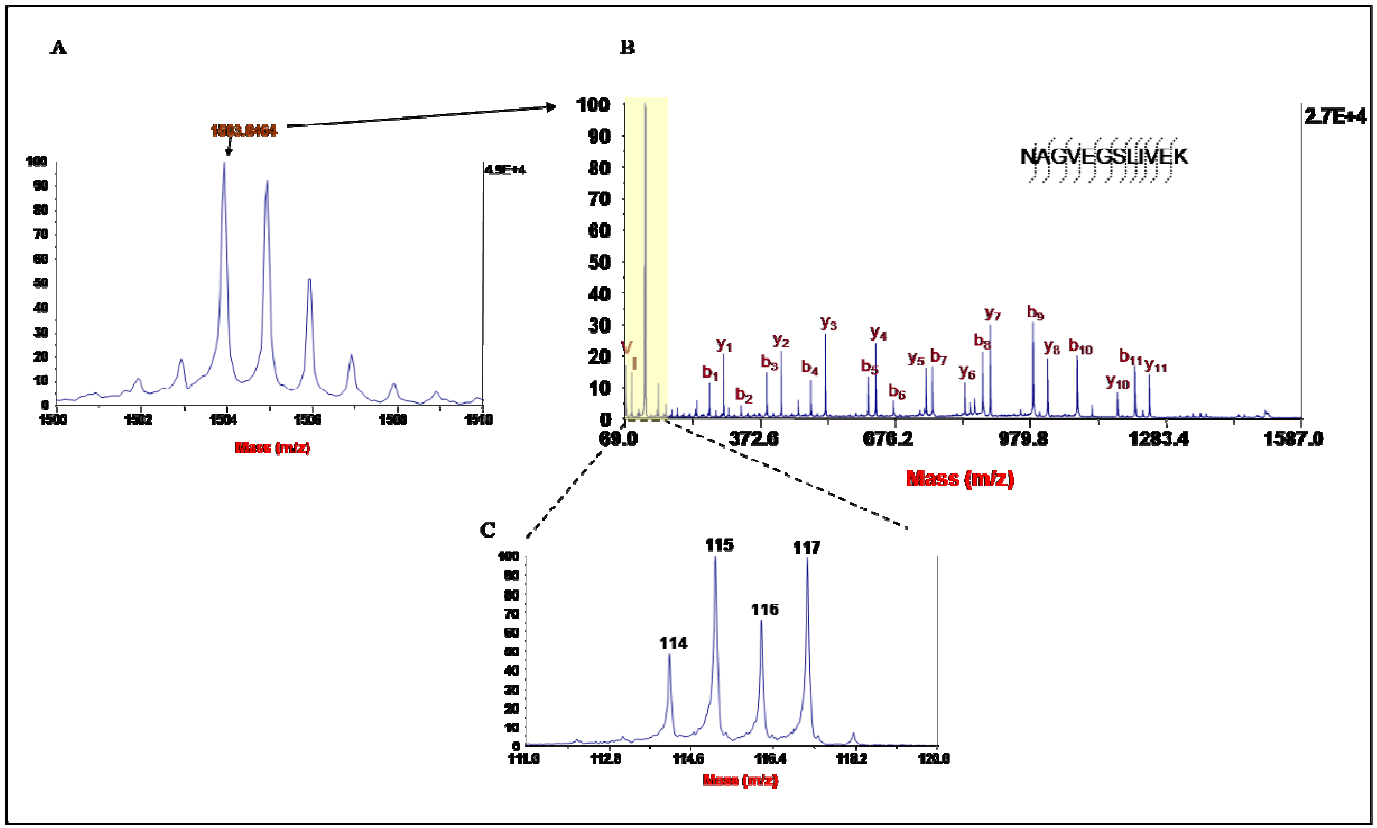


Figure 4.4: Representative iTRAQ mass spectra of 60kDa heat shock protein (HSP60) analyzed by MALDI-TOF/TOF MS upon tryptic digestion. (A) MS spectrum with tryptic peptides of HSP60; arrow indicates ion at *m/z* = 1503.8 selected for MS/MS (B) MS/MS spectrum of the peptide NAGVEGSLIVEK (*m/z* = 1503.8), where y- and b-ions are denoted along with immonium ions (V, valine; L, leucine); y- and b-fragmentations are also indicated with tilted dotted lines above and below the sequence, respectively. (C) Reporter ion region of MS/MS *m/z* 1503.8.

4.2 Identification of differentially expressed proteins

The differentially expressed proteins identified from all 3 techniques were grouped according to their biological functions as annotated in the Gene Ontology database. Table 4.1 and 4.2 contains the list of proteins identified from moderately and poorly differentiated HCC respectively. Down arrows in each column in 2-D DIGE, cICAT and iTRAQ indicated the under-expression of the protein identified while the up arrows showed over-expression. The value of protein regulation can be obtained from the individual dataset available in Appendix I, II and III.

Table 4.1 : Significantly regulated proteins in moderately-differentiated HCC as identified by 2-D DIGE, cICAT and iTRAQ are summarized according to their respective biological functions. Expression levels are summarized by arrows; down and up arrows indicate down-regulation or up-regulation respectively.

Accession No.	Protein Name	2-D DIGE	cICAT	iTRAQ	Remarks
Metabolism					
P50053	Ketohexokinase	⇩		⇩	Glycolysis
P05062	Fructose-bisphosphate aldolase B (liver)	⇩	⇩	⇩	Glycolysis
P60174	Triosephosphate isomerase	⇩			Glycolysis
P18669	Phosphoglycerate mutase 1		⇩		Glycolysis
Q96C23	Aldose 1-epimerase		⇩		Carbohydrate metabolism
P36871	Phosphoglucomutase-1		⇩	⇩	Carbohydrate metabolism
Q9UJM8	Hydroxyacid oxidase 1			⇩	Carbohydrate metabolism (Glyoxylate metabolism)
Q00796	Sorbitol dehydrogenase		⇩	⇩	Carbohydrate metabolism
P09467	Fructose-1,6-bisphosphatase 1	⇩		⇩	Gluconeogenesis
Q16822	Phosphoenolpyruvate carboxykinase			⇩	Rate-limiting step in the metabolic pathway that produces glucose from lactate

Q16851	UTP-glucose-1-phosphate uridylyltransferase			↓	Glucosyl donor in metabolic pathways
P07954	Isoform mitochondrial of Fumarate hydratase, or Isoform cytoplasmic of Fumarate hydratase,	↓			Tricarboxylic acid cycle
P30038	Aldehyde dehydrogenase 4 family (ALDH4A1)	↓		↓	Involved in connecting TCA and Urea cycle
Q53FB6	Mitochondrial aldehyde dehydrogenase 2 variant (ALDH2)			↓	Urea and glycolysis
P21695	Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	↓			Glycerol lipid metabolism
P30084	Enoyl-CoA hydratase, mitochondrial precursor	↓	↓	↓	Fatty acid elongation / Beta-oxidation
P33121	Long-chain-fatty-acid CoA ligase 1			↓	Activation of Beta-oxidaton
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic (ACAT1)	↓	↓		Beta-oxidation
P24752	Acetyl-CoA acetyltransferase, mitochondrial precursor (ACAT2)			↓	Beta-oxidation
P16219	Short-chain specific Acyl CoA dehydrogenase, mitochondrial precursor	↓			Beta-oxidation
P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial			↓	Beta-oxidation
P42765	3-ketoacyl-CoA thiolase, mitochondrial			↓	Beta-oxidation
P80404	4-aminobutyrate aminotransferase, mitochondrial precursor		↓	↓	Amino acid metabolism
P49448	Glutamate dehydrogenase 2, mitochondrial precursor		↓		Glutamate metabolism (connecting TCA and Urea cycle)
P11586	C-1-tetrahydrofolate synthase			↓	Amino acid biosynthesis
P00439	Phenylalanine-4-hydroxylase		↓		Amino acid biosynthetic process
O43175	Phosphoglycerate dehydrogenase			↓	Amino acid metabolism (Glycine/threonine/serine metabolism)

Q96GK7	Fumarylacetoacetate hydrolase domain containing 2A	↓			Tyrosine Catabolism
P50440	Isoform Cytoplasmic of Glycine amidinotransferase		↓		Urea Cycle (Amino acid metabolism)
Q03154	Aminoacylase-1	↓		↓	Urea Cycle (Amino acid metabolism)
P31327	Isoform 1 of Carbamoyl-phosphate synthase			↓	Urea Cycle (Amino acid metabolism)
P00966	Argininosuccinate synthase			↓	Urea cycle
P04424	Arginosuccinate Lyase			↓	Urea cycle
P05089	Arginase-1	↓	↓	↓	Urea cycle
Q7Z4W1	L-xylulose reductase		↓	↓	Participates in the uronate cycle of glucose metabolism.
P24298	Alanine aminotransferase 1			↓	Glutamate metabolism / Liver gluconeogenesis
Q00266	S-adenosylmethionine synthetase			↓	Methionine / Selenoamino acid metabolism
Q93088	Betaine-homocysteine S-methyltransferase 1			↓	Methionine / Homocysteine metabolism
P25325	3-mercaptopyruvate sulfurtransferase	↓			Cysteine metabolism
Q96N76	Urocanase family protein	↓			Histidine catabolic process
Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria			↓	Valine and pyrimidine metabolism / fatty acyl-CoA.
O94760	NG, NG-dimethylarginine dimethylaminohydrolase 1	↓			Arginine catabolic process
P61457	Pterin-4-alpha-carbinolamine dehydratase		↓		Tetrahydrobiopterin biosynthesis

Q59HD5	3-mercaptopyruvate sulfurtransferase variant (Fragment)		↓		Involved in cyanide degradation and in thiosulfate biosynthesis
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	↓	↓		Pentose phosphate shunt
P54819	Isoform 1 of Adenylate kinase isoenzyme 2, mitochondrial		↓		Nucleic acid metabolic process
P14550	Alcohol dehydrogenase	↓			Catalyzes the NADPH-dependent reduction
P07327	Alcohol dehydrogenase 1A			↓	Cellular alcohol metabolic processes
P00325	Alcohol dehydrogenase 1B			↓	Cellular alcohol metabolic processes
P08319	Alcohol dehydrogenase 4			↓	Cellular alcohol metabolic processes
P00352	Retinal dehydrogenase 1 (ALDH1A1)			↓	Retinol metabolism
P21549	Serine-pyruvate aminotransferase			↓	Amino acid metabolism (forms pyruvate)
P00915	Carbonic anhydrase 1	↓			Carbon compund metabolic process
P00918	Carbonic anhydrase 2	↓			Reversible hydration of carbon dioxide
P07099	Epoxide hydrolase 1, microsomal		↓		Biotransformation enzyme that catalyzes the hydrolysis of arene and aliphatic epoxides to less reactive
P16083	Ribosyldihydronicotinamide dehydrogenase / NAD(P)H dehydrogenase	↓			Quinone reductase
O60218	*Aldo-keto reductase family 1 member B10*		↑		Aldehyde metabolic process
P15531	*Nucleoside diphosphate kinase A / Nucleoside diphosphate kinase B*	↑		↑	Major role in the synthesis of nucleoside triphosphates other than ATP

Detoxification					
P21964	*Isoform Soluble of Catechol O-methyltransferase*		↓		Shortens the biological half-lives of certain neuroactive drugs
P16152	*Carbonyl reductase [NADPH] 1*		↓	↓	Catalyzes reduction carbonyl compounds including antitumor anthracycline antibiotics
P50225	*Sulfotransferase 1A1*			↓	Steroid metabolic process
O00748	*Carboxylesterase 2 Isoform 1*			↓	Involved in the detoxification of xenobiotics and in the activation of ester and amide prodrug
P05181	*Cytochrome P450 2E1*			↓	Inactivates a number of drugs and xenobiotics
P16662	UDP-glucuronosyltransferase 2B7 precursor			↓	Amino acid metabolism (elimination of toxic xenobotics)
O75795	UDP-glucuronosyltransferase 2B17 precursor			↓	Amino acid metabolism (elimination of toxic xenobotics)
Defense related protein - Antioxidants					
P04040	*Catalase*	↓	↓	↓	Hydorgen peroxide catabolic process
P00441	*Superoxide dismutase [Cu-Zn]*	↓	↓	↓	Removal of superoxide radicals
P30043	*Flavin reductase*	↓	↓	↓	Converts biliverdin to bilirubin (protects from oxidative damage & iron metabolism)
Q93099	*Homogentisate 1,2-dioxygenase*		↓		Oxidation / reduction
Q99497	*Protein DJ-1*	↓	↓		Sensor for oxidative stress / Positive regulator of androgen receptor-dependent transcription
Q16762	*Thiosulfate sulfurtransferase*		↓		Iron-sulfur complexes
P78417	Glutathione transferase omega-1	↓			Redox Homeostasis
P08263	Glutathione S-transferase A1			↓	Redox Homeostasis
P09210	*Glutathione S-transferase A2*			↓	Redox Homeostasis

P07203	Glutathione peroxidase 1		↓		Response to oxidative stress
Q06278	*Aldehyde oxidase 1(AOX1)*			↓	FAD and NADH binding
Q9NVS9	*Pyridoxine-5'-phosphate oxidase*	↓	↓		Involved in pyridoxamine-phosphate oxidase activity
P30041	*Peroxiredoxin-6*	↓			Involved in redox regulation of the cell
P30039	*Phenazine biosynthesis-like domain-containing protein (MAWD binding protein)*	↓			
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial percursor	↓			Involved in redox regulation of the cell
P07237	Protein disulfide-isomerase precursor		↑		Redox Homeostasis / Catalyzes rearrangement of disulfide bonds
Q15084	Isoform 1 of Protein disulfide-isomerase A6 precursor		↑		Catalyzes the rearrangement of -S-S- bonds in proteins
Defense related proteins - Inflammation response					
P01009	*Alpha-1-antitrypsin precursor*	↑			Acute-phase response. Inhibitor of serine proteases.
Defense related protein - Heat Shock Proteins (HSPs)					
P61604	10 kDa heat shock protein, mitochondrial (HSP10)			↑	Probable involvement with caspase activation
P04792	Heat shock protein beta-1 (HSP27)	↓		↑	Stress resistant and actin organization
Q38L19	60kDa Heat shock protein (HSP60)	↑	↑	↑	Interacts with HBV X gene
P08107	Heat shock 70kDa protein 1A (HSP70)			↑	Molecular chaperone
P17066	Heat shock 70 kDa protein 6 (HSP70B)			↑	Molecular chaperone
P11142	Isoform 1 of Heat shock cognate 71 kDa protein (HSP73)			↑	Molecular chaperone

Q12931	Heat shock protein 75 kDa, mitochondrial (TRAP1)			⇧	Molecular chaperone
P08238	*Heat shock protein HSP 90-beta (HSP90B)*			⇧	Molecular chaperone
P38646	*Stress-70 protein, mitochondrial precursor (GRP75)*			⇧	Implicated in cell proliferation and anti-apoptosis
Protein Binding - Iron related					
P02787	*Serotransferrin precursor*	⇩			Iron binding transport protein / Heme degradation
P02794	Ferritin heavy chain		⇩		Stores iron in a soluble, non-toxic, readily available form. Important for iron homeostasis.
Q86WI9	*Ferritin light chain*		⇩		Stores iron in a soluble, non-toxic, readily available form. Important for iron homeostasis
P00738	*Haptoglobin precursor*	⇩			Haptoglobin combines with free plasma hemoglobin and protecting the kidneys from damage
P68871	*Hemoglobin subunit beta*	⇩	⇩		Involved in oxygen transport
P02790	*Hemopexin precursor*		⇧		Binds heme and transport to liver for breakdown
Protein Binding					
Q13228	Selenium binding protein 1	⇩	⇩	⇩	Selenium binding / protein transport
Q15493	Regucalcin (Senescence marker-30)	⇩			Calcium binding (regulates in liver and kidney)
P27797	Calreticulin		⇩		Calcium binding chaperone promoting folding, quality control in the ER via the calreticulin/calnexin cycle
P02768	*Serum albumin precursor*	⇩			
P28838	*Cytosol aminopeptidase*		⇩	⇩	Presumably involved in the processing and regular turnover of intracellular proteins

P00167	*Isoform 1 of Cytochrome B5*			↓	Membrane bound hemoprotein which function as an electron carrier for several membrane bound oxygenases.
P11712	*Cytochrome P450 2C9*			↓	NADPH-dependent electron transport pathway
P22307	*Sterol carrier protein 2 isoform 2*			↓	Mediates in vitro the transfer of phospholipids, cholesterol and gangliosides between membranes
P14854	Cytochrome c oxidase subunit VIb isoform 1		↓		
P07108	Isoform 2 of Acyl-CoA-binding protein			↓	Fatty acid binding
P30040	Endoplasmic reticulum protein ERp29 percursor	↓			Processing of secretory proteins within ER
Q06323	Proteasome activator complex 1	↓			Implicated in immunoproteasome assembly and its down-regulation leads to possible loss of antigen processing
Q9UL46.3	Proteasome activator complex subunit 2 (PA28)	↓			Needed for presentation of viral MHC class I epitopes, down-regulation in tumour cells results in impaired representation
P19652	Alpha-1-acid glycoprotein 2 precursor		↓		Modulate activity of immune system during acute-phase reaction.
Q6IAT8	Beta-2 microglobulin		↓		Related to immune response, beta-chain of major histocompatibility complex class I molecules.
P14317	Hematopoietic lineage cell-specific protein		↓		Substrate of the antigen receptor-coupled tyrosine kinase / Transcription factor activity
P06748	Isoform 1 of Nucleophosmin			↑	Involved in diverse cellular processes such as protein chaperoning, cell proliferation and regulation of tumor
P10909	Clusterin isoform 1			↑	Associated with apoptosis - function not clear
P63104	*14-3-3 protein zeta/delta*			↑	Adaptor protein / Anti-apoptosis
P02649	*Apolipoprotein E precursor*			↑	Binding of lipoprotein particles
P62937	*Peptidyl-prolyl cis-trans isomerase A*		↑		Accelerate the folding of proteins / Involved in initiation of viral induction

P07355	Annexin A2			↑	Calcium-regulated membrane-binding protein
P17931	Galectin-3			↑	Required for terminal differentiation of columnar epithelial cells during early embryogenesis
Q9Y3C8	Ubiquitin fold modifier 1-conjugating enzyme 1		↑		E2-like enzyme which forms an intermediate with UFM1
Q1JUQ4	FK506 binding protein12			↑	Involved in protein folding
P02749	*Beta-2-glycoprotein 1 precursor*		↑		Binds to various kinds of negatively charged substances
Nucleic Acid Binding					
P52758	*Ribonuclease UK114*			↓	Inhibition of the translation by cleaving mRNA / Upregulated during cellular differentiation
Q96AE4	*Far upstream element-binding protein 1*	↑			Regulates MYC expression by binding to a single-stranded far-upstream element (FUSE)
P05455	*Lupus La protein*		↑		Plays a role in the transcription of RNA polymerase III
P62992	Ubiquitin and ribosomal protein S27a precursor			↑	Involves in translation
P09651	*Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1*			↑	Involved in the packaging of pre-mRNA into hnRNP particles
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	↓		↑	Involved with pre-mRNA processing
Cytoskeletal modelling / Cell Motility					
P26038	Moesin			↑	Connections of cytoskeletal structure to plasma membrane
P06753	Isoform 2 of Tropomyosin alpha-3 chain			↑	Binds to actin filament
P67936	Isoform 1 of Tropomyosin alpha-4 chain			↑	Binds to actin filament
P24844	Myosin regulatory light chain 2, smooth muscle isoform		↑		Cell locomotion

Q01995	Transgelin (SMP22)		↑		Actin cross-linking
P37802	Transgelin (TAGLN2 / SMP22 homolog)			↑	Actin binding protein, early markers of differentiated smooth muscle. Exact function is not clear
P02545	Isoform C of Lamin-A/C			↑	Components of nuclear lamina
P13668	Stathmin 1/oncoprotein 18	↑			Involved in the regulation of the microtubule (MT) filament system by destabilizing microtubules
P40121.1	Gelsolin-like capping protein / Macrophage capping protein	↑			Calcium-sensitive protein which reversibly blocks the fast growing ends of actin filaments but does not sever preformed
P15311	Ezrin			↑	Probably involved in connections of major cytoskeletal structures such as actin filament bundle formation.
P04004	Vitronectin precursor			↑	Cell adhesion and spreading factor in serum and tissues
Q15063	Isoform 2 of Periostin precursor			↑	Induces cell attachment and spreading. Plays a role in cell adhesion
P07858	Cathepsin B precursor		↑		Thiol protease (intracellular degradation) / implicated in tumor invasion and metastasis.
Q01082	Isoform Short of Spectrin beta chain			↑	Interacts with camodulin in a calcium dependant manner / movement of cytoskeleton at the membrane
P08670	Vimentin	↑	↑		Class-III intermediate filaments found in various non-epithelial cells, especially mesenchymal cells
P07437	*Tubulin beta chain*			↑	Major constituent of microtubules
P68371	*Tubulin beta-2C chain*			↑	Major constituent of microtubules
Fibrin formation					
P30086	*Phosphatidylethanolamine-binding protein 1*	↓			Serine protease inhibitor which inhibits thrombin
P05783	*Keratin, type I cytoskeletal 18*	↓			Involved in the uptake of thrombin-antithrombin complexes by hepatic cells / cell proliferation inducing gene
P02675	*Fibrinogen beta chain precursor*			↑	Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
P02751	Isoform 1 of Fibronectin precursor		↑	↑	Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape.

P02671	Isoform 2 of Fibrinogen alpha chain precursor			⇧	Platelet aggregation
P08758	*Annexin A5*			⇧	Anticoagulant protein that acts as an indirect inhibitor of the thromboplastin-specific complex
Others					
Q9H0W9	*Ester hydrolase*	⇩	⇩		
O94903	Proline synthetase co-transcribed bacterial homolog protein	⇩			
Q96LK9	3-OXO-5-Beta-Steroid 4-Dehydrogenase		⇩		
Q6UW68	Transmembrane protein 205			⇩	Multi-pass membrane protein
P30042	Isoform Long of ES1 protein homolog, mitochondrial precursor	⇩			
P35237	Serine (or cysteine) proteinase inhibitor (SERPINB6)			⇧	
A6NBZ8	*Putative uncharacterized Albumin*		⇧		
P04264	Keratin, type II cytoskeletal 1	⇩	⇩		Structural protein
Q6MZU6	Hypothetical protein DKFZp686C15213		⇧		

Table 4.2 : Significantly regulated proteins in poorly-differentiated HCC as identified by 2-D DIGE, cICAT and iTRAQ are summarized according to their respective biological functions. Expression levels are summarized by arrows; down and up arrows indicate down-regulation or up-regulation respectively.

Accession No.	Protein Name	2-D DIGE	cICAT	iTRAQ	Remarks
Metabolic proteins					
P50053	Ketohexokinase			↓	Glycolysis
P05062	Fructose-bisphosphate aldolase B (Liver)	↓	↓	↓	Glycolysis
Q00796	Sorbitol dehydrogenase		↓	↓	Glucose metabolic process
P06737	Glycogen Phosphorylase (liver form)			↓	Involved in glycogen metabolic processes
P09467	Fructose-1,6-bisphosphatase 1	↓		↓	Gluconeogenesis
P11498	Pyruvate carboxylase, mitochondrial precursor			↓	Gluconeogenesis
Q16822	Phosphoenolpyruvate carboxykinase			↓	Rate-limiting step in the metabolic pathway that produces glucose from lactate
Q16851	UTP-glucose-1-phosphate uridylyltransferase			↓	Glucosyl donor in metabolic pathways
P07954	Isoform mitochondrial of Fumarate hydratase, or Isoform cytoplasmic of Fumarate hydratase, mitochondrial	↓			Tricarboxylic acid cycle
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondria			↓	Tricarboxylic acid cycle electrons transfer from succinate to ubiquinone.
Q96I99	Succinyl-CoA ligase			↓	Tricarboxylic acid cycle

P21399	Cytoplasmic aconitate hydratase (Iron-responsive element-binding protein 1)			↓	Tricarboxylic acid cycle
P48735	Isocitrate dehydrogenase [NADP], mitochondrial precursor			↓	Tricarboxylic acid cycle
Q53FB6	Mitochondrial aldehyde dehydrogenase 2			↓	Urea and glycolysis
P30038	Aldehyde dehydrogenase 4 family, member A1			↓	Involved in connecting TCA and Urea cycle
P00367	Glutamate dehydrogenase 1			↓	Glutamate metabolism (connecting TCA and Urea cycle)
P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor			↓	Cholesterol biosynthesis
Q06520	Bile salt sulfotransferase			↓	Lipid metabolism (Catalyzes bile acids in the liver and adrenal glands)
Q14032	Bile acid CoA:amino acid N-acyltransferase			↓	Bile acid metabolism in hepatocytes catalyzes the 2nd step
P07148	Fatty acid binding protein		↓		Binds free fatty acid and free coenzyme A/billirubin Organ morphogenesis
P30084	Enoyl-CoA hydratase, mitochondrial percursor	↓	↓	↓	Fatty acid elongation / Beta-oxidation
P33121	Long-chain-fatty-acid--CoA ligase 1			↓	Activation of Beta-oxidaton
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial precursor			↓	Beta-oxidation / Carnitine shuttle
Q08426	Enoyl-CoA hydratase (Peroxisomal bifunctional enzyme)			↓	Beta-oxidation
Q5R1W7	3-ketoacyl-CoA thiolase (Trifunctional enzyme beta subunit)			↓	Beta-oxidation
P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial			↓	Beta-oxidation
P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial			↓	Beta-oxidation

P16219	Short chain specific acyl-CoA dehydrogenase, mitochondrial precursor	↓			Beta-oxidation
Q16836	Isoform 2 of Hydroxyacyl-coenzyme A dehydrogenase			↓	Beta-oxidation
P24752	Acetyl-CoA acetyltransferase, mitochondrial precursor			↓	Beta-oxidation
P42765	3-ketoacyl-CoA thiolase, mitochondrial			↓	Beta-oxidation
P09110	3-ketoacyl-CoA thiolase, peroxisomal precursor			↓	Beta-oxidation
Q16698	2,4-dienoyl-CoA reductase, mitochondrial precursor			↓	Auxiliary enzyme of beta-oxidation (unsaturated fatty acids)
Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria precursor			↓	Binds fatty acyl-CoA / Amino acid metabolism (Plays a role in valine and pyrimidine metabolism)
Q6IB77	Isoform 1 of Glycine N-acyltransferase			↓	Acyl-CoA metabolic process
P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid			↓	Fatty acid degradation (Acyl-CoA biosynthesis)
Q3LXA3	Dihydroxyacetone kinase			↓	Glycerol metabolic process
P00505	Aspartate aminotransferase, mitochondrial precursor (GOT2)			↓	Amino acid metabolism (aspartate)
P36269	Isoform 2 of Gamma-glutamyltransferase 5 precursor			↓	Amino acid metabolism (Glutathione biosynthesis)
P32754	4-hydroxyphenylpyruvate dioxygenase (HPD)			↓	Amino acid metabolism (Phenylalanine catabolism)
P34896	Isoform 2 of Serine hydroxymethyltransferase, cytosolic			↓	Amino acid metabolism (Serine catabolism)
P21549	Serine-pyruvate aminotransferase			↓	Amino acid metabolism (forms pyruvate)
P24298	Alanine aminotransferase 1			↓	Glutamate metabolism / Liver gluconeogenesis

P11586	C-1-tetrahydrofolate synthase, cytoplasmic			↓	Amino acid biosynthesis
P80404	4-aminobutyrate aminotransferase, mitochondrial precursor			↓	Amino acid metabolism
Q93088	Betaine--homocysteine S-methyltransferase 1			↓	Methionine / Homocysteine metabolism
Q00266	S-adenosylmethionine synthetase isoform type-1			↓	Methionine / Selenoamino acid metabolism
P50440	Isoform Cytoplasmic of Glycine amidinotransferase			↓	Urea Cycle (Amino acid metabolism)
P00480	Ornithine carbamoyltransferase, mitochondrial precursor			↓	Urea Cycle (Amino acid metabolism)
P31327	Isoform 1 of Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor			↓	Urea Cycle (Amino acid metabolism)
Q03154	Aminoacylase-1	↓		↓	Urea cycle
P00966	Argininosuccinate synthase			↓	Urea cycle
P05089	Arginase-1	↓	↓	↓	Urea cycle
P30837	Aldehyde dehydrogenase X, mitochondrial precursor			↓	Major role in the detoxification of alcohol-derived acetaldehyde
P05091	Aldehyde dehydrogenase, mitochondrial precursor	↓			Carbohydrate / Cellular alcohol metabolic processes
P22033	Methylmalonyl-CoA mutase, mitochondrial precursor			↓	Degradation of amino acids, odd-chain fatty acids and cholesterol via propionyl-CoA to TCA
Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor			↓	Converts hydroxybutyrate to acetoacetate
P07099	Epoxide hydrolase 1			↓	Biotransformation enzyme that catalyzes the hydrolysis of arene and aliphatic epoxides to less reactive
P38117	Isoform 2 of Electron transfer flavoprotein subunit beta			↓	Electron transport chain, specific electron acceptor for dehydrogenases, (five acyl-CoA dehydrogenases, glutaryl-CoA

P61457	Pterin-4-alpha-carbinolamine dehydratase		⇩	⇩	Tetrahydrobiopterin biosynthesis
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor		⇩		Pentose phosphate shunt
O75891.2	Formyltetrahydrofolate dehydrogenase isoform a variant			⇩	Carbon compound metabolic process
Q15181	Inorganic pyrophosphatase	⇧			Phosphate metabolic process
Q14117	Dihydropyrimidinase			⇩	Catalyzes the second step of the reductive pyrimidine degradation.
P07327	Alcohol dehydrogenase 1A			⇩	Cellular alcohol metabolic processes
P00325	Alcohol dehydrogenase 1B			⇩	Cellular alcohol metabolic processes
P00326	Alcohol dehydrogenase 1C			⇩	Cellular alcohol metabolic processes
P08319	Alcohol dehydrogenase 4			⇩	Cellular alcohol metabolic processes
P14550	Alcohol dehydrogenase			⇩	Cellular alcohol metabolic processes
P00352	Retinal dehydrogenase 1 (ALDH1A1)	⇩		⇩	Retinol metabolism
Q7Z4W1	L-xylulose reductase			⇩	Participates in the uronate cycle of glucose metabolism.
P04075	Fructose-bisphosphate aldolase A (Muscle)			⇧	Glycolysis
P06733	Alpha-enolase			⇧	Glycolysis
Q53EM5	Transketolase variant (Fragment)		⇧		Pentose phosphate pathway
O60218	*Aldo-keto reductase family 1 member B10*			⇧	Aldehyde metabolic process
P15531	*Nucleoside diphosphate kinase A / Nucleoside diphosphate kinase B*	⇧			Major role in the synthesis of nucleoside triphosphates other than ATP

Metabolic proteins - Detoxification					
P21964	*Isoform Soluble of Catechol O-methyltransferase*			↓	Shortens the biological half-lives of certain neuroactive drugs
P05181	*Cytochrome P450 2E1*			↓	Inactivates a number of drugs and xenobiotics
P50225	*Sulfotransferase 1A1*			↓	Catalyzes the sulfate conjugation of catecholamines, phenolic drugs and neurotransmitters
P16152	*Carbonyl reductase [NADPH] 1*			↓	Catalyzes reduction carbonyl compounds including antitumor anthracycline antibiotics
O00748	*Carboxylesterase 2 isoform 1*			↓	Involved in the detoxification of xenobiotics and in the activation of ester and amide prodrug
O95154	Aflatoxin B1 aldehyde reductase member 3			↓	Protection of liver against the toxic and carcinogenic effects of AFB1, a potent hepatocarcinogen.
P40261	Nicotinamide N-methyltransferase			↓	Important for biotransformation of many drugs and xenobiotic compounds.
Q86WA6	Isoform 1 of Valacyclovir hydrolase precursor			↓	Serine hydrolase that catalyzes the hydrolytic activation of amino acid ester prodrugs of nucleoside analogs
P16662	UDP-glucuronosyltransferase 2B7 precursor			↓	Major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics
P22309	UDP-glucuronosyltransferase 1-1 precursor			↓	Major importance in the conjugation and elimination of potentially toxic xenobiotics
Defense related proteins - Antioxidants					
P04040	*Catalase*	↓		↓	Hydorgen peroxide catabolic process
P00441	*Superoxide dismutase [Cu-Zn]*	↓	↓	↓	Removal of superoxide radicals
P04179	Superoxide dismutase isoform B [Mn]	↓			Removal of superoxide radicals
P30043	*Flavin reductase*		↓	↓	Converts biliverdin to bilirubin (protects from oxidative damage & iron metabolism)

Q93099	*Homogentisate 1,2-dioxygenase*			↓	Oxidation / reduction
P09210	*Glutathione S-transferase A2*			↓	Redox Homeostasis
Q16762	*Thiosulfate sulfurtransferase*		↓	↓	Iron-sulfur complexes
Q99497	*Protein DJ-1*	↓	↓		Sensor for oxidative stress / Positive regulator of androgen receptor-dependent transcription
Q06278	*Aldehyde oxidase (AOX1)*			↓	Oxidation / reduction
Q9NVS9	*Pyridoxine-5'-phosphate oxidase*	↓			Involved in pyridoxamine-phosphate oxidase activity
P30041	*Peroxiredoxin-6*	↓			Involved in redox regulation of the cell
P30039	*Phenazine biosynthesis-like domain-containing protein (MAWD binding protein)*			↓	
P10632	Cytochrome P450 2C8			↓	In liver microsomes, this enzyme is involved in an NADPH-dependent electron transport pathway / Oxidaton Reduction
Defense related proteins - Inflammation response					
P01009	*Alpha-1-antitrypsin precursor*			↑	Acute-phase response. Inhibitor of serine proteases.
P02763	Alpha-1-acid glycoprotein 1 precursor		↑	↑	Appears to function in modulating the activity of the immune system during the acute-phase reaction.
P05164	Myeloperoxidase precursor			↑	It is responsible for microbicidal activity against a wide range of organisms.
P59666	Neutrophil defensin 3 precursor			↑	Defensin 2 and defensin 3 have antibiotic, fungicide and antiviral activities.
P33241	Lymphocyte-specific protein 1			↑	Mediating neutrophil activation / Actin binding protein
P61626	Lysozyme C precursor			↑	Lysozymes have primarily a bacteriolytic function; associated with the monocyte-macrophage system and enhance the activity
P05109	S100A8 Protein S100-A8			↑	Expressed by macrophages in chronic inflammations

P06702	S100A9 Protein S100-A9			⇧	Expressed by macrophages in acutely inflammated tissues and in chronic inflammations / Probable inhibitor of protein kinases
P25815	S100P Protein S100-P			⇧	?
Defense related proteins - Heat Shock Proteins (HSPs)					
P11021	HSPA5 / Glucose regulated protein 78 (GRP78)	⇧			Probably plays a role in facilitating the assembly of multimeric protein complexes inside the ER
P38646	*Stress-70 protein, mitochondrial precursor (GRP75)*	⇧			Implicated in cell proliferation and anti-apoptosis
P08238	*Heat shock protein HSP 90-beta (HSP90B)*			⇧	Molecular chaperone
Q58FF6	Heat shock protein 90Bd			⇧	Putative molecular chaperone
Protein Binding - Iron related					
P02787	*Serotransferrin precursor*	⇩			Iron binding transport protein / Heme degradation
Q86WI9	*Ferritin light chain*		⇩	⇩	Stores iron in a soluble, non-toxic, readily available form. Important for iron homeostasis
P00738	*Haptoglobin precursor*	⇩			Haptoglobin combines with free plasma hemoglobin and protecting the kidneys from damage by hemoglobin
P68871	*Hemoglobin subunit beta*		⇩		Involved in oxygen transport
Q16743	Cytochrome P-450 II C (Fragment)			⇩	Heme / Iron binding
P02790	*Hemopexin precursor*		⇧		Binds heme and transport to liver for breakdown
P02788	Lactotransferrin			⇧	Iron binding and transport/ iron homeostasis
Protein Binding					
P02768	*Serum albumin precursor*	⇩			

P28838	*Cytosol aminopeptidase*			↓	Presumably involved in the processing and regular turnover of intracellular proteins.
P00167	*Isoform 1 of Cytochrome b5*			↓	Membrane bound hemoprotein which function as an electron carrier for several membrane bound oxygenases.
P11712	*Cytochrome P450 2C9*			↓	NADPH-dependent electron transport pathway
P22307	*Sterol carrier protein 2 isoform 2*			↓	Mediates in vitro the transfer of all common phospholipids, cholesterol and gangliosides between membranes
P80297	Metallothionein-1X			↓	Binds to various heavy metals
Q96KP4.2	Cytosolic non-specific dipeptidase			↓	Involves in proteolysis / Zinc ion binding
P61026	RAB10 Ras-related protein Rab-10			↑	Involved in protein transport and vesicular trafficking
Q00610	Isoform 2 of Clathrin heavy chain 1			↑	Intracellular protein transport
P02774	Vitamin D-binding protein precursor (GC globulin)			↑	Multifunctional protein found in plasma, cerebrospinal fluid, urine and cell surfaces. Carries Vit.D sterols in plasma; may prevent
P27348	14-3-3 protein theta (YWHAQ)			↑	Adapter protein implicated in the regulation of a large spectrum of both general and specialized signaling pathway.
P63104	*14-3-3 protein zeta/delta (YWHAZ)*			↑	Adapter protein
P02649	*Apolipoprotein E precursor*			↑	Binding of lipoprotein particles
P62937	*Peptidyl-prolyl cis-trans isomerase A*		↑		Accelerates protein folding
P04080	Cystatin-B			↑	Intracellular liver thiol proteinase inhibitor; binds tightly to reversible inhibitor of cathepsins L, H and B.
O14828	Isoform 2 of Secretory carrier-associated membrane protein 3			↑	Functions in post-Golgi recycling pathways. Acts as a recycling carrier to the cell surface.
P02749	*Beta-2-glycoprotein 1 precursor*		↑		Binds to various kinds of negatively charged substances
P30740	Leukocyte elastase inhibitor (SERPINB1)			↑	Regulates the activity of the neutrophil proteases elastase, cathepsin G, proteinase-3, chymase, chymotrypsin, and kallikrein

O15260	Surfeit 4			↑	Endoplasmic reticulum membrane; multi-pass membrane protein
Nucleic Acid Binding Proteins					
P52758	*Ribonuclease UK114*			↓	Endoribonuclease responsible for the inhibition of the translation by cleaving mRNA
Q96AE4	*Far upstream element-binding protein 1 (FUBP1)*	↑			Regulates MYC expression by binding to a single-stranded far-upstream element (FUSE)
Q92945	KH-type splicing regulatory protein (FUBP2)	↑			Regulates MYC expression by binding to a single-stranded far-upstream element (FUSE)
P62828	RAN 26 kDa protein			↑	Required for the import of protein into the nucleus and also for RNA export / Involved in chromatin condensation and control of
P68105	Elongation factor 1-alpha (EF-Tu)			↑	This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis
P19338	Isoform 1 of Nucleolin			↑	Major nucleolar protein, induces chromatin decondensation by binding to histone H1
P55209	Nucleosome assembly protein 1 like 1 (NAP1L1)			↑	May be involved in modulating chromatin formation and contribute to regulation of cell proliferation.
P05455	*Lupus La protein*		↑		Plays a role in the transcription of RNA polymerase III
Q08211	ATP-dependent RNA helicase A			↑	Transcriptional activator (Unwinds double-stranded DNA and RNA in a 3' to 5' direction).
Q9Y5S9	Isoform 2 of RNA-binding protein 8A			↑	Part of a post-splicing multiprotein complex involved in both mRNA nuclear export and mRNA surveillance.
Q13185	Chromobox protein homolog 3		↑		Seems to be involved in transcriptional silencing in heterochromatin-like complexes.
P23246	Isoform Long of Splicing factor, proline- and glutamine-rich			↑	mRNA processing ; DNA binding and repair protein
P78527	Isoform 2 of DNA-dependent protein kinase catalytic subunit			↑	DNA recombination / Double stranded break repair
Q59F68	CD68 antigen variant			↑	Nucleic acid binding
P09651	*Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1*			↑	Involved in the packaging of pre-mRNA into hnRNP particles

P51991	Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3			⇧	Plays a role in cytoplasmic trafficking of RNA and pre-mRNA splicing.
P31943	Heterogeneous nuclear ribonucleoprotein H1			⇧	Involves in processing events that pre-mRNAs undergo before becoming functional, translatable mRNAs in the cytoplasm.
P52272	Isoform 2 of Heterogeneous nuclear ribonucleoprotein M			⇧	Plays a role in pre-mRNA splicing.
O60506	Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q		⇧		Binds to mRNA and has high affinity for scaffold-attached region DNA.
Q00839	Heterogeneous nuclear ribonucleoprotein U isoform a			⇧	Plays a role in pre-mRNA splicing and processing
Cytoskeletal modelling / Cell Motility					
P05787	Keratin, type II cytoskeletal 8			⇩	Involved in cytoskeletal organization / Known to interact with HCV core protein
Q5XKE5	Keratin, type II cytoskeletal 79 (K6L)			⇩	Expressed in skeletal muscle, skin and scalp.
P02452	Collagen alpha-1(I) chain precursor			⇩	Collagen fibril organization / Blood vessel development
P12109	Collagen alpha-1(VI) chain precursor			⇩	Cell adhesion protein
P47756	F-actin-capping protein subunit beta (CAPZB)			⇧	Binds in a Ca2+-independent manner to the fast growing ends of actin filaments thereby blocking the exchange of subunits at
P29966	Myristoylated alanine-rich C-kinase substrate (MARCKS)			⇧	Most prominent cellular substrate for protein kinase C, binds calmodulin, actin, and synapsin / A filamentous (F) actin cross-
P13796	Plastin-2			⇧	Actin-binding protein found in intestinal microvilli
Q01518	Adenylyl cyclase-associated protein			⇧	Directly regulates filament dynamics / Actin binding
P07437	*Tubulin beta chain*			⇧	Major constituent of microtubules
Q6P9V9	Tubulin alpha-1B chain			⇧	Major constituent of microtubules
Q13885	Tubulin beta-2A chain			⇧	Major constituent of microtubules

P68371	*Tubulin beta-2C chain*			⇧	Major constituent of microtubules
Q13509	Tubulin beta-3 chain			⇧	Major constituent of microtubules
Fibrin formation					
P30086	*Phosphatidylethanolamine-binding protein 1*	⇩		⇩	Serine protease inhibitor which inhibits thrombin
P05783	*Keratin, type I cytoskeletal 18*			⇩	Involved in the uptake of thrombin-antithrombin complexes by hepatic cells / cell proliferation inducing gene
P02675	*Fibrinogen beta chain precursor*			⇧	Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
P08758	*Annexin A5*			⇧	Anticoagulant protein that acts as an indirect inhibitor of the thromboplastin-specific complex, which is involved in the blood
P02679	Isoform Gamma-A of Fibrinogen gamma chain precursor			⇧	Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
Others					
Q9H0W9	*Ester hydrolase*	⇩			
Q8WY24	SNC66 protein		⇧		Ig-like? (down in CRC)
Q6PI81	IGHM IGHM protein		⇧		
Q6NWZ1	CKAP4 protein (Fragment)			⇧	
A6NBZ8	*Putative uncharacterized Albumin*		⇧		?

4.2.1 Summary of proteins identified

The total number of regulated proteins that were identified in moderately and poorly differentiated HCC tissues are summarized in Table 4.3. The use of the same samples in all techniques enabled direct comparisons between the methods with respect to their sensitivity in identifying the differentially expressed proteins. It is observed that iTRAQ is the most sensitive method identifying a total of 241 proteins. While cICAT, appears to be as sensitive as 2-D DIGE detected a total of 81 and 80 differentially expressed proteins respectively (Table 4.3). It should be noted that a third of the proteins identified by 2-D DIGE were protein isoforms arising from post-translational modification.

Table 4.3 : Total number of proteins identified from each technique.

Analysis Used		Total number of proteins	Moderately Differentiated HCC	Poorly Differentiated HCC
2-D DIGE	**No. of spots selected**	**119**	79	40
	No. of proteins identified (excl. isoforms)	**80**	54	26
cICAT	**No. of proteins identified**	**81**	57	24
iTRAQ	**No. of proteins identified**	**241**	90	151

4.2.2 Common proteins identified in different techniques

A Venn diagram is used to illustrate the type of proteins identified in both 2-D gel based and stable isotope labelling based techniques. Note that proteins that were identified as multiple spots in 2-D DIGE; possibly due to post translational modificationd or isoforms are represented as a single identification. In moderately-differentiated HCC, 30 out of 201 proteins were common in at least 2 techniques and only 8 proteins are common in all 3 techniques. Similarly in poorly-differentiated HCC only a small subset of proteins were identified in more than 1 technique (13 out of 201 proteins were common in at least 2 techniques with only 4 proteins identified in all techniques). This therefore results in a total of 344 proteins identified as differentially expressed in this study.

All overlapping proteins except two were regulated in the same direction (either over-expressed or down-regulated). These were heat shock protein β1 (HSPβ1) and heterogeneous nuclear ribonucleoproteins A2/B1 (HNRNP A2/B1), which were identified as down-regulated in 2-D DIGE but up-regulated in iTRAQ. The difference observed in the regulation level of these proteins can be attributed to the possible presence of different isoforms of the protein such as mature/processed forms or protein fragments.

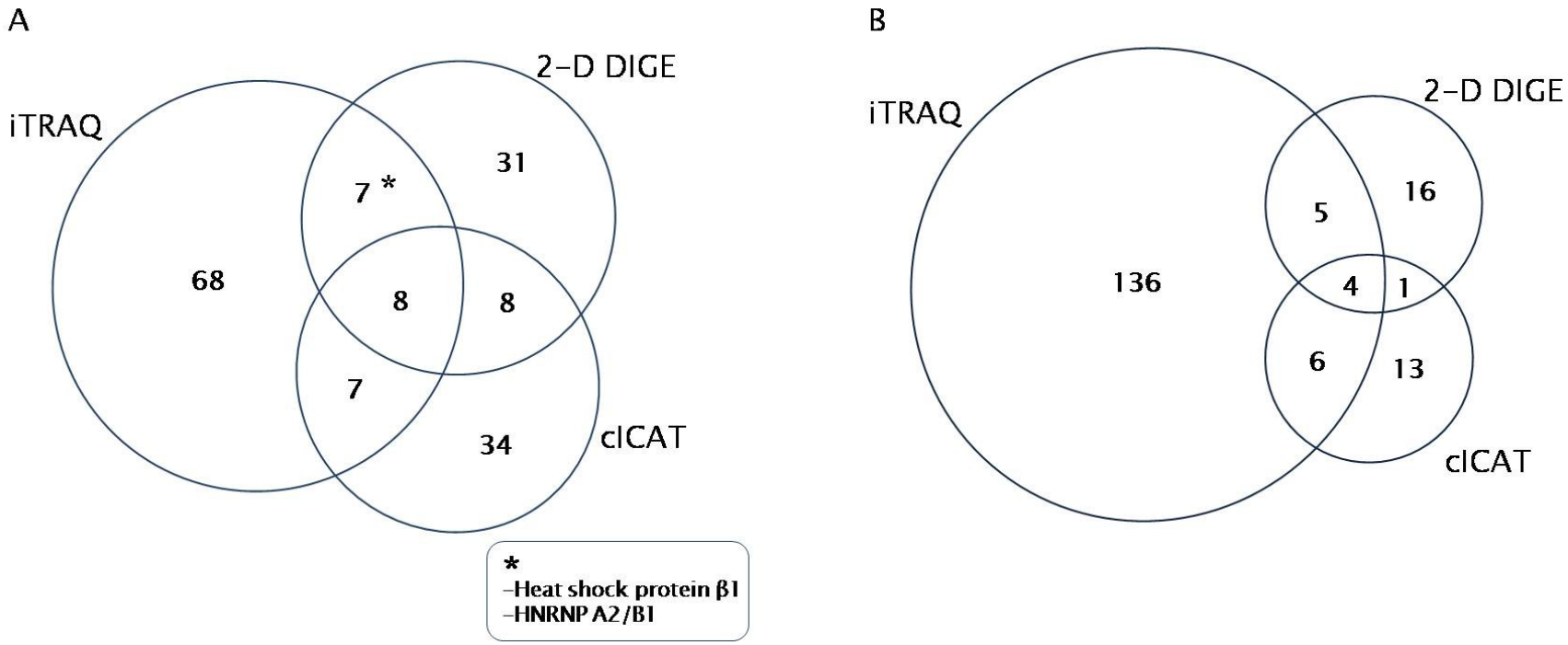


Figure 4.5 : Venn diagram of proteins identified from 2-D DIGE, cICAT and iTRAQ approaches in (A) moderately differentiated HCC and (B) poorly differentiated HCC. * denotes the presence of additional 2 proteins identified in 2-D DIGE and iTRAQ techniques but are differentially regulated

4.3 Protein physiochemical and biological properties

Disparity in proteins identified was expected as it is known that each method has its inherent biasness and limitations. In order to better portray these differences, we classified all the proteins identified by each technique according to several physiochemical properties. These include molecular weights, isoelectric points, total number of cysteines and protein hydrophobicity. Proteins were also grouped according to the cellular localization and biological function as described by Gene Ontology (GO) consortium. For ease of analysis, proteins identified in moderately- and poorly-differentiated HCC were classified together.

4.3.1 Molecular weight and Isoelectric point

Theoretical molecular weight and isoelectric point (pI) were obtained from SwissProt database. The molecular weight and pI of the regulated proteins are represented in the scatter plot (Fig. 4.6). All the proteins identified by 2-D DIGE are in the molecular mass range of 12 kDa to 82 kDa. In cICAT technique, the majority of the proteins identified were also smaller than 100 kDa with the exception of one protein, fibronectin precursor (Accession No.: P02751, MW of 221 kDa). Proteins identified via iTRAQ labels have a wider coverage with an estimate of 10% of the proteins having molecular masses being greater than 100 kDa. The largest protein identified is DNA-dependent protein kinase (Accession No.: P78527) with a theoretical molecular mass of 508 kDa.

The proteins identified by 2-D DIGE and cICAT are clustered at the pI range of 5 – 9. The majority of the 2-D DIGE proteins are located in the pI 6 – 7 region which is most expanded in a non-linear IPG strip. In addition, basic proteins were under-represented by 2-D

DIGE in comparison to cICAT and iTRAQ methods. Lastly, the proteins identified by the iTRAQ technique have a slightly wider pI range of 4.5 – 10. This is advantageous as it enables the technique to identify proteins with extreme pI that are often missed in 2-D gel based techniques.

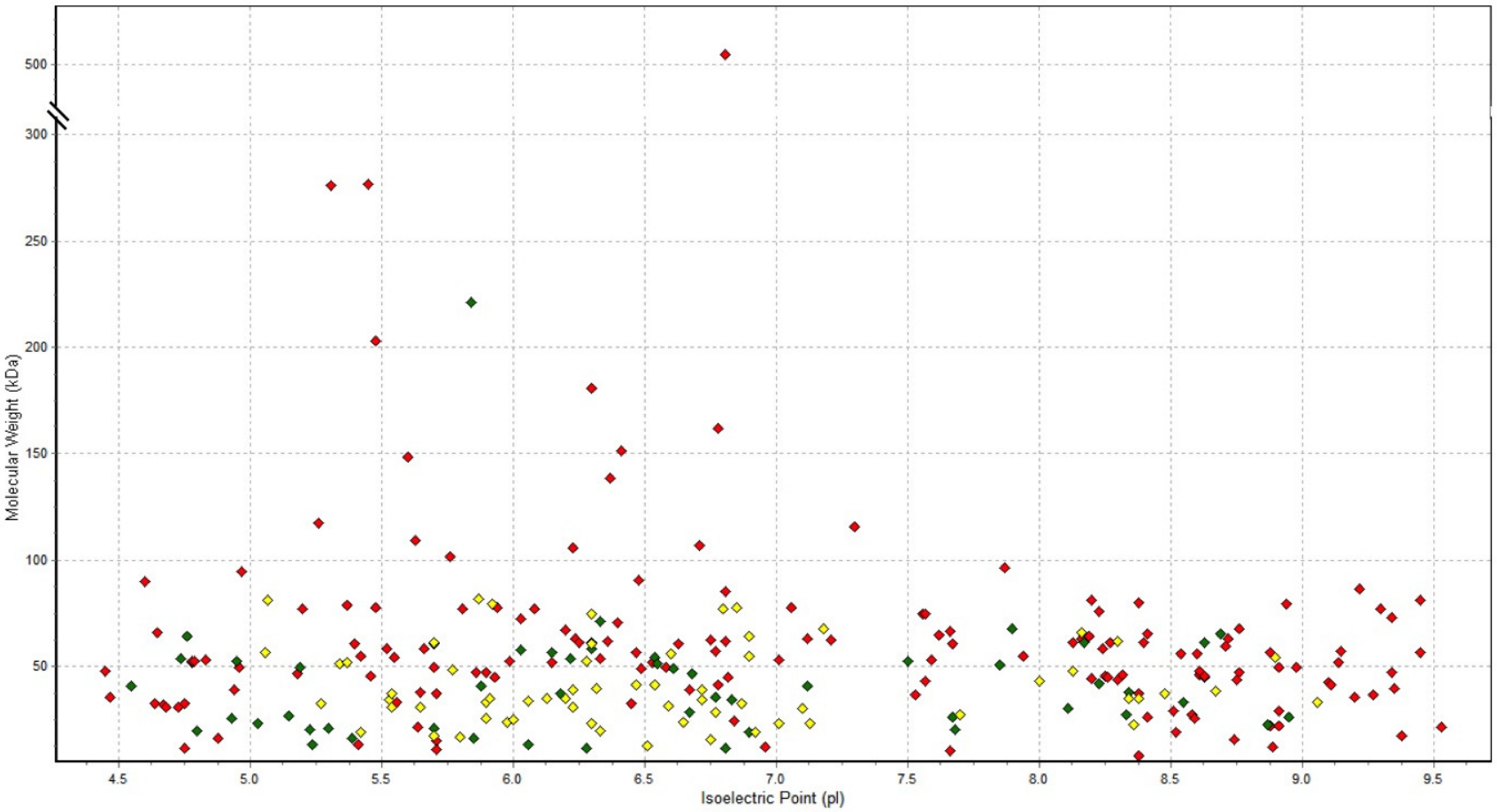


Figure 4.6 : Scatter plot of molecular weight (kDa) and isoelectric point (pI) of all the proteins identified by (A) 2-D DIGE; yellow, (B) cICAT; green and (C) iTRAQ ; red.

4.3.2 Hydrophobicity plot

The extent of hydrophobicity is obtained from the general average hydropathicity (GRAVY) score obtained from ProtParam Tool. GRAVY score is calculated as the mean of the sum of the hydropathic indices of amino acids. According to Kyte and Doolittle (1982), integral membrane proteins typically have higher GRAVY scores than globular proteins. This score however is not able to reliably predict the structure without the help of hydropathy plots.

The GRAVY scores of all the proteins identified are represented in histograms in Fig. 4.7. Bars in darker grey hue indicate possible hydrophobic proteins. Interestingly, the GRAVY score of proteins identified by 2-D DIGE are in the range of -0.9 to 0.2 (with 11% having positive scores) and a similar coverage from -1.0 to 0.3 were observed in the cICAT and iTRAQ methods (with only an average of 10% of the proteins had positive scores). Proteins identified with positive GRAVY scores include membrane proteins such as a peripheral membrane protein, L-xylulose reductase (Accession No: Q7Z4W1) and a multi-pass membrane protein, Transmembrane protein 205 (Accession No.: Q6UW68) identified via cICAT and iTRAQ respectively. However, in general all the 3 methods seemed to show under representation of hydrophobic proteins.

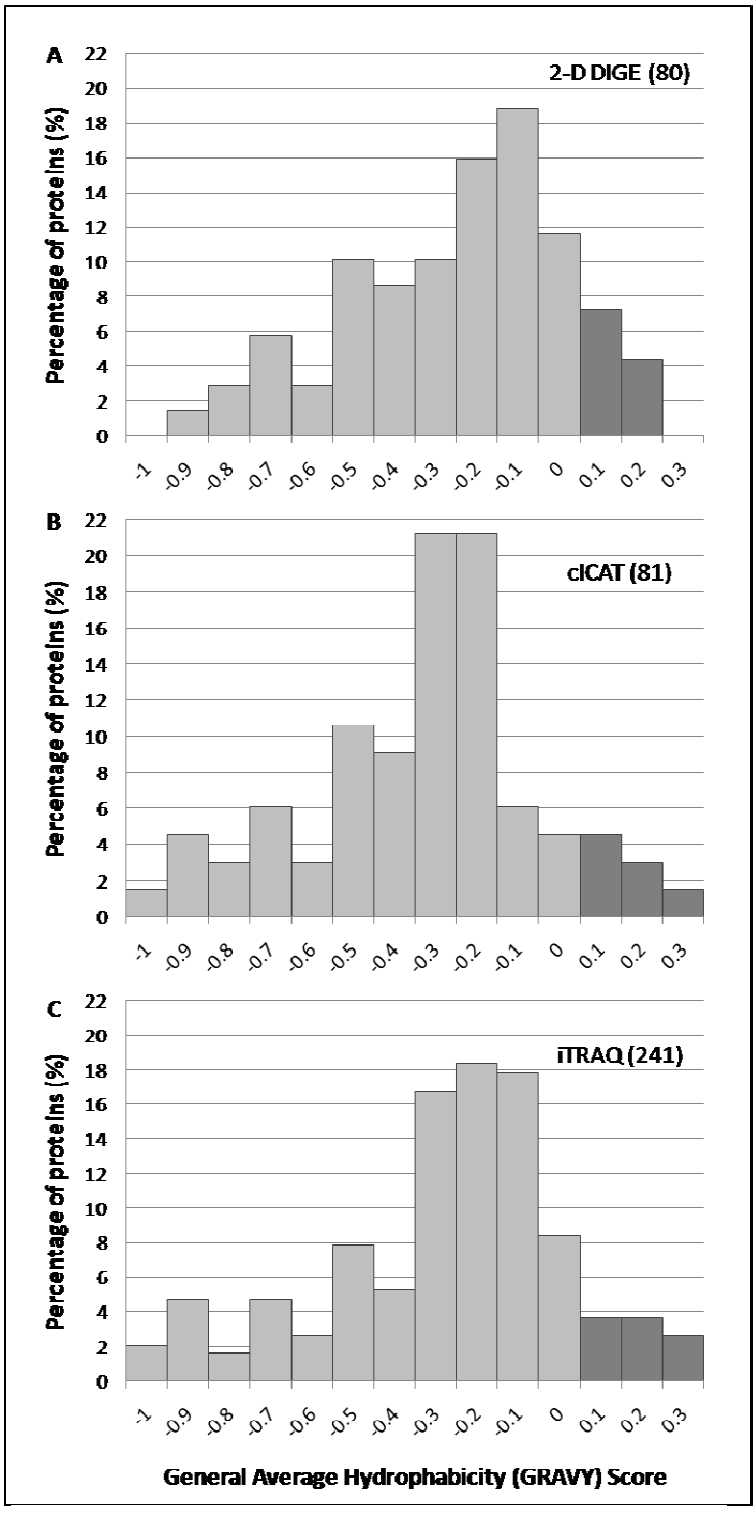


Figure 4.7 : Plots of the GRAVY values of all the proteins identified via (A) 2-D DIGE, (B) cICAT (C) iTRAQ. Bars in darker grey hue indicate proteins with positive GRAVY scores. The numbers in brackets indicate the total number of proteins identified by each technique.

4.3.3 Localization and biological functions

The cellular localization and biological functions of these dysregulated proteins as obtained from Gene Ontology (http://www.geneontology.org/) were shown in Figs. 4.8. Interestingly, there are no differences between the cellular localization and functions of proteins identified by the 3 methods. In all approaches, an average of 50% of the proteins identified in all the different techniques is localized in the cytoplasm. The majority of them were identified as metabolic proteins followed by binding proteins.

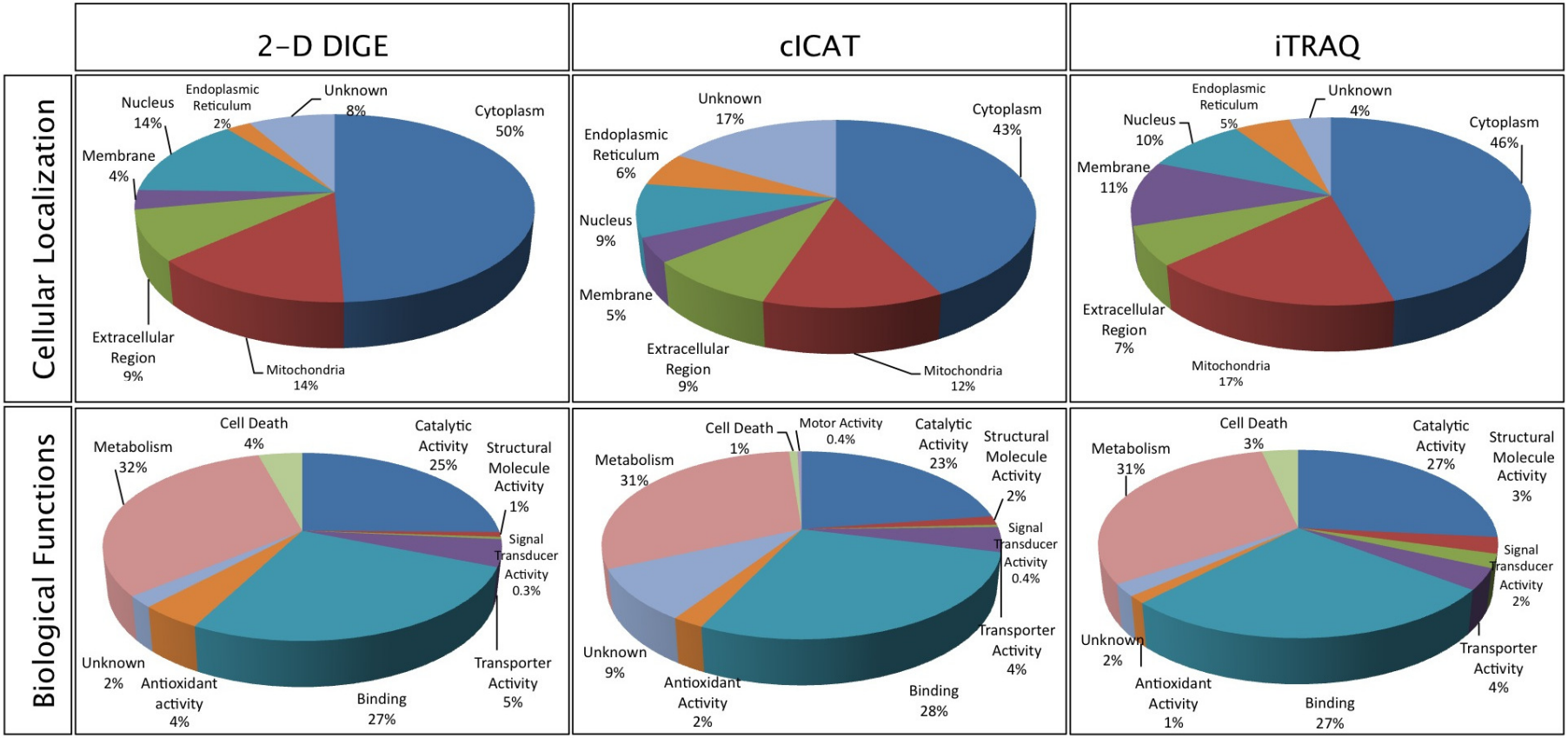


Figure 4.8 : Distribution of the identified proteins according to (A) cellular localization and (B) biological functions based on GO consortium. (A) moderately-differentiated HCC tissues and (B) poorly-differentiated HCC tissues

4.3 Biological functions of regulated proteins

Regardless of the technique used for separation and identification, the differentially expressed proteins were subsequently analyzed based on differentiation status : *viz*, moderately and poorly differentiated HCC. A total of 85 common proteins were found to be regulated in both HCC stages (Fig. 4.9). These proteins are listed in italics in Table 4.1 and 4.2. The 3 major groups of proteins that are affected include those that are involved in metabolic and catalytic activities and binding (Fig 4.10). A significant portion (>30%) proteins being affected are those involved in energy metabolism.

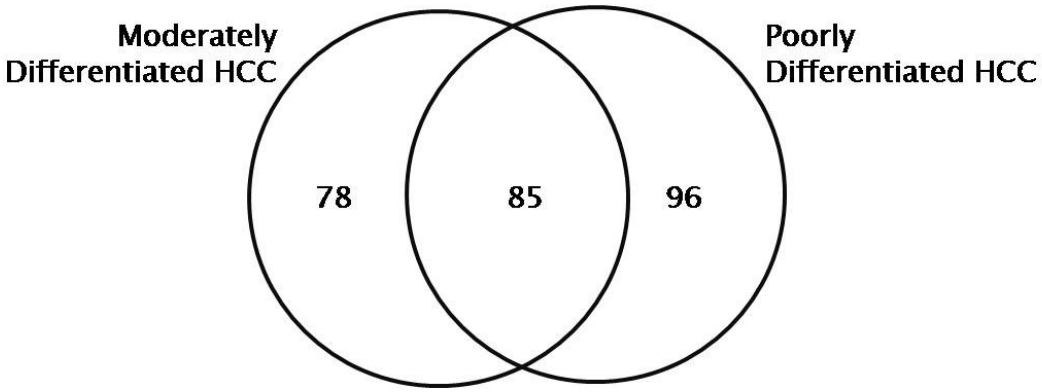


Figure 4.9 : Distribution of the moderately and poorly differentiated proteins. (Proteins that were identified in more than one technique or with multi-isoforms are counted as a single / unique protein)

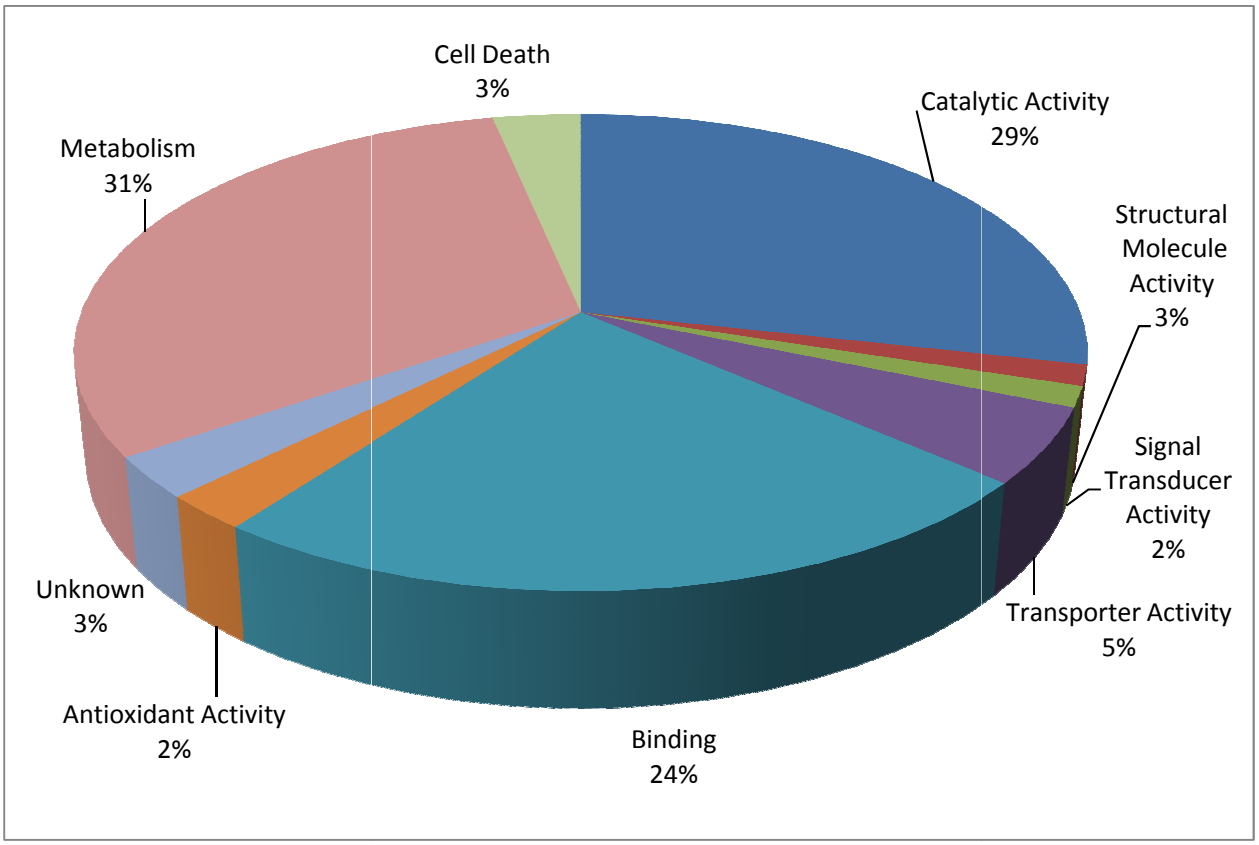


Figure 4.10 : Distribution of the biological functions of the common dysregulated proteins from moderately- and poorly-differentiated HCC.

Selected proteins of interests from Table 4.1 and 4.2 are represented as stacked bar charts according to their biological functions as annotated by KEGG and Gene Ontology (Fig. 4.11). These consist of mainly enzymes involved in amino acid metabolism (e.g. arginase), glucose catabolism (e.g. fumarate hydratase) and fatty acid β-oxidation (e.g. enoyl-CoA hydratase). Down-regulation of these proteins had also been reported earlier by various gene and protein profiling studies of HCC.

These groups of proteins were selected based on their importance with respect to proper maintenance of liver function and tumourigenesis. Proteins that are over-expressed include inflammation response, heat shock proteins, cell motility and nuclear proteins. The functions of these proteins are elaborated in later section of the thesis.

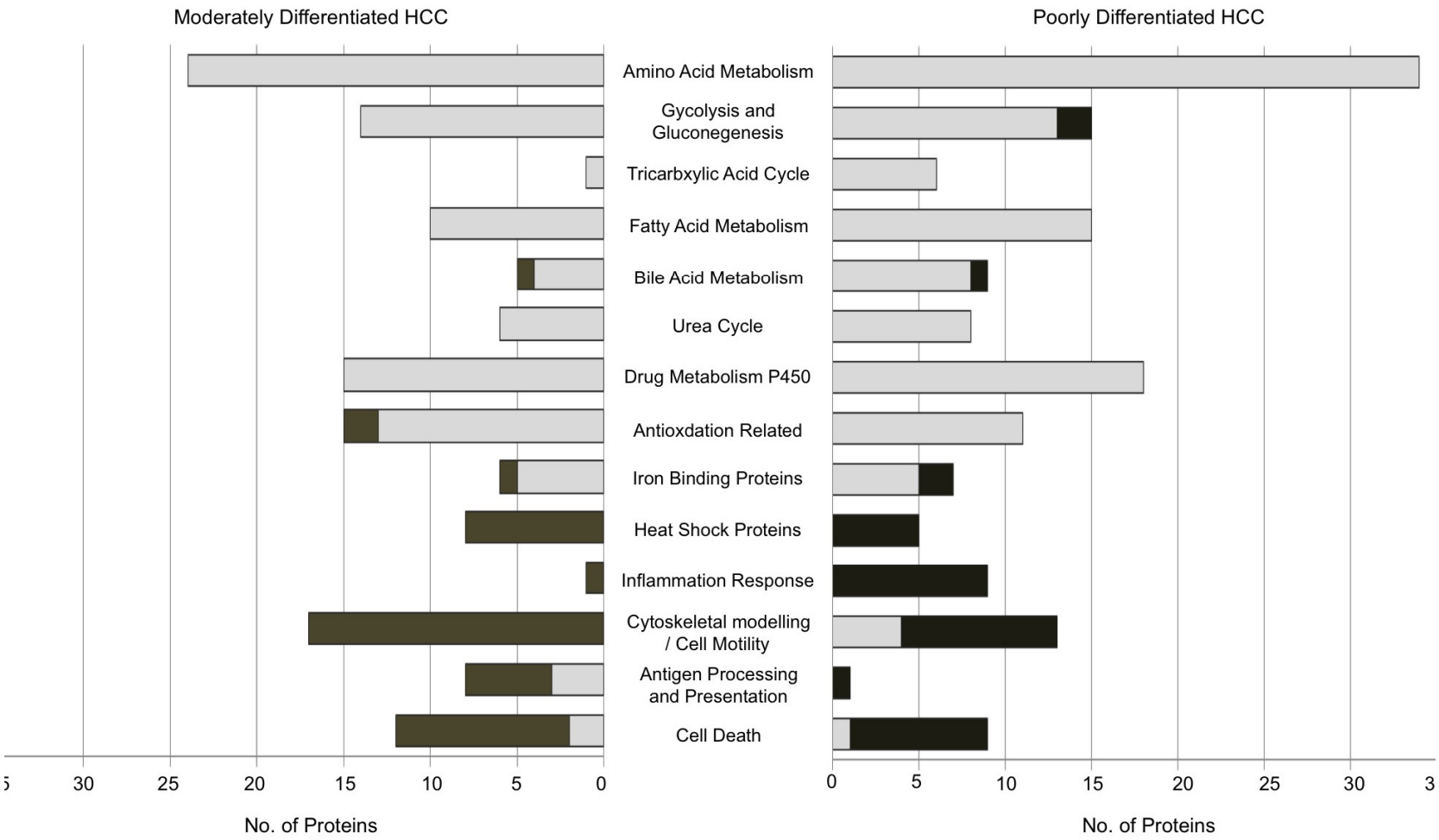


Figure 4.11 : Distribution of selected moderately and poorly differentiated proteins according to KEGG and Gene Ontology biological functions. (Grey bars represent total number of proteins that are down-regulated; Black bars represent total number of proteins that are up-regulated proteins.)

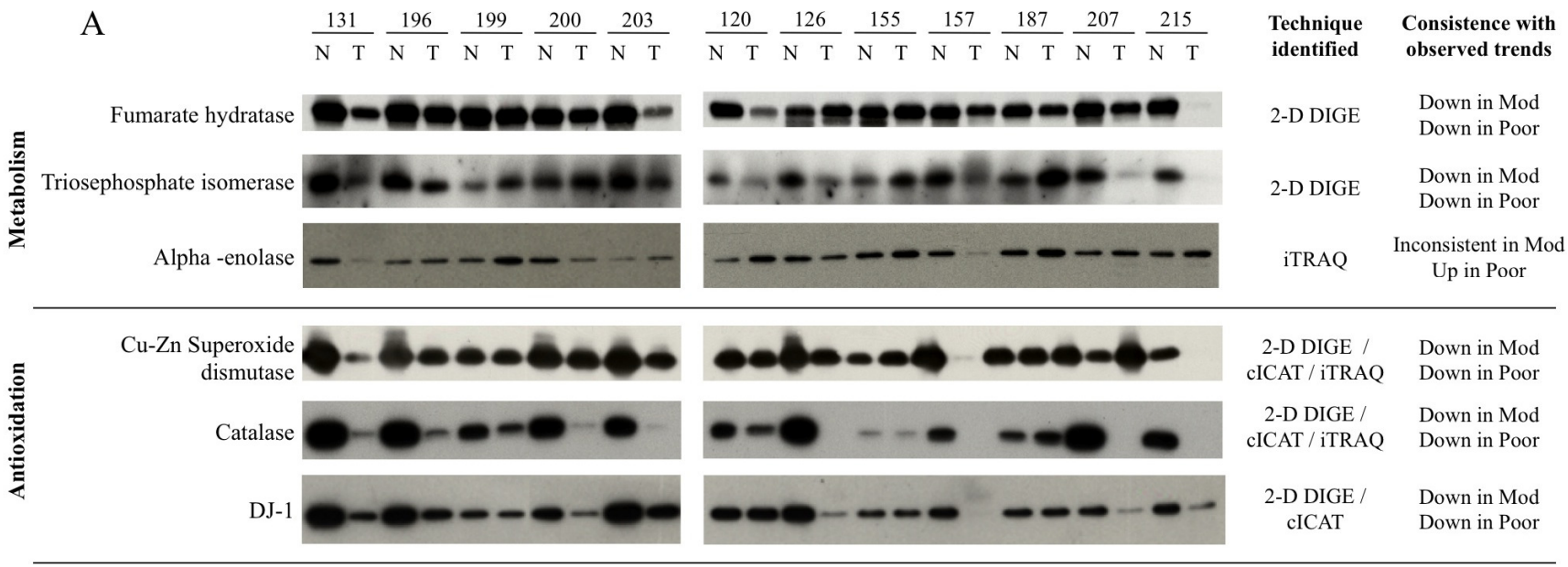
4.4 Verification of protein regulation

4.4.1 Western blotting

A group of proteins were further selected for western blot verification using commercially available antibodies. All 12 pairs of samples used in this study, were separated via 1- or 2-dimensional SDS-PAGE and probed for the respective antibodies. The concentration of the antibodies used and duration of exposure was listed in Table 3.4. This verification was carried out to confirm the identification and, most importantly, the regulation level of the proteins as identified from the each technique.

As illustrated in Fig. 4.12 and 4.13, a selected group of proteins identified from the different techniques (5 proteins from 2-D DIGE; 1 protein from cICAT; 5 proteins from iTRAQ; 3 proteins were identified by multiple techniques) were selected for verification. A protein was determined as regulated by comparing its expression level between tumour and its paired non-tumour. The extent of regulation between a pair of tumour and its non-tumour sample was also observed to vary across the different pairs of tissues. All the proteins verified using western blots confirmed the regulation level as that observed in the proteomic screening.

Actin and GAPDH (Fig. 4.12 C) were also immunoblot as controls to ensure equal loading of proteins. These common housekeeping proteins were also observed to be regulated and vary extensively across the patient samples. The limitations of using housekeeping proteins as normalizations of protein samples in western blotting had also been discussed by Ferguson *et al.,* (2005). Hence, in this study silver colloidal stains of the PVDF membranes were used instead to confirm equal loading of protein samples (Fig. 4.14).


A
131 196 199 200 203 120 126 155 157 187 207 215
N T N T N T N T N T N T N T N T N T N T N T N T
Technique identified
Consistence with observed trends
Metabolism
Fumarate hydratase
2-D DIGE
Down in Mod
Down in Poor
Triosephosphate isomerase
2-D DIGE
Down in Mod
Down in Poor
Alpha -enolase
iTRAQ
Inconsistent in Mod
Up in Poor
Antioxidation
Cu-Zn Superoxide dismutase
2-D DIGE / cICAT / iTRAQ
Down in Mod
Down in Poor
Catalase
2-D DIGE / cICAT / iTRAQ
Down in Mod
Down in Poor
DJ-1
2-D DIGE / cICAT
Down in Mod
Down in Poor

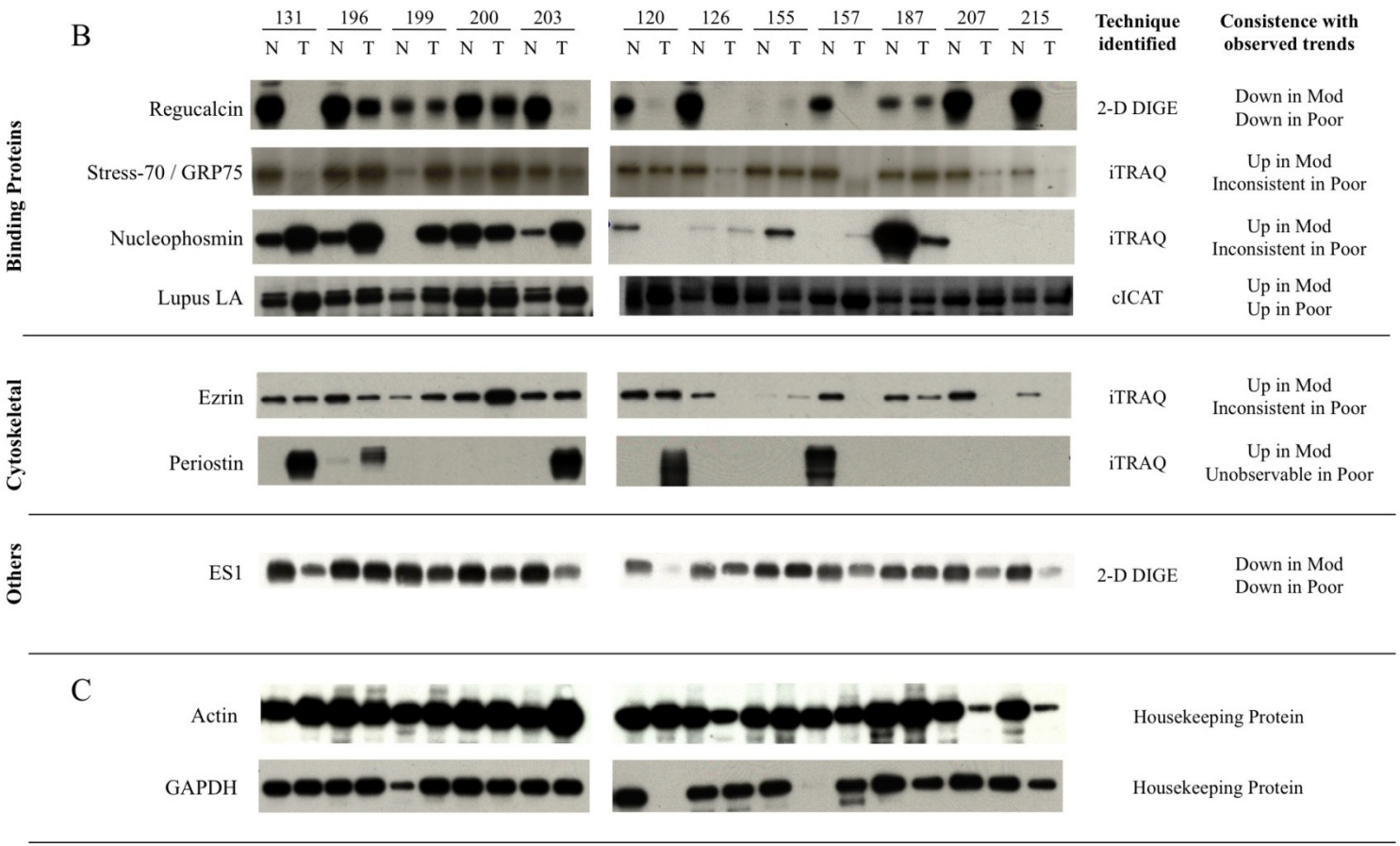


Figure 4.12 : Verification of selected proteins using 1D western blot; (A) down-regulated proteins, (B) up-regulated proteins and (C) housekeeping proteins. (N: non-tumour, T: tumour)

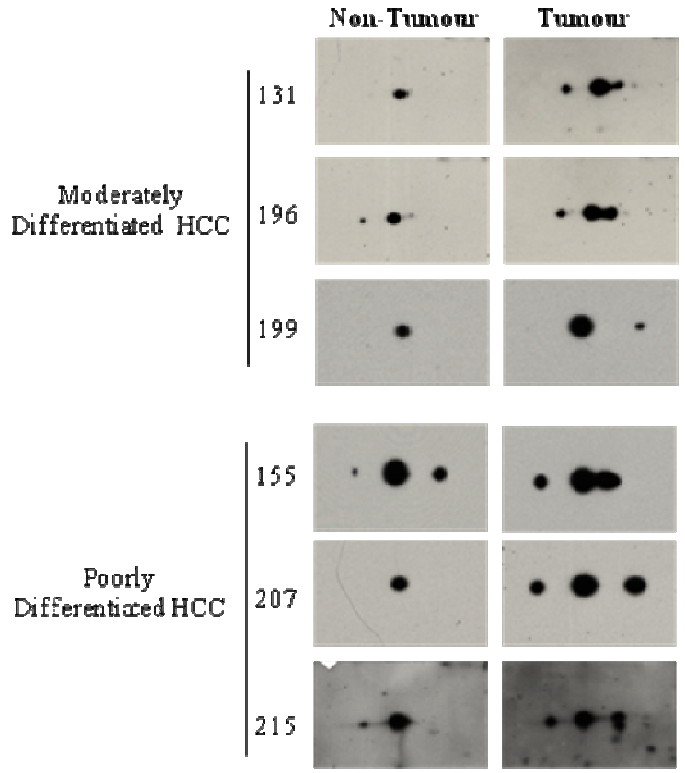


Figure 4.13 : Western blot images of nucleotide diphosphate kinase A (NDKA) of 6 representative tissues for moderately- and poorly-differentiated HCC tissue lysates. (N: non-tumour, T: tumour)

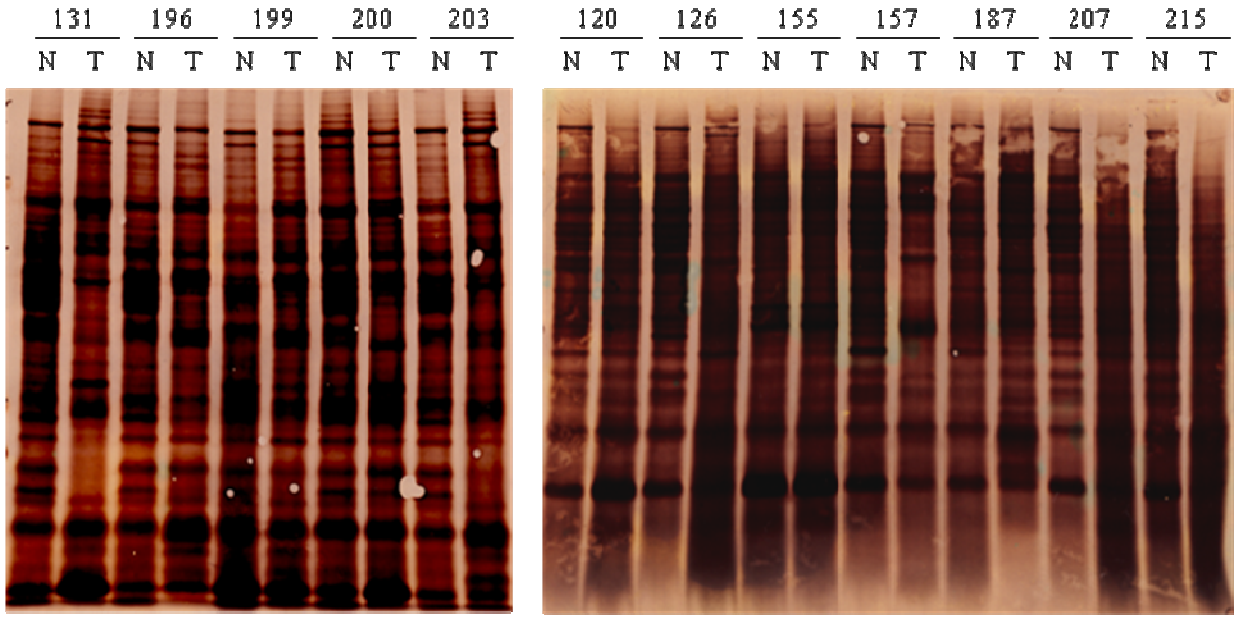


Figure 4.14 : Silver colloidal membrane of 1D western blots representative. (N: non-tumour, T: tumour)

4.4.2 Over expression of FUSE binding protein (FUBP)

Over-expression of protein spots from two members in the far upstream binding protein (FUBP) family[1] [FUBP1 and FUBP2 (KHSRP)[2]] were identified from 2-D DIGE / MS-MS analysis. Three over-expressed protein spots were identified as FUBP1 in moderately-differentiated HCC tissues. These protein spots (# 977, # 985 and # 992) have experimental pIs of 6.7, 6.9 and 7.2 and molecular mass of 83 kDa (Fig. 4.15 A). In poorly differentiated HCC samples, two of the FUBP1 protein spots (# 882 and # 895) with a experimental pIs of 6.9 and 7.2 were observed to be significantly over expressed. In addition, 2 over-expressed protein spots corresponding to FUBP2 (# 681 and # 694) with experimental pIs 6.6 and 6.9 and with a molecular mass of 94 kDa were also observed in patients with poorly differentiated tumours (Fig. 4.15 B). Table 4.4 summarizes the average ratio and frequency of occurrences of these FUBP protein spots in the tissue samples as obtained by DeCyder analysis.

[1] Far upstream binding protein (FUBP) is also reported in literature as FUSE binding protein, FBP and FABP.

[2] FUBP2 is also known as KH-splicing regulatory protein (KHSRP).

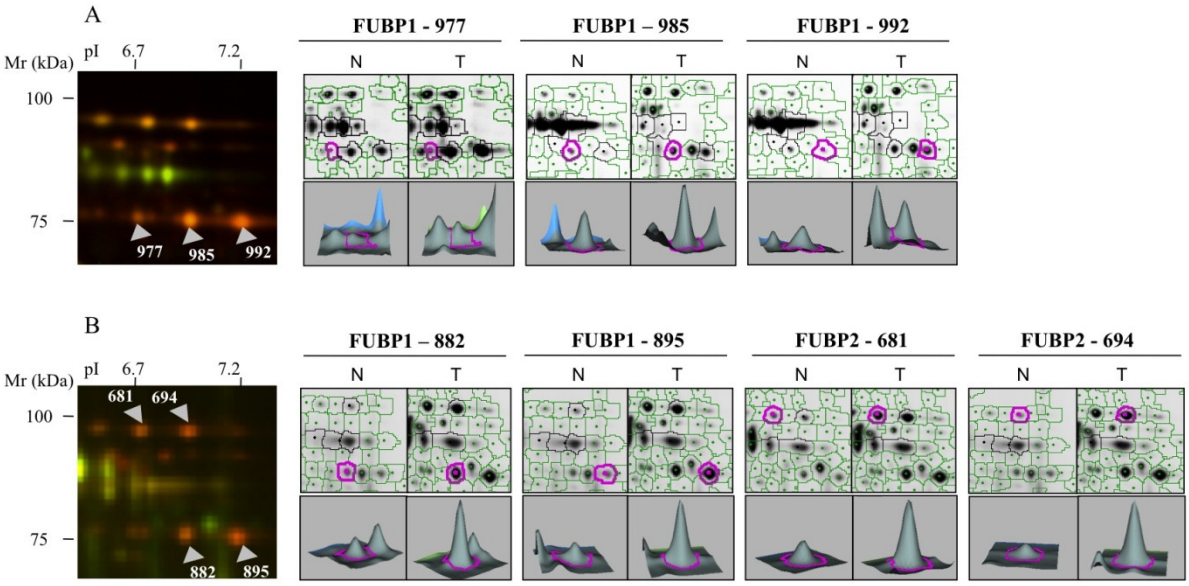


Figure 4.15 : Representative image of ImageQuant and DeCyder analysis of (A) moderately-differentiated HCC – 3 protein spots of FUBP1 977, 985 and 992 with average ratios of 3.65, 1.60 and 1.99 respectively, (B) poorly-differentiated HCC – FUBP1 882 and 895 with average ratio of 1.68 and 1.90; FUBP2 681 and 694 with average ratios of 1.86 and 2.34. (N: non-tumour, T: tumour ; Image view and 3-D view obtained from DeCyder)

4.4.2.1 Mass spectra of FUSE binding protein (FUBP)

The mass spectra of the tryptic digests of FUBP1 and FUBP2 are shown in Figs. 4.16 A and 4.16 C. It can clearly distinguish the 2 FUBP isoforms. This was further confirmed and supported by the MS/MS analysis of one of the peptides from each of the isoforms selected for fragmentation (Figs. 4.16 B and 4.16 D).

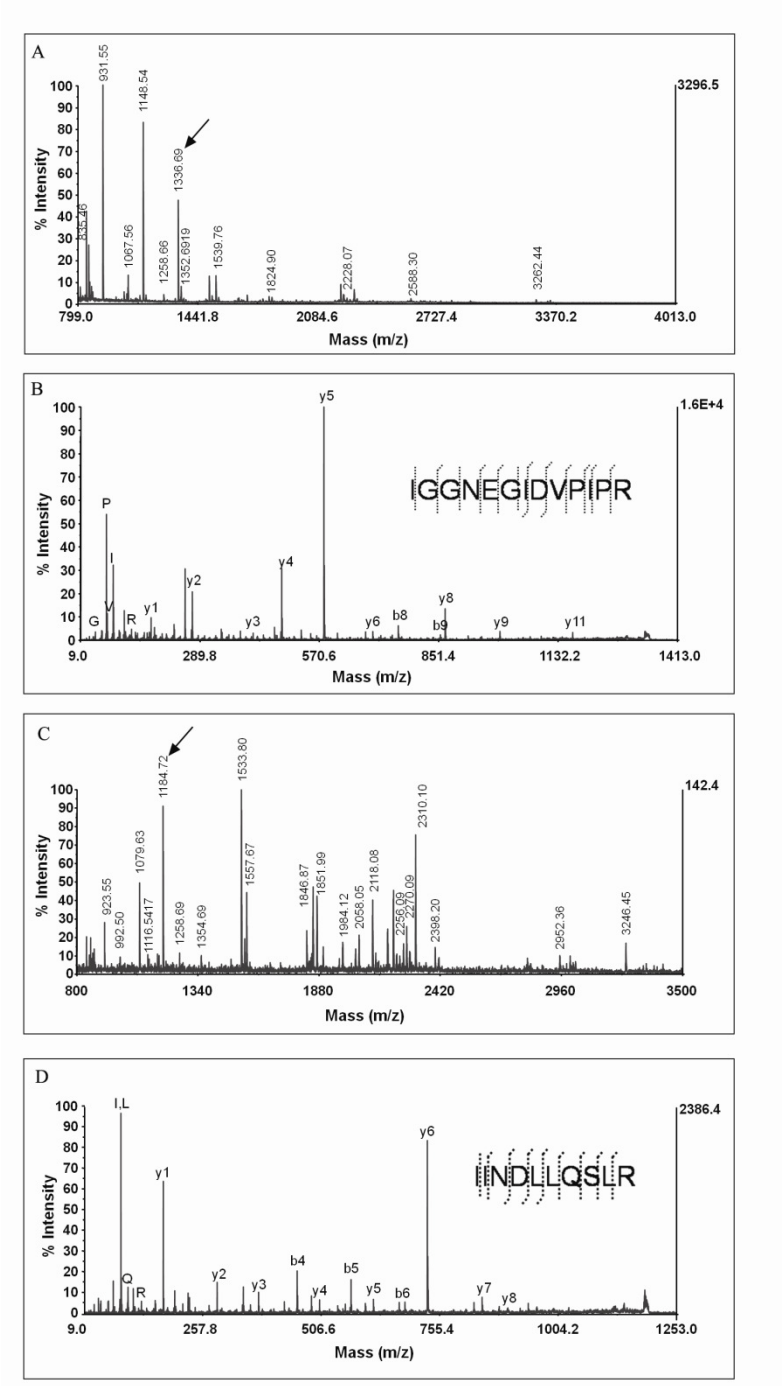


Figure 4.16 : Representative mass spectra of FUBP1 and FUBP2 analyzed by MALDI-TOF/TOF MS upon tryptic digestion. (A) MS spectrum with tryptic peptides of FUBP1; arrow indicates ion at *m/z* = 1336.70 selected for MS/MS (B) MS/MS spectrum of the peptide IGGNEGIDVPIPR (m/z = 1336.69), where y- and b-ions are denoted along with immonium ions (G, glycine; P, proline; V, valine; I, isoleucine; R, arginine); y- and b-fragmentations are also indicated with tilted dotted lines above and below the sequence, respectively. (C) MS

spectrum with tryptic peptides of FUBP2; arrow indicates ion at m/z 1184.72 selected for MS/MS and (D) MS/MS spectrum of the peptide IINDLLQSLR (m/z = 1184.72), where y- and b-ions are denoted along with immonium ions (I, isoleucine; L, leucine; Q, glutamine; R, arginine); y- and b-fragmentations are also indicated with tilted dotted lines above and below the sequence, respectively.

Table 4.4 : Summary of FUBP1 and FUBP2 protein spots based on DeCyder analysis.

Master No.	Swissprot No.	Protein Name	Theoretical M_r /pI	Experimental M_r /pI	Av. Ratio	T-test	Freq+
Moderately differentiated HCC							
977	Q96AE4	**Far upstream element-binding protein 1** FUBP1	67.6 / 7.2	83.3 / 6.7	3.65	3.90E-08	5 / 5
985	Q96AE4	**Far upstream element-binding protein 1** FUBP1	67.6 / 7.2	83.3 / 6.9	1.60	0.0018	3 / 5
992	Q96AE4	**Far upstream element-binding protein 1** FUBP1	67.6 / 7.2	83.3 / 7.2	1.99	8.30E-05	4 / 5
Poorly differentiated HCC							
882	Q96AE4	**Far upstream element-binding protein 1** FUBP1	67.6 / 7.2	84.6 / 6.9	1.68	0.035	4 / 7
895	Q96AE4	**Far upstream element-binding protein 1** FUBP1	67.6 / 7.2	83.3 / 7.2	1.90	6.00E-04	5 / 7
681	Q92945	**Far upstream element-binding protein 2** FUBP2, KHSRP	73.1 / 6.8	94.4 / 6.6	1.86	0.024	5 / 7
694	Q92945	**Far upstream element-binding protein 2** FUBP2, KHSRP	73.1 / 6.8	94.0 / 6.9	2.34	0.0052	5 / 7

+ Frequency denotes the number of paired samples in which the spot has same alteration

4.4.2.2 Over expression of FUSE binding protein (FUBP)

To confirm the 2-D DIGE results, FUBP1 and FUBP2 were validated in 6 individual tissue samples using western blots. As shown in Fig. 4.17, both moderately- and poorly-differentiated HCC tumour tissues showed over-expression of FUBP1 and FUBP2 in all of the 6 tumour tissue lysates.

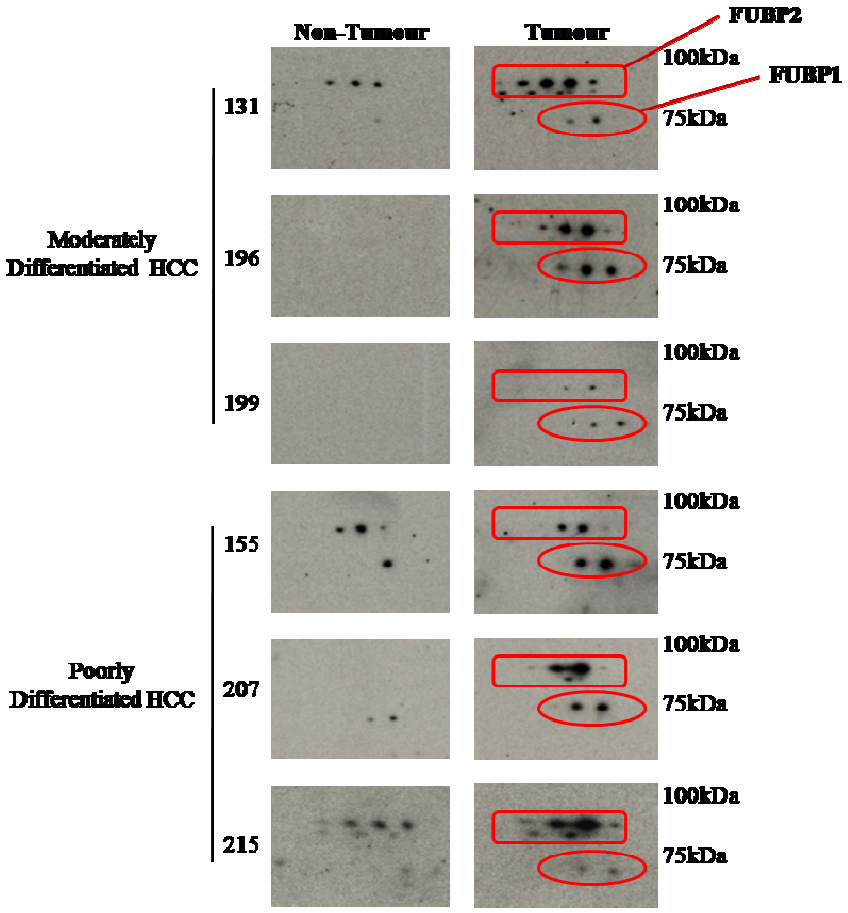


Figure 4.17 : Western blot images of FUSE binding protein (FUBP1/2) of the 6 representative tissues for moderately- and poorly-differentiated HCC tissue lysates.

4.4.2.3 c-myc validation by western blot

FUBP1 and FUBP2 are known to be involved in the transcriptional control of the proto-oncogene, c-myc. Thus a western blot analysis was conducted to check the protein expression level of c-myc in our HCC tissues (Fig. 4.18). As shown, the c-myc levels are higher in the tumour tissues especially the poorly-differentiated HCC tissues that were analysed. The significance of this result will be discussed later.

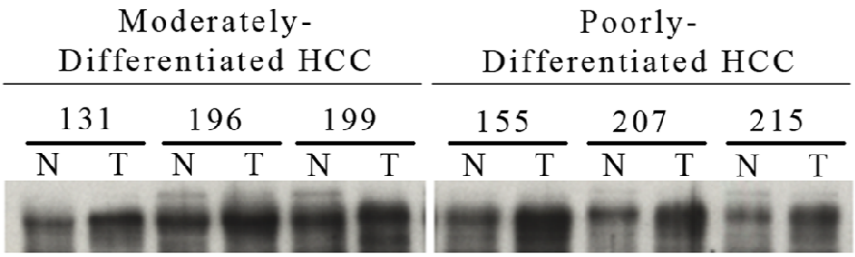


Figure 4.18 : 1-D Western blot images of c-myc of the 6 representative tissues for moderately- and poorly-differentiated HCC tissue lysates. Equal loading of proteins were confirmed in a colloidal stained membrane (data not shown). (N: non-tumour, T: tumour)

4.5 In vitro study on FUBP

As observed in the tissue lysates, over-expression of FUBP 1 and 2 is involved in HCC. In order to investigate if changes in FUBP levels might directly influence tumourigenesis, knock-downs of each of FUBP isoforms using siRNA from Dharmacon RNAi Technologies, on liver cell lines as a model was carried out.

4.5.1 Optimization of concentration of siRNA

HepG2 liver cell lines grown in 24 well plates were used for optimization. Three different concentrations of siRNA (25 nM, 50 nM and 100 nM) against FUBP 1, 2, 3 and siRNA cocktail of all 3 FUBP isoforms at 33 nM each (FUBPmix) were also introduced. siRNA against GAPDH at similar concentrations were used as a positive control to ensure the technique employed is successful. HepG2 control cells without any treatment, transfectant only and non-targeting (NTC) siRNA with are used as negative controls. Cells were treated at 70% confluence for 48 hours before they were lysed in urea/thiourea buffer.

10μg of proteins from each treatment was separated in 1-D western blot and probed against FUBP 1, 2, 3 and GAPDH. Figure 4.19 showed that the knockdown was successful in all the concentrations used. Subsequently, 50 nM of siRNA were used for all the following experiments on HepG2 and Hep3B cell lines.

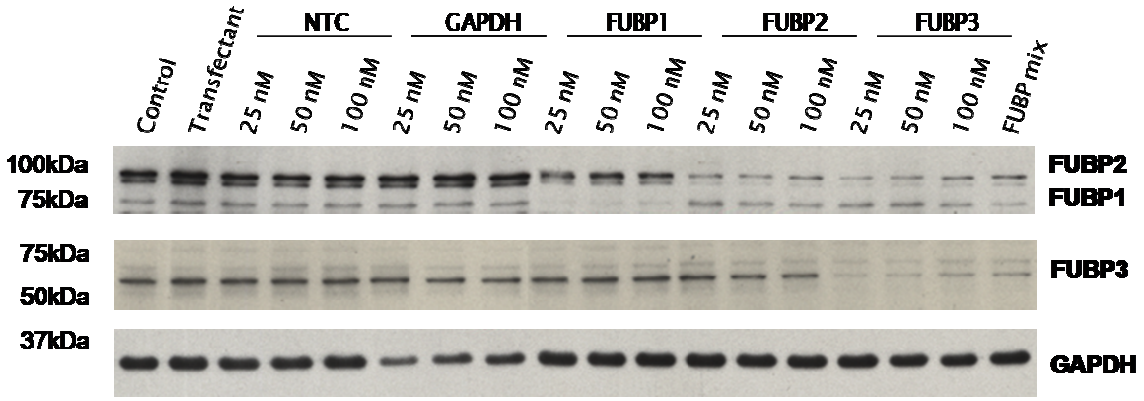


Figure 4.19 : 1-D Western blot images of FUBP 1 / 2 / 3 and GAPDH on HepG2 whole cell lysates following addition of 3 different concentration of siRNA, NTC : non-targeting control, GAPDH, FUBP 1 / 2 / 3.

In view that each FUBP has multiple isoforms a 2-D western blot was performed on the HepG2 cell lysates after siRNA treatment. A total of 10µg of proteins from each treatment were probed against FUBP 1, 2, 3. As illustrated by Figure 4.20, all the isoforms were concomitantly expressed at lower levels, indicating that the siRNA treatment was not preferentially affecting any isoforms. This also showed that the multi protein spots of FUBP 1 / 2 / 3 observed were likely due to post-translational modifications.

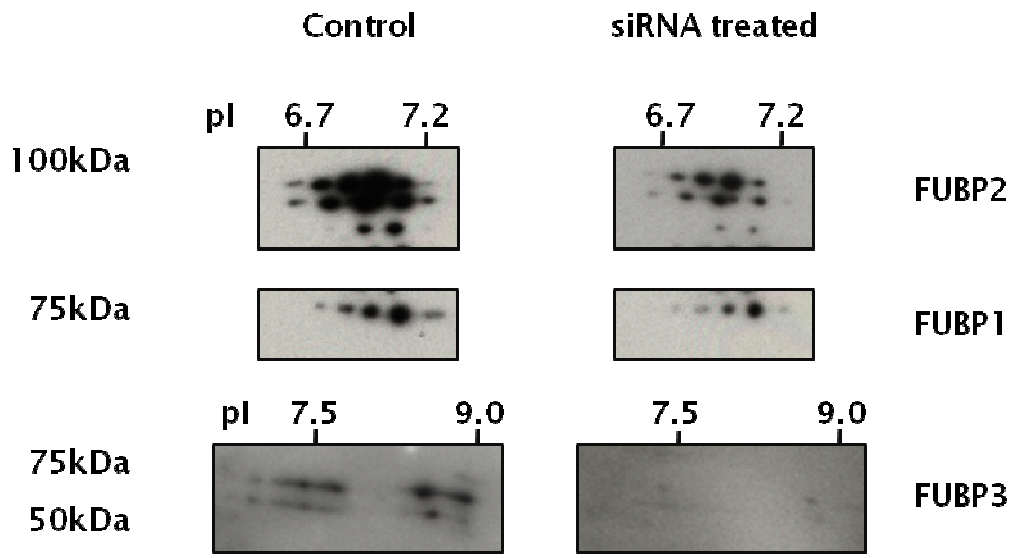


Figure 4.20 : 1-D Western blot images of FUBP 1 / 2 / 3 and GAPDH on HepG2 whole cell lysates following addition of 3 different concentration of siRNA, NTC : non-targeting control, GAPDH, FUBP 1 / 2 / 3.

4.5.2 Effects of FUBP knockdown on c-myc levels

50nM of siRNA against FUBP 1 / 2 / 3 were treated for 72 hrs in HepG2 and Hep3B. 10µg of proteins were separated on 1-D SDS PAGE and probed for c-myc levels. As shown in Figure 4.21, despite effective knockdowns of the respective FUBPs, the levels of c-myc did not vary significantly in both cell lines. FUBPmix which contains all 3 FUBP siRNA showed a slight decrease in c-myc level in Hep3B.

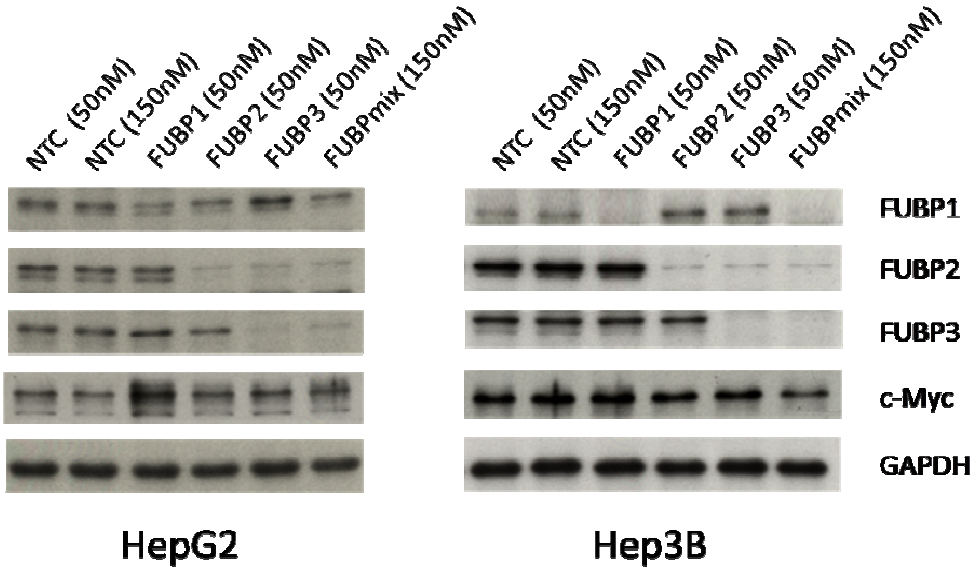


Figure 4.21 : 1-D Western blot images of (A) HepG2 and (B) Hep3B upon FUBP 1 / 2 / 3 siRNA treatment. GAPDH levels are used as loading controls.

4.5.3 Effects of FUBP knockdown in cell viability

In addition to c-myc western blots, cell viability assay were conducted on both HepG2 and Hep3B cells using MTT reagent (Fig. 4.22). As shown above, viability of HepG2 cells were not affected upon siRNA treatment. Hep3B cells on the other hand showed significant decrease in viable cells in each of the siRNA treatment. All experiments were conducted in 4 sets of wells. All 3 separate batches of cells used showed similar changes in viability levels.

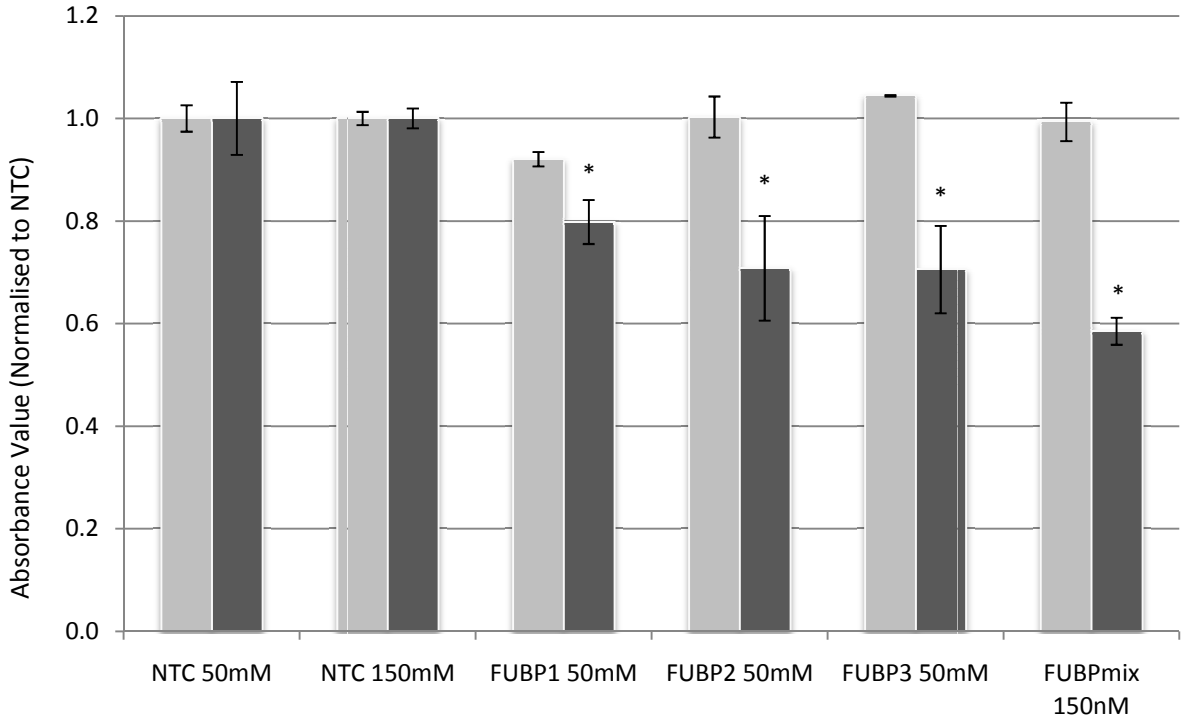


Figure 4.22 : Cell viability were measured using absorbance value at 550nM upon treatment of FUBP siRNA. All absorbance values were normalized to the respective non-targeting controls (NTC). X-axis indicates the concentration of siRNA used. Grey bars represent HepG2 cells and black bars represent Hep3B cells ($p < 0.05$).

5. DISCUSSION

This study is the first report using multiple quantitative proteomic approaches to identify differentially expressed proteins with the aim to understand the molecular pathogenesis of HBV-associated HCC. With the use of three complementary approaches (2-D DIGE, cICAT and iTRAQ), we successfully identified a total of 344 dysregulated proteins excluding isoforms from HCC tumour versus non-tumour tissues (Table 4.3).

The use of multiple but complementary techniques on the same set of tissues has been proposed to enable a more comprehensive identification of regulated proteins (Choe *et al.,* 2005; Wu *et al.,* 2006). As observed in this study, the significance of this approach is evident by the total number of dysregulated protein targets identified in comparison to previous HCC proteomic studies (Table 1.4). In addition, it was also observed that each of the 3 techniques identified different sets of proteins (as illustrated in Fig. 4.5). This thus further emphasized that the use of only one proteomic technique in global profiling studies may provide insufficient information. Most significantly, the use of complementary techniques in this study had substantially improved the coverage of differentially regulated proteins in hepatocarcinogenesis. This should enable us to better understand the molecular events that are involved in HBV-associated HCC.

5.1 Protein expression of moderately- and poorly-differentiated HCC

Out of the total of 344 proteins identified, 163 and 181 proteins were expressed in moderately- and poorly-differentiated HCC respectively. Eighty-five of these proteins were observed to be common in both stages of HCC (Fig. 4.9). Most of these commonly affected proteins are involved in metabolism, catalytic activity and binding properties (Fig. 4.10).

It was initially anticipated that critical molecular players of HCC would reveal stepwise increasing or decreasing regulation levels between the 2 stages of HCC tissues. While all 85 proteins indicated common direction of regulation between moderately- and poorly-differentiated stages, only a handful of these proteins revealed such a progressive change in their regulation levels. It is therefore probable that to delineate the significant molecular events in tumour progression, emphases should not be on individual players but on the combinatory effects of proteins from a common pathway.

5.1.1 Alterations of proteins from common pathways

Proteins identified were further analysed according to their known pathways and interactions as annotated by Ingenuity Pathway Analysis (IPA). As illustrated in Figure 4.11, we observed a significant increase in regulated proteins of a specific pathway as tumour progress from moderately- to poorly-differentiated HCC. The number of dysregulated proteins in metabolic activities for example increased from moderately- to poorly-differentiated HCC. This increasing aberration of proteins will result in perturbation of important molecular and cellular events.

We anticipate that these pathways or groups of proteins will aid in understanding the progression of hepatocarcinogenesis. The functional roles of major clusters of differentially expressed proteins identified in this study are described in the following sections : metabolic proteins, oxidative stress related proteins and c-myc associated proteins. Emphases were also made on protein clusters that showed a progressive loss or gain of function across the 2 stages of HCC.

5.2 Dysregulation of Metabolic Proteins

Metabolic pathways represent one of the major groups of proteins that showed increasing dysregulation from moderately- to poorly-differentiated HCC (Table 4.1 and 4.2, Fig 4.12). This includes glucose, amino acids and lipid metabolism (Fig. 4.10 and Fig. 4.11). Dysregulations of these metabolic pathways had also been observed in other tumour phenotypes (Warburg, 1956; Dang and Semenza, 1999). Differential expressions of these enzymes are also likely a reflection of the gross effect of the loss of liver function across the various stages of HCC (Liang *et al.,* 2005). Although metabolic defects may not be fundamental in causing cancer, they may confer a common advantage that ensures the survivability of tumour cells (Dang and Semenza, 1999).

5.2.1 Glucose metabolism and oxidative phosphorylation

One of the most frequent and well studied metabolic alterations is glucose metabolism. It is commonly accepted that most tumours invest heavily in glycolysis as their main source of energy (Altenberg and Greulich, 2004) even in aerobic conditions, exhibiting a phenomenon described as Warburg effect (Warburg, 1956). Most tumour cells including HCC has been shown to alter their glycolytic and mitochondrial machinery resulting in a preference to produce lactic acid to obtain immediate energy rather than catabolising glucose via tri-carboxylic acid (TCA) cycle (Kim and Dang, 2006). Maintaining a high glycolytic rate also implies a "longer tumour survival time" when these rapidly proliferating cells are exposed to a hypoxia micro-environment (Pedersen, 2007).

In addition, these enzymes can also be activated during hypoxia by transcription factors such as hypoxia inducible factors-1α (HIF-1α) (Maxwell, 2005; Esteban and Maxwell, 2005).

Alterations in glycolysis can also be attributed to various tumour suppressors (such as loss of p53 affects TIGAR pathway, Bensaad *et al.,* 2006; Corcoran *et al.,* 2006) as well as oncogenes (c-myc, Dang and Semenza, 1999). Although the "cause and effect" of glycolysis and cancer is controversial (Zu and Guppy, 2004, Pan and Mak, 2007), elevated levels of glycolysis in cancer cells ensures survivability and enhances proliferation.

5.2.1.1 Alterations in glycolytic pathway

In this study, we also observed over-expression of glycolytic enzymes such as muscle type aldolase A and alpha-enolase in poorly-differentiated HCC. Transketolase, an enzyme involved in pentose phosphate pathway, was also identified as up-regulated only in poorly differentiated HCC. However, several other glycolytic enzymes such as ketohexokinase (KHX), aldolase B, triosephosphate isomerase (TPI) (Fig. 4.12A) and phosphoglycerate mutase (PGM) were shown to be down-regulated (Table 4.1 and 4.2). Figure 5.1 highlights the different glycolytic enzymes identified in moderately- and poorly-differentiated HCC.

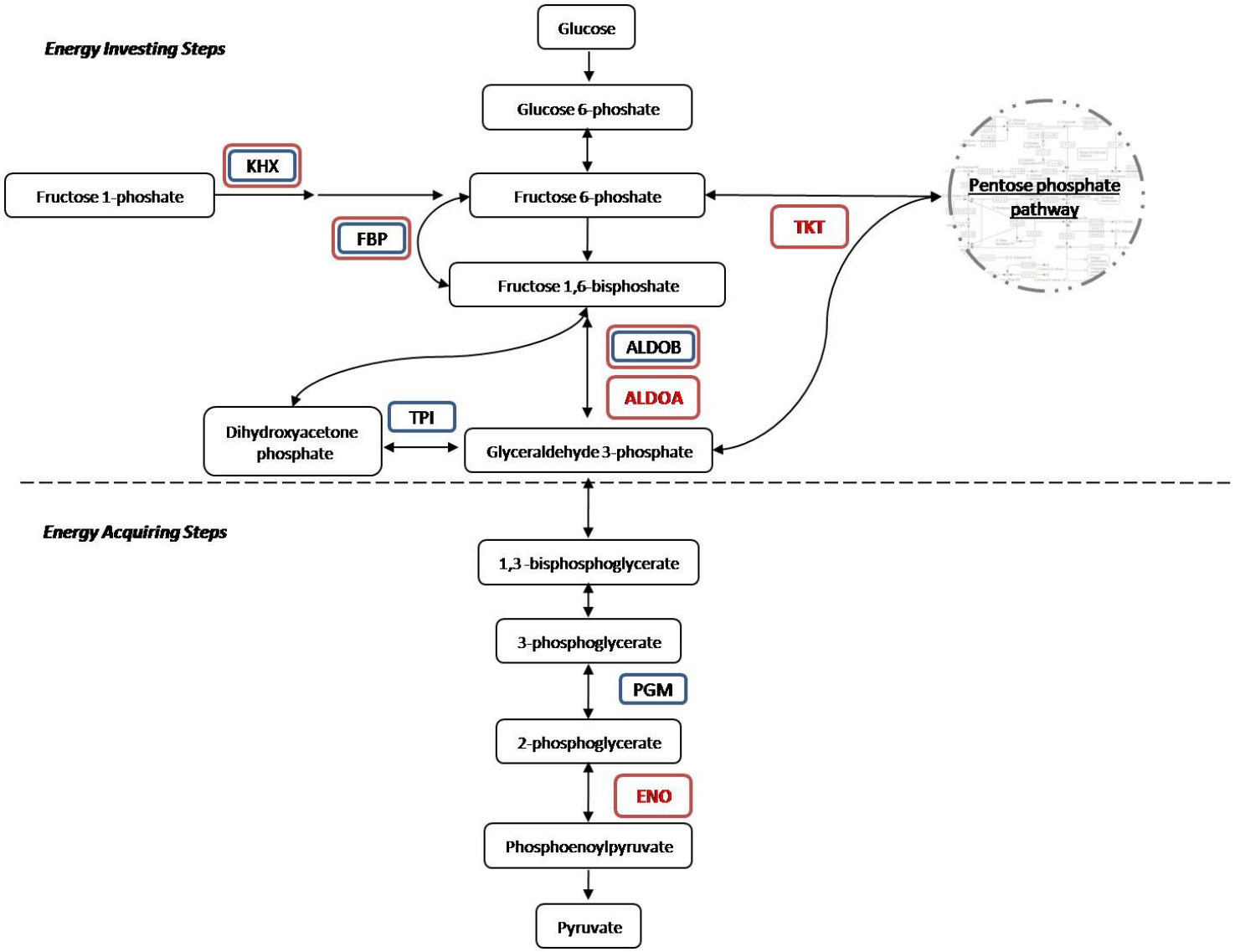

Energy Investing Steps
Glucose
Glucose 6-phoshate
KHX
Fructose 1-phoshate
Fructose 6-phoshate
Pentose phosphate pathway
FBP
TKT
Fructose 1,6-bisphoshate
ALDOB
ALDOA
TPI
Dihydroxyacetone phosphate
Glyceraldehyde 3-phosphate
Energy Acquiring Steps
1,3 -bisphosphoglycerate
3-phosphoglycerate
PGM
2-phosphoglycerate
ENO
Phosphoenoylpyruvate
Pyruvate

Figure 5.1 : Diagrammatic representation of glycolysis and the various dysregulated enzymes. Enzymes that were identified in moderately- and poorly-differentiated HCC are boxed in blue and red respectively. In addition, enzymes that were over-expressed are in red and those that are down-regulated are in black. (KHK, ketohexokinase; FBP, fructose-1,6 bisphosphatase; ALDO A / B, aldoalase A / B; TKT, transketolase; PGM, phosphoglucomutase; ENO, alpha-enolase.)

Under-expression of these enzymes in HCC tumour tissues had also been reported in other proteomic studies (Yokoyama *et al.,* 2004; Liang *et al.,* 2005; Blanc *et al.,* 2005). Contrary to Warburg effect, low levels of glycolytic enzymes in tumour tissues would hamper glucose utilization and hence energy production. With the exception for PGM, these discrepancies can be best explained by analyzing energy flux for glycolysis (Fig. 5.1).

Glycolysis is composed of firstly, energy investment followed by energy acquiring steps. Aldolase A / B, KHX and TPI are involved in the first half of glycolysis. It is thus tempting to suggest that the down regulation of these enzymes allows the tumour to utilize other less energy investing route to produce ATP. This might have been achieved as observed via up regulation of transketolase (identified in our poorly differentiated HCC samples) through the pentose phosphate pathway. This also ensures nucleotide biosysnthesis which is necessary in proliferating cells. Thus low expression of enzymes in the energy investment steps (such as KHX and TPI) coupled with the up-regulation of energy acquiring step (*e.g.* enolase) could be beneficial for the tumour. These observations suggest that HCC might have successfully identified alternative pathways that can feed into the energy acquiring steps of glycolysis. This might add a 'twist' to the Warburg effect.

5.2.1.2 Over-expression of aldolase A but not liver specific aldolase B

Most vertebrates have 3 different aldolase isozymes (Izzo *et al.,* 1987). Aldolase A is identified predominantly in foetal liver as well as adult muscle. While aldolase B is found exclusively in the adult liver and aldolase C in the brain (Mamczur and Dzugaj, 2008). Aldolase is involved in cleaving of fructose-1,6-bisphosphate into two carbon-3 molecules in the energy investing step of glycolysis. In this study we observed differential regulation levels of 2

isozymes of aldolase. Down-regulation of liver specific aldolase B was observed in both stages of HCC and over-expression of aldolase A was shown in only poorly-differentiated HCC.

The under expression of aldolase B had also been reported in several HCC studies (Kinoshita and Miyata, 2002, Yokoyama *et al.,* 2004, Lee *et al.,* 2005; Liang *et al.,* 2005) and were correlated with poor prognosis and early HCC recurrence (Peng *et al.,* 2008). Elevated levels of aldolase A was first observed more than 20 years ago and was proposed as a serum marker for HCC (Asaka *et al.,* 1983). Castaldo *et al.,* (2000) also reported up-regulation of mRNA transcript levels of specifically aldolase A in HCC tissues compared to cirrhotic liver. In addition, HIF-1α is also able to induce expression levels of aldolase A suggesting its role for tumour survival in hypoxia environment (Dang and Semenza, 1999).

The interplay of aldolase isoforms suggests that tumours in the late stage have de-differentiated from normal hepatocytes. Thus, it is capable to enhance glycolysis by utilizing embryonic form of aldolase. Further investigation of the different levels of aldolase isozymes may be useful in understanding HCC initiation and progression.

5.2.1.3 Elevated levels of alpha-enolase

Another glycolytic enzyme, alpha-enolase was also identified to be up-regulated in poorly differentiated HCC only (Table 4.2, Fig. 4.12A). Alpha-enolase is responsible for formation of phosphoenolpyruvate in the second half of glycolysis. Over-expression of alpha-enolase was described in vascular endothelial cells as protective response in hypoxia environment (Aaronson *et al.,* 1995) and it is a target of HIF-1α (Semenza *et al.,* 1996). High expression levels of alpha-enolase have been reported in various cancers such as colon cancer

cell lines (Katayama *et al.,* 2006), breast cancer (Somiari *et al.,* 2003) and cervical cancer (Lee *et al.,* 2004).

In HCC, elevated levels of alpha-enolase were associated with increasing tumour size and venous invasion in late stage HCV-associated tumour tissues (Takashima *et al.,* 2005). However, down-regulation of alpha-enolase was reported in early HBV-associated HCC using Grade I and II human tissues (comparable to well and moderately-differentiated HCC) (Kim *et al.,* 2003). This correlates with identification of higher levels of alpha-enolase in only poorly differentiated HCC tissues analysed in this study (Fig. 4.12A). This suggests a prognostic value of alpha-enolase in identification of late stage HCC tumours. Additional studies will be necessary to confirm these differences in expression levels.

5.2.1.4 Tri-carboxylic acid (TCA) cycle

The TCA cycle is the main source of reducing molecules (NADH and $FADH_2$) that sustains the mitochondrial respiratory chain activity for producing ATP. It consists of a series of 8 progressive oxidative decarboxylations of acetyl-coA. It takes place in the mitochondrial matrix and it is an essential cycle connecting various molecular pathways.

In this study, a progressive loss of TCA cycle was observed from moderately- to poorly-differentiated HCC. In the earlier stage, only 1 enzyme, fumarate hydratase was identified as down-regulated. While in poorly differentiated HCC, a total of 5 TCA cycle enzymes (aconitate hydratase, isocitrate dehydrogenase, fumarate hydratase, scuccinyl Co-A ligase and succinate dehydrogenase) were shown to be down-regulated (Table 4.1, 4.2 and Fig 5.2). Though low expression levels of fumarate hydratase (Liang *et al.,* 2005) and succinyl CoA-ligase (Blanc *et al.,* 2005) had been reported earlier, this is the first report that identified dysregulation of 5 out

of 8 TCA enzymes . Regulation levels of fumarate hydratase levels in both stages of HCC were also verified using western blots (Fig 4.12A). Disruption of TCA cycle had been suggested as one of the mechanisms employed by tumours to ensure rapid energy production via glycolysis (Pedersen, 2007).

Recent discoveries had also implicated direct involvement of succinate dehydrogenase and fumarate hydratase in tumour formation. Mutations or low expression levels of these 2 enzymes had been implicated in paraganglioma, uterine leiomyosarcoma and renal cancer (Baysal *et al.,* 2000; Launonen *et al.,* 2001; Tomlinson *et al.,* 2002). It was shown that the accumulation of succinate and fumarate due to defects in succinate dehydrogenase and fumarate hydrates lead to inhibitin of HIF prolyl hydolases (PHD) (Isaacs *et al.,* 2005; Briere *et al.,* 2005, 2006; Sudarshan *et al.,* 2009). In the absence of PHD, HIF-1α is translocated into the nucleus and results in the subsequent activation of target genes (King *et al.,* 2006). Therefore, dysfunctional TCA cycle may induce glycolysis (as suggested by Warburg effect) and also activate other the tumourigenic properties such as angiogenesis via HIF-1α (Dang and Semenza; 1999)

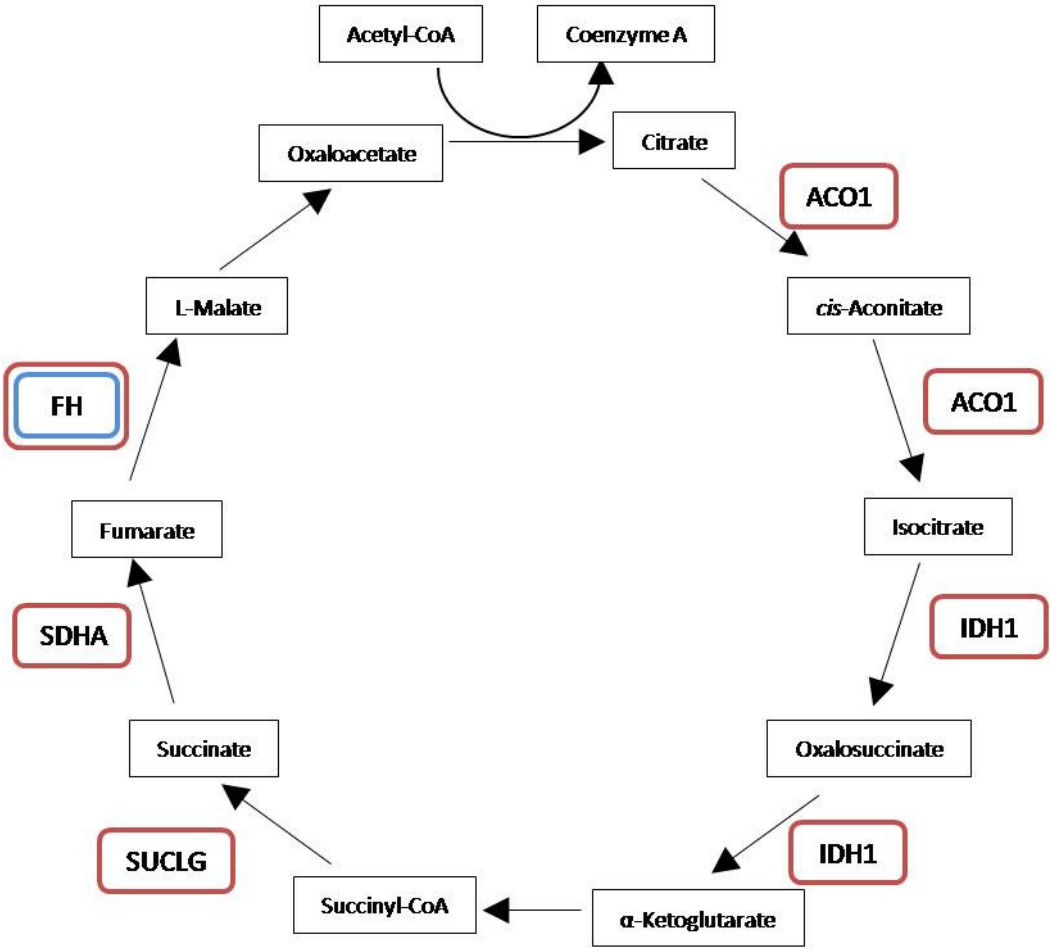


Figure 5.2 : Schematic representation of tri-carboxylic acid (TCA) cycle and dysregulation of enzymes observed in both stages of HCC. Proteins identified in moderately- and poorly-differentiated are in blue and red boxes respectively. All the enzymes identified were down-regulated. (ACO1, aconitate dehydrogenase; IDH1, isocitrate dehydrogenase; SUCLG, succinyl-CoA ligase; SDHA, succinate drhydrogenase; FH, fumarate hydratase).

5.2.2 Lipid metabolism

Under normal physiological conditions, liver is necessary for lipid homeostasis. In this study, we observed that during HCC progression β-oxidation levels are affected. Four mitochondrial enzymes of β-oxidation (fatty acid coA ligase, acetyl-coA acetyltransferase, acyl-coA dehydrogenase and ketoacyl-coA thiolase) recurring steps were down-regulated in moderately and poorly differentiated HCC. In addition, enzymes responsible of activating β-oxidation (fatty acid-CoA ligase and carnithine palmitoyltransferase) and other peroxisomal localized isozymes were also identified as down regulated in only poorly differentiated HCC. This again describes the successive loss of metabolic integrity from moderately- to poorly-differentiated HCC. Dysregulation of lipid metabolism will lead to accumulation of free fatty acid that may eventually lead to hepatic steatosis and hepatocellular injury (Browning and Horton, 2004).

Impairment of β-oxidative and fatty acid metabolic enzymes has also been observed in other profiling studies (Sun *et al.,* 2007). High levels of free fatty acid increased the susceptibility of lipid peroxidation damage that may occur in the presence of reactive oxygen species (Browning and Horton, 2004). This may lead to oxidative stress, liver inflammation and fibrosis. Interestingly, down-regulation of fatty acid enzymes are more prominent in HCV-related than in HBV-related HCC. In addition, steatosis has also been associated with chronic HCV infection and changes in lipid level can affect HCV replication (Powell *et al.,* 2005). Aberration in the enzyme levels have been credited to both host and direct HCV viral factors.

5.2.3 Down-regulation of methylation cycle proteins

In agreement with previous HCC omics analyses (Shen *et al.,* 1998; Avila *et al.,* 2000; Liang *et al.,* 2005), we also observed down-regulation of enzymes in the methylation cycle (S-adenosylmethionine synthetase and betaine-homo cysteine S-methyltransferase). Oxidative stress, high levels of nitric oxide and hypoxia has been associated with inactivation of S-adenosylmethionine synthetase (Corrales *et al.,* 2002). Synthesis of S-adenosylmethionine (AdoMet) is essential in all cells but methylation occurs mainly in the liver (Avila *et al.,* 2002).

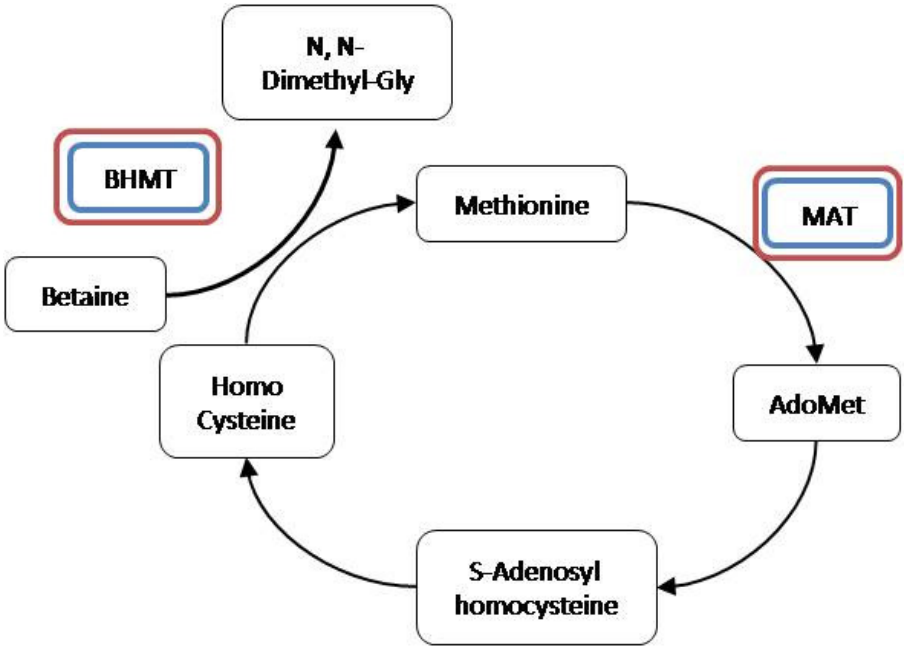


Figure 5.3 : Schematic illustration of the methylation cycle. Proteins identified in moderately- and poorly-differentiated are in blue and red boxes respectively. All the enzymes identified were down-regulated. (MAT, methionine adonesyltransferase; BHMT, betaine homocysteine N-methyltransferase; Adomet, adenosylmethionine).

This cycle is hence crucial as this determined the proper methylation of DNA, RNA and other macromolecules (Tsukada *et al.,* 1985). DNA methylation is also an important epigenetic factor (Laird and Jaenisch, 1996). Hypomethylation of liver DNA, was described to increase expression of oncogenes (c-jun, c-myc, ras) and generation of liver tumours in rats (Christman *et al.,* 1993; Simile *et al.,* 1994).

Low AdoMet levels were shown to impair mitochondrial function (Santamaria *et al.,* 2003) and generate oxidative stress in the liver (Corrales *et al.,* 2002; Martinez-Chantar *et al.,* 2002). Mice without adenosylmethionine synthetase showed spontaneous steatosis and HCC (Martinez-Chantar *et al.,* 2002). In another study, AdoMet administration is able to reduce liver damage and improve alcohol dependant cirrhosis (Vendemiale *et al.,* 1989). This thus provides additional evidence that the imbalance in methionine metabolism is an important player in tumourigenesis.

5.3 Oxidative stress in HCC

Oxidative stress is one of the earliest cellular responses during chronic viral infections and rapid cell growth. This cluster of proteins includes pathways that augmented production of oxidative stress, inactivation of scavenging mechanism and over-expression of anti-inflammatory proteins.

5.3.1 Perturbation in iron homeostasis results in oxidative stress

The liver is the major site for iron storage. It regulates iron traffic around the body and synthesizes major proteins involved in iron metabolism (Anderson and Frazer, 2005). The liver maintains iron homeostasis in the body mainly by uptake of circulating iron via serotransferin, hemoglobin, heme and ferritin. Our data collected suggests that the integrity of basic iron regulatory system is greatly compromised.

Elevated hemopexin is observed in both moderately- and poorly-differentiated HCC. This implies an increase in the uptake of heme into the liver, which will be degraded to biliverdin and free iron. Free iron is normally bound to iron-binding proteins such as tissue ferritin and serotransferin for storage or degradation. In these tumour tissues however, these proteins were both down regulated. This now indicate high level of unbound iron in the liver.

It has been suggested that untreated iron overload may lead to liver fibrosis, cirrhosis and cancer (Kowdley, 2004; Asare *et al.,* 2006). This can be mediated by either direct and/or indirect mechanisms. Direct mechanism would include possible DNA damage, inactivation of tumour suppressor and cell proliferation (Dong-yun *et al.,* 2003). Indirect effects would comprise of free iron forming reactive oxidative species (ROS) such as the hydroxyl radicals

($OH^{\cdot}$), superoxide and singlet oxygen (Cadenzas, 1989). This can lead to oxidative damage to DNA, proteins and lipids (Cheeseman, 1993) which have been implicated in inflammatory diseases and cancer including HCC (Wiseman and Halliwell, 1996; Jungst *et al.,* 2004). It is proposed that oxidative damage due to excess hepatic iron may result in chronic inflammatory hepatic disease. This will result in more ROS and oxidative damage (Hagen *et al.,* 1994; Jungst *et al.,* 2004).

5.3.2 Inactivation of scavenging mechanisms

Under normal conditions, the presence of ROS and free radicals in the body usually leads to an increase in antioxidant proteins to protect the cells. This scavenging mechanism is however, abolished in many cancer cells including HCC (Sun *et al.,* 2005). Similarly in the HCC tissues that we had analysed, we observed diminished levels of a repertoire of antioxidant proteins. Proteins such as superoxide dismutase, catalase, peroxiredoxin 6, thioredoxin-dependent peroxide reductase and glutathione peroxidase were all also shown to be down regulated in both moderately and poorly differentiated HCC. The regulation of superoxide dismutase and catalase were also verified by western blots (Fig. 4.12A). This under expression could result in prolonged oxidative insult.

Diminished antioxidant defense mechanism, in concert with iron overloading, would lead to excessive oxidative stress in the hepatocytes. At present, there is little doubt that oxidative stress is important in the pathophysiological component of tumourigenesis. There is also evidence that ROS could also directly promote cell proliferation and the invasive ability of hepatoma cells (Miura *et. al.,* 2003). ROS and free radicals have the ability to react with a wide range of cellular constituents such as amino acids, membrane lipids to initiate a chain of free

radical reactions known as lipid peroxidation and insult on pyrimidine residues of DNA. All these could possibly lead to mitochondrial and DNA damage that will contribute to initiating and promoting tumorigenesis.

5.3.3 Elevated heat shock protein and inflammatory response

In concert with liver inflammation, hypoxia and high levels of free radicals, a cluster defense related proteins were identified to be up-regulated. This consists of a family of heat shock proteins (HSPs), glucose regulated proteins (GRPs) and inflammatory response proteins. With the exception of HSPs, we observed a progressive increase in the number of dysregulated proteins involved in inflammatory response across the two stages of HCC (Fig. 4.12). The over-expression of inflammatory responses enables the tumour cells to protect from high levels of oxidative stress. These inflammatory response proteins also display tumourigenic properties. The following sections describe the current literature on these chaperone proteins and their possible prognostic value.

5.3.3.1 Dysregulations of heat shock proteins

Heat shock proteins (HSPs) are protein chaperones responsible for facilitating protein folding and translocation (Bukau and Horwich, 1998). Some members have also been shown to promote cancer cell growth and survival (Rohde *et al.,* 2005). In this study, over-expression of a myriad of heat shock proteins such as HSP 70 isoforms and HSP 90 isoforms were identified in both stages of HCC.

The HSP 70 protein family for example, had been well characterized and had shown to play a crucial role in caspase de-activation leading to its anti-apoptotic effect (Beree *et al.,* 2000). Elevated levels of HSPs had also been reported earlier in HCC studies (Kim *et al.,* 2002; Takashima *et al.,* 2003; Kim *et al.,* 2003; Kim *et al.,* 2006; Luk *et al.,* 2006).

Interestingly, HSP27 was identified in moderately differentiated HCC as down regulated using 2-D DIGE approach but up-regulated in our iTRAQ results. This difference in regulation level may be due to a specific isoform identified in 2-D DIGE. In the literature, variable levels of HSP 27 had also been reported. Kim *et al.,* (2002) analysed 11 HCC tissues and reported down-regulation of HSP27. Another group (Kim *et al.,* 2003) identified over-expression and down-regulation of HSP27 in HBV- and HCV-associated HCC respectively. A recent study on HBV-associated HCC however identified over-expression of HSP27 (Luk *et al.,* 2006). This discrepancies observed by these studies may have been due to different aetiology of HCC or simply a different protein isoforms.

5.3.3.2 Up-regulation of glucose regulated proteins (GRPs)

In addition to HSPs, a family of glucose regulated proteins (GRPs) had also been of great interest in carcinogenesis. GRPs are endoplasmic reticulum (ER) chaperones that can be induced under glucose starvation and other ER perturbations (Lee, 2001). Elevated levels of GRP75 were identified in both moderately- and poorly- differentiated HCC and GRP78 was found in poorly differentiated HCC tissues used in this study. High levels of GRPs had been associated in several HCC studies (Kim *et al.,* 2003; Takashima *et al.,* 2003).

GRP75 was recently shown to indicate high metastatic potential and early recurrence in HCC (Yi *et al.,* 2008). Preliminary test indicated that GRP75 showed far superior sensitivity in predicting early recurrence compared to AFP (90.90 % (GRP75) versus 33.33% (AFP)) and had comparable specificity value at 71.4 % (GRP75) versus 80.0% (AFP). Yi *et al.,* (2008) also suggested the use of GRP75 in combinatory with AFP to improve diagnostic performance for identification of early HCC recurrence. Additionally, GRP75 autoantibodies had also been identified in HCC patients' serum (Uemura *et al.,* 2003) further suggesting its application for surveillance after curative surgery to prevent tumour recurrence.

Levels of GRP78 had also been evaluated by several HCC studies (Lim *et al.,* 2002; Luk *et al.,* 2006). Shuda *et al.,* (2003) showed exclusive over-expression of GRP78 transcript levels in poorly differentiated HCC and highlighted a potential involvement of ER stress pathway in HCC progression. GRP78 was also shown to be strongly correlated with HCC progression (Lim *et al.,* 2005).

Although the mechanistic value of GRPs are not clear, it was shown that reduced levels of GRP75 in immortalized cells can cause senescence like growth arrest (Wadhwa *et al.,* 2003; Deocaris *et al.,* 2007). Using an animal model on fibrosarcoma, Jamora *et al.,* (1996) had also demonstrated that inhibition of GRP78 can lead to tumour regression. It is therefore hopeful that in addition to prognostic value for HCC progression or recurrence, these proteins are also potential candidates for cancer therapy.

5.3.3.3 Over expression of S100 proteins in only poorly differentiated HCC

In addition to elevation of protein chaperones, we also identified a family of S100 proteins- S100A8, S100A9 and S100P that were up-regulated in only poorly-differentiated HCC tissues. S100 proteins are calcium-binding protein with diverse roles in a spectrum of tissues (Salama *et al.,* 2008). These S100 proteins were identified by the iTRAQ approach only. Its low relative molecular mass (10- 12 kDa) probably makes it difficult to be detected by 2-D DIGE method.

Over-expression of S100A4 (another member of this protein family) had been proposed as a marker for tumour invasion and metastasis using a HCC cell line model (Ding *et al.,* 2004; Cui *et al.,* 2006). In another study, higher levels of S100A6 were indentified in colon-derived liver metastases compared to HCC (Melle *et al.,* 2008). To our knowledge, this is the first HCC study to identify elevated levels of these three additional members of S100 proteins.

S100A8 has been shown to have chemo-attraction for leukocytes and S100A9 are involved in the regulation of cytoskeleton components (Salama *et al.,* 2008). Both proteins have been shown to be up-regulated in gastric cancer (Yong and Moon, 2007), prostate cancer (Hermani *et al.,* 2006), colorectal cancer (Stulik *et al.,* 1999) and breast cancer (Arai *et al.,* 2008). These two protein isoforms can form a heterodimer complex and have been hypothesized to act as chemo-attractants to prepare the tumour cells to pre-metastatic state (Hermani *et al.,* 2006). Most importantly, both proteins had also been implicated in poor prognosis and metastatic potential in invasive ductal carcinoma of the breast (Arai *et al.,* 2008).

S100P another member of the S100 family of proteins was first purified from placenta (Becker *et al.,* 1992). Its over-expression had also been positively correlated with tumour malignancy in pancreatic cancer (Logsdon *et al.,* 2003, Arumugam *et al.,* 2005), decrease

patient survival in lung cancer (Beer *et al.,* 2002) and resistance to chemotherapy in colon cancer (Bertram *et al.,* 1998). S100P levels were also associated with cellular immortalization of human breast epithelial cells (Guerreiro *et al.,* 2000). Expression levels of S100P have not been highlighted or directly examined in any HCC studies.

In our tissue samples, over-expression of S100A8, S100A9 and S100P were only identified in poorly differentiated HCC. Although S100 proteins lack tissue specificity, their involvement in late stage tumour and poor prognosis entails them as potential prognostic marker.

5.4 Dysregulation of c-myc associated proteins

Another prominent cluster of proteins identified were c-myc associated proteins. c-myc, proto-oncogene, is a transcriptional factor known to be crucial in various biological processes and is often over-expressed during tumourigenesis. It is capable of acting as either an activator or repressor. c-myc was shown, via gene expression studies and *in vivo* mapping of binding, sites to govern up to 10 – 15% of genes (Chung and Levens, 2005).

c-myc appears to be tightly regulated in resting cells and even in tumours, with RNA and protein levels of an order of 1 transcript and 500 proteins per fibroblast (Lockhart and Winzeler, 2000; Warrington *et al.,* 2000). Moreover, this oncogene has very short half lives in the range of 20 – 30 min (Eisenman, 2001). Therefore, slight dysregulation of c-myc levels can lead to a myriad of undesirable chain of events. This includes uncontrolled cell-proliferation, DNA damage, mitochondrial biogenesis, ROS production and even apoptosis (Vafa *et al.,* 2002; Morrish and Hockenbery, 2003; Dang *et al.,* 2005).

5.4.1 Central role of c-myc in HBV-associated HCC

In this study, c-myc was observed as a central node to 33 proteins identified in this study (as illustrated by Ingenuity Pathways Analysis, Fig. 5.4). These interactions are based primarily on a curated database collected from publications maintained by Ingenuity Systems. Though c-myc was not identified in this proteomic screening, its over-expression in the HCC samples used in this study was confirmed using western blotting (Fig. 4.19).

A similar study using microarray analysis on HBV-associated HCC tissues (Iizuka *et al.,* 2006) also reported 17 of the top most regulated genes were directly associated with c-myc.

Alike the observations in our study, transcription level of c-myc was also not identified in the genome-wide microarray analysis but direct analysis using RT-PCR showed an over-expression of 1.4 fold times between tumour and non-tumour samples. It is thus possible that the large heterogeneity of human HCC tissues as well as low abundance and short half live of c-myc renders it difficult to be captured using a large scale screening approach.

It is however generally accepted that c-myc plays an active role in HCC (Thorgeirsson and Grisham, 2002; Feitelson *et al.,* 2004). High levels of c-myc in HCC tissues has been identified by various groups using southern blot (Peng *et al.,* 1993), differential polymerase chain reaction (PCR) analysis (Abou-Elella *et al.,* 1996) and immunohistochemistry (Niu *et al.,* 2002). Frequent amplification of the chromosome arm 8q24 (where c-myc gene locus is found) in HCC tissues may also contribute to higher expression level of c-myc in liver cancer (Kusano *et al.,* 1999; Zimonjic *et al.,* 1999; Schlaeger *et al.,* 2008). Nevertheless, there were also several studies that contradict c-myc's association in hepatocarcinogenesis (Yuen *et al.,* 2001; Ikeguchi and Hirooka, 2004; Liu *et al.,* 2004).

Most significantly, data obtained from animal models showed that c-myc's over-expression can induce HCC (Murakami *et al.,* 1993; Terradillos *et al.,* 1997) and its inhibition resulted in loss of HCC neoplastic properties (Simile *et al.,* 2004). An elegant study by Shachaf *et al.,* (2004) showed that over-expression of a tet-inducible c-myc in transgenic mice not only induced liver cancer but subsequent inactivation of c-myc's transgene expression was able to cause sustained tumour regression. These liver tumours were shown to be able to re-differentiate back to normal hepatic lineages with lowered cancer markers such as alpha-feto protein (AFP) levels and induced tumour dormancy.

Although c-myc expression levels and functions in HCC is an unresolved issue, higher levels of c-myc had been consistently observed in HBV associated in liver tissues. Peng *et al.,* (1993) observed a significant correlation between elevated c-myc levels in patients with poor prognosis and HBV infections. Similar observations were made by Wu *et al.,* 2001 in microarray analysis using 7 human HBV-infected and normal liver tissues. Cell line models transfected with HBV-X gene was shown to induce elevated c-myc expression levels (Wu *et al.,* 2001; Yang *et al.,* 2008). A HBV-X transgenic mouse model also showed stronger c-myc expression in dysplastic nodules of the hepatocytes and in tumour cells than in the adjoining liver cells (Lakhtakia *et al.,* 2003). The knowledge gained thus far from the literature supports the hypothesis of c-myc's central role in HCC especially in HBV associated tumourigenesis.

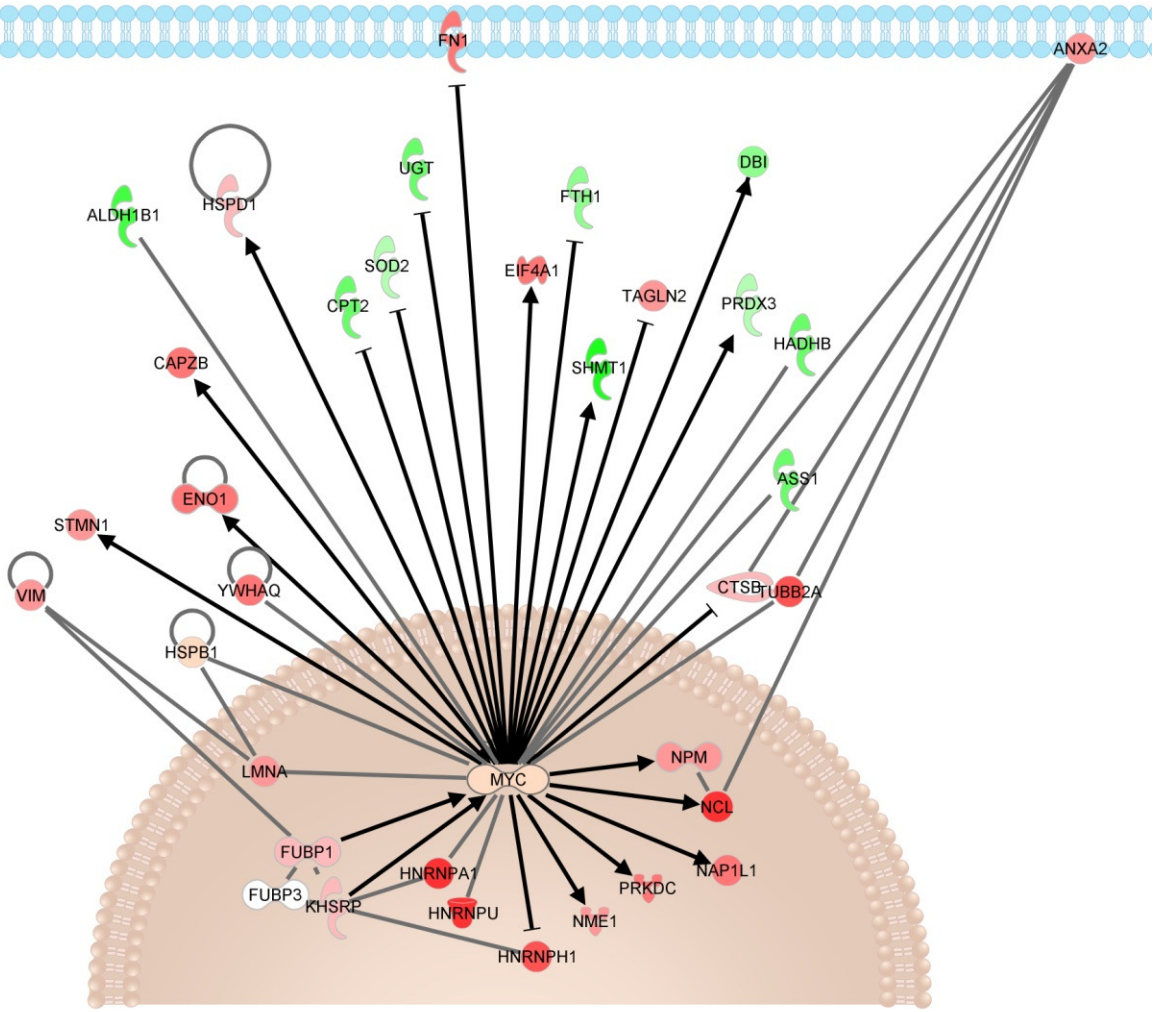


Figure 5.4 : Schematic diagram illustrating the different proteins identified that interacts with c-myc as annotated by Ingenuity Pathway Analysis (IPA). Arrows are used to describe increasing expression and inhibitory interactions are described using T-shape connectors. Protein-protein bindings are represented by solid grey lines. In addition up-regulated proteins that are identified in this study are in red and those

down-regulated are in green. (FUBP1; far upstream binding protein 1, KHSRP; far upstream binding protein 2 (FUBP2), HNRNPA1; heterogeneous nuclear ribonuclearprotein A1, HNRNPU; heterogeneous nuclear ribonuclearprotein U, HNRNPH1; heterogeneous nuclear ribonuclearprotein H1, NME1; non-metastatic cells 1 (NDKA), PRKDC; prortein kinase, DNA activated catalytic polypeptide, NAP1L1; nuclesome assembly protein 1- like 1, NCL; nucleolin, NPM; nucleophosmin, TUBB2A; tubulin beta 2A, CTSB; cathepsin B, ASS1; arginosuccinate synthetase 1, ANXA2; annexin A2, HADHB; hydroxyacyl-coenzyme A dehydrogenase beta, PRDX3; peroxiredoxin 3, DBI; diazepam binding inhibitor, TAGLN2; transgelin 2, SHNT1; serine hydroxymethyltransferase 1, FTH1; ferritin heavy polypeptide 1, EIF4A1; eukaryotic translation initiation factor 4A isoform 1, FN1; fibronectin 1, UGT; UDP-glucoronosytransferase, SOD2; superoxide dismutase 2, CPT2; carnithine palmotyltransferase 2, HSPD1; heat shock protein 60, ALDH1B1; aldehyde dehhydrogenase 1 B1, CAPZB; capping protein beta, ENO1; enolases 1, YWHAQ; tyrosine 3-monoooxygenase, STMN1; stathmin 1, HSPB1; heat shock protein 27, VIM; vimentin, LMNA; lamin A)

5.4.2 Differentially expressed proteins governed by c-myc

Akin to the numerous literature evidences, the observation made in this study also supports the importance of c-myc as a central transcriptional control in HBV-associated HCC. The 33 proteins identified displayed protein-protein interaction with c-myc as well as down-stream activators that are controlled by c-myc (Figure 5.4). Most of the proteins identified (except for 6 proteins) showed expected regulation levels as predicted from an over-expression of c-myc. These proteins include metabolic proteins such as aldehyde dehydrgenase, UDP glucoronyltranferase, carnithine palmitoyl transferase and oxidative stress related proteins such as ferritin heavy chain and superoxide dismutase. In addition to metabolic proteins, we also identified several nuclear localized proteins that are regulated by c-myc. Their interaction with the oncogene and significance in HCC is elaborated below.

5.4.2.1 Dysregulation of hnRNP protein family

Heterogeneous nuclear ribonucleoproteins (hnRNP) family consists of 19 different members that have important roles in DNA repair, telomere biogenesis and regulation of gene expression including c-myc via transcription and translation machineries (Carpenter *et al.,* 2006). In this study we identified over-expression of 2 hnRNP members (hnRNP A1 and hnRNP A2/B1) and 6 hnRNP members (hnRNP A1, hnRNP A3, hnRNP H, hnRNP M, hnRNP Q, hnRNP U) in moderately and poorly differentiated HCC respectively. The increase number of dysregulated hnRNP proteins in poorly-differentiated HCC tissues suggests its role in late stage tumourigenesis.

Several hnRNP members such as hnRNP A2/B1 (Codarin *et al.,* 2008), hnRNP C (Blanc *et al.,* 2005; Sun *et al.,* 2006), hcc-1 (similar sequences to hnRNP, Choong *et al.,* 2001),

hnRNP H (Honore *et al.,* 2004) and hnRNP K (Li *et al.,* 2005; Ng *et al.,* 2005) have also been identified as up-regulated in other HCC genomic and proteomic analyses. In addition, autoantibody against hnRNP A2 had also been identified in HCC patient's sera (Li *et al.,* 2008).

Though only a few selected members have been extensively studied, hnRNPs appear to be promiscuous and illustrated high expression levels in majority of cancers (Zech *et al.,* 2006; Matta *et al.,* 2009; Barboro *et al.,* 2009). It is unclear how hnRNPs execute its action and each protein members are likely to have its own mechanism (reviewed by Carpenter *et al.,* 2006). Gene sequences of hnRNP A1, A2, E, H and K for example were shown to contain E box elements, hence may be regulated by c-myc (Dang 1999, Carpenter *et al.,* 2006). In addition, several other *in vitro* studies highlighted various members of hnRNP could promote mRNA stabilization of c-myc (Brewer, 1991) and increase its translation activity (Kim *et al.,* 2003).

5.4.2.2 Over-expression of nucleotide diphosphate kinase

Nucleotide diphosphate kinase (NDKA/nm 23), a controversial metastatic protein was shown to be over-expressed in both moderately and poorly differentiated HCC. Its differential regulation was also confirmed via 2-D western blot (Fig 4.13). Transcription levels of NDKA was shown to be regulated by c-myc in several reports (Godfried *et al.,* 2002, Menssen and Hermeking, 2002)

Over-expression of NDKA has been shown to correlate with tumourigenicity as shown in neuroblastoma (Hailat *et al.,* 1991) and pancreatic cancer (Nakamori *et al.,* 1993) but was also shown to inhibit metastasis in breast (Russell *et al.,* 1998), melanoma (Baba *et al.,* 1995) and prostate cancer (Lim *et al.,* 1998). Similarly in HCC analyses, over-expression of NDKA

was also identified in comparative analysis between tumours and non-tumours (Li *et al.,* 2005). A recent study also showed increased levels of NDKA in HepG2 liver cell lines infected with HBV-X gene (He *et al.,* 2007). However, NDKA expression levels are down-regulated in HCC tissues with intrahepatic metastasis (Iizuka *et al.,* 1995; Fujimoto *et al.,* 1998). These evidences suggest a dual function of NDKA with a high expression levels during tumour progression and a loss of expression levels during metastasis (Boissan and Lacombe, 2006). It is possible that the high levels of NDKA observed in this study are a reflection of the association to c-myc and HBV-X during tumour progression.

5.4.2.3 Nucleophosmin

Another nuclear localized protein, nucleophosmin was identified to be up-regulated in only moderately differentiated HCC, consistent with western blot verification (Fig 4.13B). Over-expression of nucleophosmin has been noted in gastric cancer (Tanaka *et al.,* 1992), colon cancer (Nozawa *et al.,* 1996) and prostate cancer (Subong *et al.,* 1999). Recently nucleophosmin levels were also examined in 103 human HCC tissues (Yun *et al.,* 2007). The results showed correlated expression levels with other prognostic parameters such serum AFP levels and liver cirrhosis.

Nucleophosmin is a direct target of c-myc transcription factor (Zeller *et al.,* 2001; Grisendi *et al.,* 2006) and was shown to correlate with transfection of HBV-X gene in liver cell lines (Li *et al.,* 2009). High levels of nucleophosmin are believed to reflect cell's commitment in mitogenesis (Feuerstein *et al.,* 1988) and are proposed to play a role in tumourigenesis. The elevated levels of nucleophosmin in only moderately-differentiated HCC may reflect this commitment to HCC initiation in early stages. Its exact role in HCC remains to be understood.

5.4.3 Far-upstream binding proteins (FUBPs)

Another c-myc associated protein of special interest is far upstream binding proteins (FUBPs). Unlike other c-myc related proteins discussed earlier, FUBPs are transcriptional activators of c-myc. Our study shows for the first time, the over-expression of two FUBP isoforms: FUBP1 and FUBP2 were identified in both moderately- and poorly-differentiated HCC (Fig.4.15). Li *et al.,* (2005) had earlier reported up-regulation of only FUBP1 in HBV-associated HCC. However, the significance of this observation was not elaborated further.

5.4.3.1 Mechanism of FUBPs in regulating c-myc's expression

FUBPs consist of 3 members; FUBP1 was originally identified in 1990, along with closely related homologs FUBP2 and FUBP3 genes (Avigan *et al.,* 1990; Bazar *et al.,* 1995; Davis-Smyth *et al.,* 1996). Although all 3 isoforms are situated on different chromosomes, their primary amino acid sequences are highly similar (Chung *et al.,* 2006). All 3 proteins have four KH-DNA binding domains and have been shown to be able to bind with great affinity to a single stranded extended far upstream element (FUSE), about 1500 base pairs upstream of c-myc's promoter region.

A working model describes that RNA polymerase II downstream of c-myc's promoters is paused by transcriptional factor (TFIIH). In the presence of FUBPs bound to FUSE sequence, TFIIH releases RNA polymerase II and this in turn results in transcription of c-myc (He *et al.,* 2000; Lui *et al.,* 2006). Presence of FUBPs thus regulates c-myc expression by "modulating the transition from transcription initiation to promoter escape" (He *et al.,* 2000). This process can

be counteracted by FUBP interacting repressor (FIR) which can bind to FUBP and TFIIH. This results in inactivation of TFIIH and diminishes c-myc transcription (Liu *et al.,* 2006).

Binding of FUBPs to the FUSE sequence thus is an essential process in regulating the promoter activity of c-myc's transcription (He *et al.,* 2000, Chung *et al.,* 2006). Dysregulation of FUBPs will result in aberrant c-myc's expression levels. *In vitro* studies of FUBP knock-down in osteosarcoma cell line (U2OS) also showed a significant decrease in c-myc mRNA levels and arrest in cell proliferation (He *et al.,* 2000).

FUBP expression levels were also observed to be tightly regulated with cell differentiation. Higher levels of FUBPs were reported in undifferentiated cells and expression levels declines upon cell differentiation. As observed by Wang *et al.,* 1998, expression levels of FUBP decreases along development of various organs of embryonic mouse and chicken. In addition, ubiquitination of FUBP via p38 was necessary to lower c-myc expression levels for differentiation of lung cells (Kim *et al.,* 2003). Over-expresion of FUBPs were also reported in several other studies such as DAOY medullablastoma cell line (Engidawork *et al.,* 2006), melanoma cell lines induced by interferon-α (Craven *et al.,* 2004) and in hypoxia induced stress and re-oxygenation of HeLa cervix carcinoma cells (Magagnin *et al.,* 2007). The significance of these studies was however not elaborated.

5.4.3.2 Over-expression of FUBPs

In this study, 2-D DIGE approach detected the presence of multiple FUBP1 and FUBP2 protein spots (Fig. 4.15). Despite the high similarity in their protein sequences, MS/MS spectra (Fig. 4.16B and D) illustrated that both isoforms have unique tryptic peptide sequences enabling

us to differentiate the two isoforms. Regulation level of each of these proteins spots are summarized in Table 4.4. The expression levels were also verified using western blotting (Fig. 4.17). Multiple FUBPs protein spots with slightly varying pIs that ran along horizontal lines indicate the presence of post-translational modifications. The shift in pIs of these protein spots suggests the presence of various phosphorylation states of the protein. Indeed a total of 3 and 6 phosphorylation sites are listed in the IPI database (Version 3.31) for FUBP1 and FUBP2 respectively.

Interestingly, we have found similar isoforms of FUBP1 and FUBP2 in HepG2 liver cells and they were found to be down-regulated when these cells were treated with butyrate, an anti-cancer agent (unpublished data). Butyrate has previously been shown to cause growth arrest and differentiation in liver cancer cells (Emanuele *et al.,* 2004). A recent HCV study also revealed that FUBP is essential for efficient replication of the virus (Zhang *et al.,* 2008). These results suggested FUBPs significance in HCC.

5.4.3.3 Loss of FUBPs display preferential response

In this study, we observed correlated expression levels of FUBPs and c-myc in our HCC samples. Higher expression of c-myc was also more prominent in the poorly-differentiated tumour tissues paralleled with elevated levels of both FUBP1 and FUBP2 in these tissues (Fig. 4.18). He *et al.,* (2001) had also earlier showed using osteosarcoma cell lines (U2OS) that loss of FUBP resulted in lowered c-myc expression. This suggested that high expression of c-myc may be due to elevated FUBP expression observed in these HCC tissues analysed.

In consideration of evidence suggesting involvement of HBV in high expression level of c-myc, 2 different cell lines (HepG2 and Hep3B) with differing HBV properties were used for preliminary analysis. HepG2 is liver cell line has no known HBV and commonly used in numerous *in vitro* HCC studies. Hep3B another well characterized cell line on the hand, has HBV integrated genome and HBsAg present in the media (Tay *et al.,* 1990).

An *in vitro* model using siRNA transfection was conducted on these two cell lines to further characterize, FUBPs role in HBV-associated HCC. Despite, successful knock-down of FUBPs, HepG2 did not show any significant change in c-myc protein levels and cell viability (Fig.4.21 A and Fig. 4.22). In Hep3B, c-myc levels also remained unchanged in each transient knock-down of FUBP isoforms. siRNA transfection of all 3 FUBP isoforms simultaneously however showed slight down-regulation of c-myc expression level (Fig. 4.21 B). This observation is likely due to the compensatory effects of the FUBP isoforms.

Most importantly, significant loss of cell viability was observed in Hep3B cells (compared to HepG2 cells) in all the siRNA transfections (Fig. 4.22). This observation suggests that FUBPs play an important role in viability of HBV-related HCC cells. It is however unclear if the minimal changes in c-myc expression levels detected in the western blots could explain the lowered cell viability observed. This preliminary analysis suggests that FUBPs are able to promote hepatocarcinogenesis in both c-myc dependent and independent pathways.

5.4.3.4 Other possible roles of FUBPs

Though most of the earlier studies on FUBPs had revolved around its possible roles with respect to c-myc, it is expected that as a transcriptional activator, FUBPs are also able to

modulate expression levels of other genes with an upstream FUSE sequence. A recent microarray analysis (Chung *et al.,* 2006) conducted on individual FUBP knockdown showed that only a third of the 172 genes identified were common among all 3 isoforms. Another third of the genes detected showed distinct expression patterns regulated by each FUBPs. Although it is not clear, if the genes identified are directly controlled by FUBPs, this study suggests that each of the FUBP isoforms is capable of regulating a specific set of genes. Therefore it is likely that each of the FUBPs may regulate specific downstream activities in a c-myc independent manner. As described by Weber *et al.,* 2008, over-expression of FUBP1 and FUBP3 was observed in renal, prostate and bladder cancer. This expression however only correlated with high levels of c-myc in renal cancer but not in prostate and bladder cancer. Thereby, suggesting other functions of FUBP in these tumours.

In another study, Singer *et al.,* (2009) showed FUBP1 as a potential inducer of stathmin in non-small cell lung cancer. Stathmin, involved in cell motility and division, was shown to decrease significantly upon FUBP1 siRNA transferction using Calu-1 (squamous cell carcinoma cell line) and Calu-6 (adenocarcinoma cell line). Most recently, the same group showed the same association between FUBP1, FUBP2 and stathmin in HCC cancer cell lines (Malz *et al.,* 2009). The data from their study also further confirmed our observation that transient FUBP1 knock-down in Hep3B cells leads to loss of cell viability with marginal down-regulation of c-myc. They also showed that FUBP activation is necessary for proliferation and motility of human liver cancer cells. In addition, over-expression of FUBPs in HCC significantly correlated to poor patient survival.

These evidences further points to the importance of FUBPs in modulating the progression of HCC. It will thus be beneficial to evaluate the genes affected by FUBPs in a

HCC model so as to enable us to better understand the effects of its over-expression in addition to the modulation of c-myc.

6. Conclusion

This study represents the first single effort to combine three quantitative proteomic techniques to provide the most comprehensive analysis of proteome changes in liver tumourigenesis. A total of 344 regulated proteins were identified in both moderately- and poorly-differentiated HCC. The proteins identified varied significantly in the three techniques, suggests that these techniques are complementary and confirms that a combination of different approaches are essential to acquire adequate data in global profiling studies.

Differentially expressed proteins obtained from this study thus signifies the completion of the first crucial step; identification of possible molecular players in initiating and promoting hepatocarcinoma. In this thesis, only three major clusters of proteins; metabolic proteins, stress related proteins and c-myc associated proteins were further elaborated. In all these clusters, we observed a prominent increase in number of dysregulated proteins from moderately- to poorly-differentiated HCC. Stepwise abrogation of these pathways is an indicator of the loss of liver function as well as an attempt by the tumours to survive and proliferate.

Most interestingly a significant number of proteins identified, including nuclear localized proteins, were associated with the proto-oncogene, c-myc. Though c-myc was not identified in our proteomics screening but its over-expression was later confirmed using western blotting. This finding is consistent with other HCC reports, where elevated levels of c-myc have often been credited to chromosomal instability in the chromosome 8q or direct interaction of HBV-X protein. The identification of c-myc cluster of proteins thus reiterates the importance of this oncogene in HBV-related HCC as suggested by previous reports.

The non-bias approach of proteomics also confers it the capability of identifying novel proteins that have not yet been well characterized in this area of study. To our knowledge this is

the first HCC study to report over-expressin of FUBP1 and FUBP2 in moderately- and poorly-differentiated HCC. The abberation FUBPs were of particular interest due to their importance in "governing" the promoter sites for c-myc's transcription factors. Unlike the other c-myc associated proteins identified, FUBPs have been credited as essential in ensuring the tight regulation of the oncogene. *In vitro* experiments to investigate its significance in liver tumourigenesis, showed that FUBPs are required to maintain cell viability of HBV-associated liver cell lines, Hep3B but not in HepG2 (a HBV null cell line). It is thus tempting to hypothesize that FUBPs are capable of increasing c-myc expression and also necessary in promoting hepatocarcinogenesis (Fig 6.1). Nevertheless, more work needs to be done to establish FUBPs exact molecular role and function. Cell lines and / or animal models will also be required to confirm its specificity in modulating the progression of HBV-associated HCC.

It is hoped that c-myc and other prominent clusters of proteins that had been identified in this study will serve as a basis to extend our understanding in the molecular pathogenesis of HCC. Further characterization of their functions could provide insights to hepatocarcinoma and thus increase our ability for treatment and diagnosis of the disease.

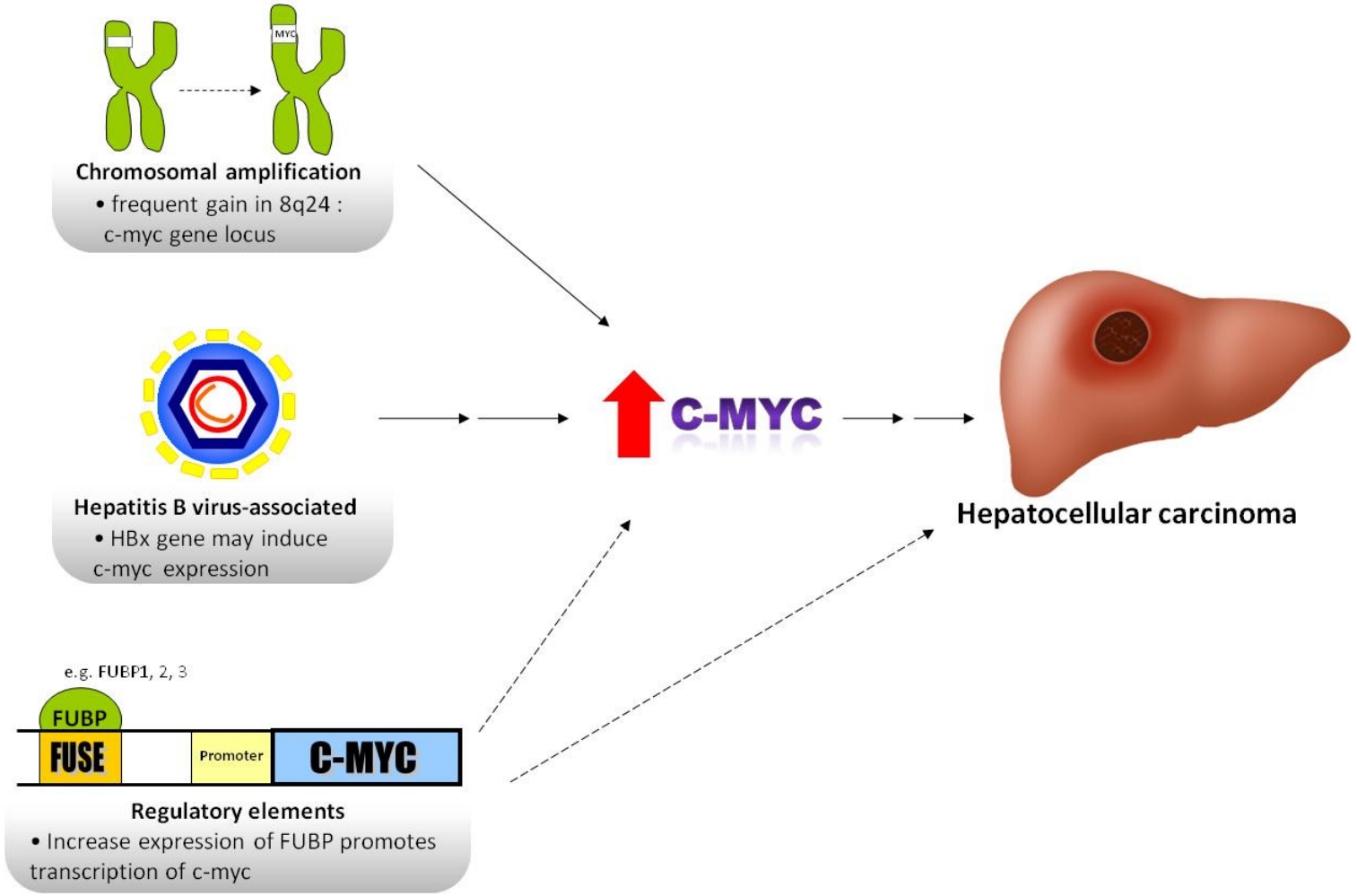


Figure 6.1 : Schematic diagram illustrating the possible mechanisms that may be involved in the amplification of the proto-oncogene, c-myc and HCC tumourigenesis.

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Appendix I

Table A : Significantly regulated proteins in moderately-differentiated HCC as identified by 2-D DIGE are listed below according to spot number.

Master No.	IPI Accession No.	Uniprot / Swissprot No.	Protein Name	Theoretical MW /pI	Experimental MW /pI	Av. Ratio	T-test	Protein Score	Protein Score CI%	Total Ion Score	Total Ion Score CI%	Percentage coverage (%)	Frequency (out of 5)	Appearance (out of 45 gels)
888	IPI00022463	P02787	Serotransferrin precursor	77.0 / 6.8	87.9 / 6.7	-2.67	1.70E-07	169	100	88	100	39	5	45 (45)
895	IPI00022463	P02787	Serotransferrin precursor	77.0 / 6.8	87.6 / 6.8	-1.97	9.60E-06	232	100	113	100	49	5	45 (45)
932	IPI00470790	Q96N76	Urocanase family protein	74.8 / 6.3	85.3 / 6.4	-2.11	1.90E-07	76	99.834	41	98.116	33	5	45 (45)
958	IPI00745872	P02768	Serum albumin precursor	69.4 / 5.9	82.4 / 6.0	-3.81	1.20E-08	353	100	201	100	58	5	45 (45)
977	IPI00853059	Q96AE4	Far upstream element-binding protein 1	67.6 / 7.2	83.3 / 6.7	3.65	3.90E-08	69	99.089	60	99.978	11	5	45 (45)
985	IPI00375441	Q96AE4	Far upstream element-binding protein 1	67.6 / 7.2	83.3 / 6.4	1.60	0.018	222	100	174	100	35	3	45 (45)
992	IPI00375441	Q96AE4	Far upstream element-binding protein 1	67.6 / 7.2	83.3 / 7.2	1.99	8.30E-05	182	100	78	100	47	4	45 (45)
1207	IPI00553177	P01009	Alpha-1-antitrypsin precursor	46.7 / 5.4	72.5 / 4.9	1.73	0.01	497	100	301	100	68	4	45 (45)
1208	IPI00472102	Q38L19	60kDa Heat shock protein	61.1 / 5.7	72.5 / 5.1	2.17	0.0015	373	100	271	100	38	4	42 (45)
1236	IPI00217871	P30038	Aldehyde dehydrogenase 4 family, member A1	61.7 / 8.3	72.9 / 6.5	-3.91	2.60E-08	86	99.983	25	9.93	33	5	45 (45)
1238	IPI00465436	P04040	Catalase	59.8 / 6.9	72.9 / 7.2	-3.18	7.40E-08	111	100	67	99.994	36	5	45 (45)
1244	IPI00465436	P04040	Catalase	59.8 / 6.9	72.2 / 7.0	-3.80	9.20E-08	519	100	361	100	56	5	45 (45)
1246	IPI00465436	P04040	Catalase	59.8 / 6.9	71.9 / 6.8	-4.27	3.40E-09	216	100	151	100	44	5	45 (45)
1250	IPI00465436	P04040	Catalase	59.8 / 6.9	71.9 / 6.7	-4.15	3.40E-09	477	100	349	100	55	5	45 (45)
1374	IPI00418471	P08670	Vimentin	53.7 / 5.1	65.0 / 4.8	3.39	0.00058	294	100	148	100	68	3	45 (45)
1389	IPI00012303	Q13228	Selenium binding protein 1	52.4 / 5.9	64.6 / 5.8	-2.49	0.0006	485	100	186	100	75	5	45 (45)
1402	IPI00012303	Q13228	Selenium binding protein 1	52.4 / 5.9	64.6 / 5.9	-1.92	5.50E-05	490	100	285	100	75	5	45 (45)
1627	IPI00296053	P07954	Isoform mitochondrial of Fumarate hydratase, or Isoform cytoplasmic of Fumarate hydratase, mitochondrial percursor	54.6 / 8.9	56.5 / 6.6	-2.83	9.60E-06	140	100	104	100	28	4	45 (45)
1633	IPI00296053	P07954	Isoform mitochondrial of Fumarate hydratase, or Isoform cytoplasmic of Fumarate hydratase, mitochondrial percursor	54.6 / 8.9	56.2 / 6.8	-2.70	8.30E-05	422	100	297	100	43	3	45 (45)
1640	IPI00759715	P07954	Isoform mitochondrial of Fumarate hydratase, or Isoform cytoplasmic of Fumarate hydratase, mitochondrial percursor	54.6 / 8.9	56.2 / 7.0	-2.31	0.00033	424	100	317	100	64	3	45 (45)
1718	IPI00654755	P68871	Hemoglobin subunit beta	16.0 / 6.7	53.6 / 7.1	-1.91	0.00022	292	100	188	100	95	5	45 (45)
1771	IPI00009268	Q03154	Aminoacylase-1	45.9 / 5.8	51.9 / 5.8	-4.27	2.70E-09	829	100	606	100	79	5	45 (45)
1802	IPI00784347	P05783	Keratin, type I cytoskeletal 18	48.1 / 5.3	50.0 / 5.0	-2.01	0.00024	339	100	222	100	58	4	45 (45)
1841	IPI00848090	P40121.1	Gelsolin-like capping protein / Macrophage capping protein	38.5 / 5.9	49.5 / 5.8	2.13	6.00E-07	114	100	93	100	19	4	45 (45)
1913	IPI00218407	P05062	Fructose-bisphosphate aldolase B	39.5 / 8.0	46.4 / 6.5	-6.62	2.80E-10	213	100	169	100	37	4	45 (45)

1917	IPI00291419	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	41.4 / 6.5	46.3 / 6.1	-2.64	3.10E-08	97	99.999	65	99.992	30	5	42 (45)
1937	IPI00398768	P05089	Arginase-1	34.7 / 6.7	46.2 / 6.8	-3.71	4.60E-06	419	100	268	100	83	5	45 (45)
1945	IPI00291419	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	41.4 / 6.5	46.2 / 6.2	-2.46	1.10E-07	64	97.377	29	88.256	39	5	45 (45)
1948	IPI00220271	P14550	Alcohol dehydrogenase	36.6 / 6.3	45.5 / 6.4	-2.40	7.00E-06	590	100	369	100	71	4	45 (45)
1962	IPI00027701	P16219	Short-chain specific Acyl CoA dehydrogenase, mitochondrial precursor	44.3 / 8.1	45.2 / 6.1	-2.61	2.00E-11	122	100	76	100	40	5	45 (45)
1963	IPI00027701	P16219	Short-chain specific Acyl CoA dehydrogenase, mitochondrial precursor	44.3 / 8.1	46.0 / 6.3	-3.70	1.60E-08	455	100	328	100	70	5	45 (45)
1990	IPI00760666	Q9H0W9	Ester hydrolase C11orf54	35.1 / 6.2	43.9 / 6.1	-3.07	5.40E-09	76	99.826	44	99.301	25	5	45 (45)
1991	IPI00073772	P09467	Fructose-1,6-bisphosphatase 1	36.8 / 6.5	44.5 / 6.5	-4.77	7.70E-09	471	100	344	100	71	5	45 (45)
1995	IPI00295777	P21695	Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	37.6 / 5.8	45.2 / 5.8	-2.16	4.80E-05	104	100	55	99.951	39	4	45 (45)
2008	IPI00220342	O94760	NG, NG-dimethylarginine dimethylaminohydrolase 1	31.1 / 5.5	44.4 / 5.5	-2.26	4.60E-06	389	100	269	100	70	4	45 (45)
2020	IPI00165360	P25325	3-mercaptopyruvate sulfurtransferase	33.2 / 6.1	43.9 / 6.2	-2.62	1.20E-09	362	100	262	100	72	5	45 (45)
2026	IPI00073772	P09467	Fructose-1,6-bisphosphatase 1	36.8 / 6.5	44.5 / 6.4	-3.05	3.30E-06	146	100	132	100	21	5	45 (45)
2037	IPI00072044	Q9H0W9	Ester hydrolase C11orf54	35.1 / 6.2	43.5 / 6.4	-2.88	9.70E-07	412	100	304	100	48	5	45 (45)
2040	IPI00061507	Q9H0W9	Ester hydrolase C11orf54	35.1 / 6.2	43.6 / 6.3	-2.45	2.10E-06	79	99.915	44	98.94	26	5	45 (45)
2152	IPI00017551	Q15493	Regucalcin	33.3 / 5.9	41.7 / 5.8	-2.06	0.00032	347	100	262	100	72	4	45 (45)
2193	IPI00165360	P25325	3-mercaptopyruvate sulfurtransferase	33.2 / 6.1	40.5 / 6.2	-2.13	9.40E-05	399	100	277	100	77	4	45 (45)
2267	IPI00329742	Q96GK7	Fumarylacetoacetate hydrolase domain containing 2A	34.6 / 8.5	39.3 / 6.7	-2.95	2.00E-07	59	91.883	27	70.667	29	5	45 (45)
2395	IPI00013860	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	35.3 / 8.4	36.3 / 5.6	-1.94	1.10E-05	100	100	53	99.901	47	5	45 (45)
2435	IPI00024896	P30039	Phenazine biosynthesis-like domain-containing protein (MAWD binding protein)	31.8 / 6.1	35.6 / 6.2	-3.96	2.40E-07	359	100	231	100	74	4	45 (45)
2436	IPI00216136	P50053	Ketohexokinase	32.7 / 5.6	35.3 / 5.9	-2.24	7.10E-06	220	100	133	100	63	4	45 (45)
2442	IPI00414696	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	37.4 / 9.0	35.8 / 6.8	-1.80	0.0015	204	100	117	100	48	4	45 (45)
2480	IPI00746205	Q9UL46.3	Proteasome activator complex subunit 2	27.4 / 5.4	34.8 / 5.3	-1.69	0.00018	269	100	192	100	54	3	45 (45)
2482	IPI00019755	P78417	Glutathione transferase omega-1	27.6 / 6.2	34.8 / 5.5	-1.77	6.10E-05	156	100	114	100	38	5	45 (45)
2494	IPI00019755	P78417	Glutathione transferase omega-1	27.6 / 6.2	34.6 / 5.7	-1.97	9.30E-05	264	100	189	100	57	4	45 (45)
2516	IPI00016346	O94903	Proline synthetase co-transcribed bacterial homolog protein	30.3 / 7.1	34.3 / 6.9	-1.61	9.90E-05	76	99.826	30	79.389	34	4	45 (45)
2522	IPI00513830	P05062	Fructose-bisphosphate aldolase	39.5 / 8.0		-2.25	5.70E-07	106	100	100	100	8	4	45 (45)
2560	IPI00479722	Q06323	Proteasome activator complex 1	28.7 / 5.8	33.3 / 5.6	-2.18	6.50E-06	568	100	340	100	65	4	45 (45)
2564	IPI00215983	P00915	Carbonic anhydrase 1	28.9 / 6.6	33.2 / 6.7	-1.64	0.04	451	100	373	100	69	5	45 (45)
2616	IPI00024911	P30040	Endoplasmic reticulum protein ERp29 percursor	29.0 / 6.8	32.4 / 5.7	-2.11	0.0001	497	100	419	100	42	5	45 (45)
2627	IPI00025512	P04792	Heat shock protein beta-1	22.8 / 6.0	32.0 / 5.5	-1.94	0.0004	207	100	134	100	41	5	45 (45)
2640	IPI00218414	P00918	Carbonic anhydrase 2	29.2 / 6.9	31.6 / 6.9	-2.34	2.30E-06	454	100	334	100	68	5	45 (45)
2645	IPI00024993	P30084	Enoyl-CoA hydratase, mitochondrial precursor	31.4 / 8.3	31.5 / 5.6	-2.26	1.30E-05	171	100	75	100	57	5	45 (45)

2652	IPI00024993	P30084	Enoyl-CoA hydratase, mitochondrial precursor	31.4 / 8.3	31.4 / 5.9	-2.58	7.00E-06	434	100	324	100	66	5	45 (45)
2671	IPI00793232	Q9NVS9	Pyridoxine-5'-phosphate oxidase	33.0 / 6.6	31.1 / 6.0	-2.50	1.50E-05	240	100	142	100	81	5	45 (45)
2729	IPI00465028	P60174	Triosephosphate isomerase	26.7 / 6.5	30.2 / 6.5	-1.86	1.70E-06	243	100	166	100	72	5	45 (45)
2737	IPI00465028	P60174	Triosephosphate isomerase	26.7 / 6.5	30.2 / 6.1	-2.33	3.30E-13	173	100	125	100	44	5	45 (45)
2738	IPI00220301	P30041	Peroxiredoxin-6	25.0 / 6.0	30.3 / 5.9	-2.29	2.50E-07	376	100	263	100	67	5	42 (45)
2751	IPI00024993	P30084	Enoyl-CoA hydratase, mitochondrial precursor	31.4 / 8.3	29.9 / 5.6	-5.41	1.50E-07	157	100	126	100	42	5	45 (45)
2782	IPI00024919	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial percursor	27.7 / 7.7	29.3 / 5.7	-1.69	1.90E-05	89	99.992	57	99.94	55	5	45 (45)
2795	IPI00219129	P16083	Ribosyldihydronicotinamide dehydrogenase / NAD(P)H dehydrogenase	26.0 / 5.9	29.3 / 5.8	-1.81	0.00021	503	100	407	100	78	4	45 (45)
2796	IPI00793677	P30042	Isoform Long of ES1 protein homolog, mitochondrial precursor	28.2 / 8.5	29.2 / 6.9	-2.69	2.40E-07	380	100	286	100	80	5	45 (45)
2812	IPI00298547	Q99497	Protein DJ-1	19.9 / 6.3	28.8 / 5.7	-2.28	8.30E-07	209	100	141	100	62	5	45 (45)
2824	IPI00298547	Q99497	Protein DJ-1	19.9 / 6.3	28.6 / 6.1	-1.62	5.40E-05	508	100	370	100	86	4	45 (45)
2827	IPI00783862	P30043	Flavin reductase	22.1 / 7.1	28.7 / 7.1	-3.61	6.10E-08	351	100	247	100	86	5	45 (45)
2950	IPI00219446	P30086	Phosphatidylethanolamine-binding protein 1	21.1 / 7.0	26.5 / 6.5	-2.91	4.60E-08	87	99.989	38	95.876	60	5	42 (45)
3162	IPI00012048	P15531	Nucleoside diphosphate kinase A / Nucleoside diphosphate kinase B	17.1 / 5.8	23.6 / 5.7	2.10	0.003	320	100	215	100	76	4	45 (45)
3208	IPI00641737	P00738	Haptoglobin precursor	45.2 / 6.1	22.9 / 6.0	-2.58	0.019	317	100	288	100	21	4	45 (45)
3241	IPI00783680	P00441	Superoxide dismutase	15.9 / 5.7	21.8 / 5.6	-3.39	9.90E-06	447	100	371	100	87	4	45 (45)
3340	IPI00643115	P13668	Stathmin 1/oncoprotein 18	17.3 / 5.8	15.0 / 5.6	2.91	1.60E-07	209	100	181	100	32	5	45 (45)
3488	IPI00418471	P08670	Vimentin	53.7 / 5.1	59.1 / 4.6	2.41	0.0052	728	100	380	100	77	3	45 (45)

Table B : Significantly regulated proteins in poorly-differentiated HCC as identified by 2-D DIGE are listed below according to spot number.

Master No.	IPI Accession No.	Uniprot / Swissprot No.	Protein Name	Theoretical MW /pI	Experimental MW /pI	Av. Ratio	T-test	Protein Score	Protein Score CI%	Total Ion Score	Total Ion Score CI%	Percentage coverage (%)	Frequency (out of 7)	Appearance (out of 63 gels)
681	IPI00479786	Q92945	KH-type splicing regulatory protein	73.1 / 6.8	94.4 / 6.6	1.86	0.024	355	100	232	100	29	5	63 (63)
694	IPI00479786	Q92945	KH-type splicing regulatory protein	73.1 / 6.8	94.0 / 6.9	2.34	0.0052	535	100	375	100	45	5	63 (63)
777	IPI00022463	P02787	Serotransferrin precursor	77.0 / 6.8	89.3 / 6.6	-3.07	5.00E-06	204	100	29	67.731	46	5	63 (63)
780	IPI00022463	P02787	Serotransferrin precursor	77.0 / 6.8	89.3 / 6.5	-1.83	0.0022	209	100	65	99.994	50	4	60 (63)
782	IPI00022463	P02787	Serotransferrin precursor	77.0 / 6.8	89.0 / 6.9	-3.16	0.00013	340	100	133	100	48	5	63 (63)
859	IPI00745872	P02768	Serum albumin precursor	69.4 / 5.9	85.9 / 6.0	-2.76	0.017	138	100	63	99.992	38	6	63 (63)
880	IPI00745872	P02768	Serum albumin precursor	69.4 / 5.9	85.9 / 5.9	1.79	0.045	305	100	172	100	56	4	63 (63)
882	IPI00375441	Q96AE4	Far upstream element-binding protein 1	67.6 / 7.2	84.6 / 6.9	1.68	0.035	378	100	257	100	43	4	63 (63)
895	IPI00375441	Q96AE4	Far upstream element-binding protein 1	67.6 / 7.2	83.9 / 7.2	1.90	0.0006	254	100	126	100	49	5	63 (63)
938	IPI00007765	P38646	Stress-70 protein, mitochondrial precursor	73.7 / 5.9	81.5 / 5.4	1.51	0.0032	292	100	224	100	44	6	63 (63)
1111	IPI00465436	P04040	Catalase	59.8 / 6.9	72.1 / 6.6	-2.57	2.70E-05	131	100	66	99.994	38	4	63 (63)
1221	IPI00218914	P00352	Retinal dehydrogenase 1	54.9 / 6.3	67.7 / 6.4	-1.77	0.00029	360	100	227	100	57	6	63 (63)
1240	IPI00006663	P05091	Aldehyde dehydrogenase, mitochondrial precursor	56.4 / 6.6	66.3 / 5.8	-2.22	0.047	391	100	221	100	60	5	63 (63)
1481	IPI00759715	P07954	Isoform mitochondrial of Fumarate hydratase, or Isoform cytoplasmic of Fumarate hydratase, mitochondrial percursor	54.6 / 8.9	56.9 / 6.8	-2.61	1.50E-05	223	100	171	100	34	6	63 (63)
1488	IPI00759715	P07954	Isoform mitochondrial of Fumarate hydratase, or Isoform cytoplasmic of Fumarate hydratase, mitochondrial percursor	54.6 / 8.9	56.7 / 7.0	-1.80	0.017	197	100	163	100	29	4	63 (63)
1496	IPI00759715	P07954	Isoform mitochondrial of Fumarate hydratase, or Isoform cytoplasmic of Fumarate hydratase, mitochondrial percursor	54.6 / 8.9	56.7 / 7.2	-1.85	0.032	506	100	468	100	47	4	63 (63)
1584	IPI00009268	Q03154	Aminoacylase-1	45.9 / 5.8	54.1 / 5.7	-2.32	2.40E-06	505	100	267	100	83	7	63 (63)
1589	IPI00009268	Q03154	Aminoacylase-1	45.9 / 5.8	54.3 / 5.8	-3.26	3.20E-05	569	100	360	100	80	5	63 (63)
1767	IPI00218407	P05062	Fructose-bisphosphate aldolase B	39.5 / 8.0	47.4 / 7.0	-2.96	1.60E-09	176	100	125	100	39	7	63 (63)
1769	IPI00218407	P05062	Fructose-bisphosphate aldolase B	39.5 / 8.0	47.4 / 7.2	-2.58	6.10E-08	119	100	89	100	17	7	63 (63)
2032	IPI00218407	P05062	Fructose-bisphosphate aldolase B	39.5 / 8.0	41.1 / 6.8	-2.30	1.60E-05	154	100	106	100	31	6	63 (63)
2060	IPI00218407	P05062	Fructose-bisphosphate aldolase B	39.5 / 8.0	40.5 / 6.2	-2.90	8.90E-06	124	100	93	100	30	6	63 (63)
2318	IPI00218407	P05062	Fructose-bisphosphate aldolase B	39.5 / 8.0	33.9 / 6.5	-2.20	0.0022	311	100	270	100	36	5	63 (63)
1774	IPI00291560	P05089	Arginase-1	34.7 / 6.7	47.2 / 6.7	-2.14	1.00E-07	207	100	133	100	48	5	63 (63)
1798	IPI00027701	P16219	Short chain specific acyl-CoA dehydrogenase, mitochondrial precursor	44.3 / 8.1	47.9 / 6.3	-2.22	0.0006	228	100	158	100	55	4	63 (63)
1845	IPI00073772	P09467	Fructose-1,6-bisphosphatase 1	36.8 / 6.5	46.5 / 6.2	-1.76	5.00E-06	72	99.584	59	99.975	23	6	63 (63)
1861	IPI00072044	Q9H0W9	Ester hydrolase C11orf5	35.1 / 6.2	44.5 / 6.4	-2.09	5.70E-05	300	100	214	100	67	6	63 (63)

1975	IPI00027701	P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	44.3 / 8.1	42.8 / 6.8	-2.19	6.80E-05	205	100	112	100	47	6	63 (63)
2039	IPI00015018	Q15181	Inorganic pyrophosphatase	32.7 / 5.5	40.9 / 5.5	1.76	0.039	242	100	164	100	66	5	63 (63)
2425	IPI00024993	P30084	Enoyl-CoA hydratase, mitochondrial percursor	31.4 / 8.3	31.8 / 5.6	-2.33	5.00E-07	72	99.574	72	99.998	7	6	63 (63)
2440	IPI00024993	P30084	Enoyl-CoA hydratase, mitochondrial percursor	31.4 / 8.3	31.5 / 5.9	-2.82	6.20E-08	217	100	166	100	48	5	63 (63)
2455	IPI00793232	Q9NVS9	Pyridoxine-5'-phosphate oxidase	30.0 / 6.6	31.4 / 6.0	-1.92	1.50E-05	244	100	143	100	83	6	63 (63)
2496	IPI00003362	Q2KHP4	HSPA5 protein / GRP78	72.4 / 5.1	30.2 / 5.1	1.68	0.0037	346	100	308	100	23	4	63 (63)
2519	IPI00220301	P30041	Peroxiredoxin-6	25.0 / 6.0	30.3 / 5.8	-1.97	8.00E-07	384	100	281	100	66	6	63 (63)
2602	IPI00298547	Q99497	Protein DJ-1	19.9 / 6.3	29.1 / 5.7	-2.11	3.90E-07	113	100	96	100	52	5	63 (63)
2749	IPI00219446	P30086	Phosphatidylethanolamine-binding protein 1	21.1 / 7.0	26.4 / 7.4	-2.35	0.00065	334	100	249	100	80	5	63 (63)
2981	IPI00375531	P15531	Nucleoside diphosphate kinase A / Nucleoside diphosphate kinase B	17.1 / 5.8	24.6 / 5.7	1.99	4.20E-05	257	100	189	100	60	7	63 (63)
3028	IPI00641737	P00738	Haptoglobin precursor	45.2 / 6.1	23.9 / 6.0	-2.93	7.70E-07	111	100	39	95.68	35	7	63 (63)
3082	IPI00783680	P00441	Superoxide dismutase	15.9 / 5.7	23.0 / 5.6	-2.70	2.50E-06	357	100	281	100	87	6	63 (63)
3512	IPI00607577	P04179	manganese superoxide dismutase isoform B precursor	24.7 / 8.4	27.5 / 6.4	-2.20	7.90E-06	72	99.554	46	97.552	21	5	63 (63)

Appendix II

Table A : Significantly regulated proteins in moderately-differentiated HCC as identified by cICAT are listed below.

Acc No	Uniprot	Name	131NT	196NT	199NT	200NT	203NT
IPI00783862	P30043	Flavin reductase	0.000	0.612	0.603	0.553	0.006
IPI00760666	Q9H0W9	Isoform 4 of Ester hydrolase C11orf54	0.469	0.591	0.707	0.486	0.000
IPI00291560	P05089	Isoform 1 of Arginase-1	0.000	0.458	0.661	0.326	0.396
IPI00783680	P00441	Superoxide dismutase	0.000	0.641	0.390	0.629	0.000
IPI00465436	P04040	Catalase	0.111	0.150	0.462	0.268	0.147
IPI00013860	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	0.000	0.536	0.444	0.536	0.327
IPI00215901	P54819	Isoform 1 of Adenylate kinase isoenzyme 2, mitochondrial	0.000	1.158	0.672	0.273	0.173
IPI00852596	Q86WI9	Ferritin light chain	0.000	0.000	0.642	0.292	0.825
IPI00654755	P68871	Hemoglobin subunit beta	0.473	0.027	0.554	0.815	0.446
IPI00549725	P18669	Phosphoglycerate mutase 1	0.674	0.792	0.665	0.625	0.000
IPI00024993	P30084	Enoyl-CoA hydratase, mitochondrial precursor	0.000	0.723	0.374	0.531	0.002
IPI00784231	Q4AEI2	GPX1 16 kDa protein	0.544		0.692	0.554	0.240
IPI00219526	P36871	Isoform 1 of Phosphoglucomutase-1		0.333	0.629	0.309	0.000
IPI00797249	Q7Z4W1	DCXR 26 kDa protein	0.000	0.407		0.000	0.000
IPI00060200	Q96C23	Aldose 1-epimerase	0.000		0.316	0.559	0.004
IPI00375513	P21964	Isoform Soluble of Catechol O-methyltransferase	0.000	0.001	0.669		0.000
IPI00017579	P00439	Phenylalanine-4-hydroxylase	0.000	0.000		0.000	0.000
IPI00009532	P80404	4-aminobutyrate aminotransferase, mitochondrial precursor	0.000	0.363		0.006	0.000
IPI00745729	A6NML9	SELENBP1 53 kDa protein	0.000	0.009		0.695	0.003
IPI00216293	Q16762	Thiosulfate sulfurtransferase	0.261	2.136	0.401	0.360	0.045
IPI00797738	P14854	- 12 kDa protein	0.285	29.697	0.648	0.578	0.113
IPI00746782	Q59HD5	3-mercaptopyruvate sulfurtransferase variant (Fragment)	0.474	0.722		0.614	0.156
IPI00026156	P14317	Hematopoietic lineage cell-specific protein	0.716	0.627	0.635		0.682
IPI00218568	P61457	Pterin-4-alpha-carbinolamine dehydratase	0.316	0.768	0.599		0.000
IPI00793232	Q9NVS9	PNPO 19 kDa protein	0.000	0.781		0.551	0.165
IPI00303174	Q93099	Homogentisate 1,2-dioxygenase		0.553		0.451	0.138
IPI00218407	P05062	Fructose-bisphosphate aldolase B	0.000	0.005			0.000
IPI00789806	P28838	Isoform 2 of Cytosol aminopeptidase		0.599	0.239		0.406
IPI00220327	P04264	Keratin, type II cytoskeletal 1		0.001		0.034	0.447
IPI00554521	P02794	Ferritin heavy chain	0.000	0.000		0.181	
IPI00640017	P07099	Epoxide hydrolase 1, microsomal	0.000	0.597			0.559
IPI00295386	P16152	Carbonyl reductase [NADPH] 1		0.421	0.667		0.000
IPI00027146	P49448	Glutamate dehydrogenase 2, mitochondrial precursor	0.408	0.004		0.443	

IPI00216057	Q00796	Sorbitol dehydrogenase	0.068	0.008			0.164
IPI00065073	Q96LK9	AKR1D1 highly similar to 3-OXO-5-BETA- S	0.000	0.000			0.000
IPI00793605	P27797	CALR 37 kDa protein	0.565	0.818	1.469	0.643	0.241
IPI00291419	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	0.000	1.508		0.283	0.355
IPI00216279	P50440	Isoform Cytoplasmic of Glycine amidinotransferase	0.000	2.032		0.000	0.008
IPI00298547	Q99497	PARK7 Protein DJ-1	0.440	1.757	0.497		0.003
IPI00020091	P19652	ORM2 Alpha-1-acid glycoprotein 2 precursor	0.639	0.677		6.199	0.099
IPI00796379	Q6IAT8	B2M B2M protein	0.622		0.532	2.732	0.381
IPI00010796	P07237	Protein disulfide-isomerase precursor	0.006	3.168	1.647	77.276	0.000
IPI00784154	P10809	60 kDa heat shock protein, mitochondrial precursor	0.503	2.945	2.360	1.859	0.550
IPI00022434	A6NBZ8	Serum albumin	1.575	1.550	1.014	2.648	0.073
IPI00022488	P02790	HPX Hemopexin precursor	1.564	1.513	0.769	1.873	0.457
IPI00216138	Q01995	TAGLN Transgelin	4.626	0.422		2.570	4.751
IPI00827679	P08670	VIM 50 kDa protein	2.003	0.648		3355.970	3.133
IPI00295741	P07858	CTSB Cathepsin B precursor	1.410	1.592	0.396	2.291	
IPI00644989	Q15084	Isoform 1 of Protein disulfide-isomerase A6 precursor	1.582	1.864		1.466	0.000
IPI00294495	Q9Y3C8	UFC1 Ufm1-conjugating enzyme 1	1.803	1.667		1.824	0.522
IPI00419585	P62937	Peptidyl-prolyl cis-trans isomerase A	1.570	3.361	1.494		
IPI00556632	P02751	Isoform 12 of Fibronectin precursor		3399.395	3225.625	4732.048	
IPI00105407	O60218	Aldo-keto reductase family 1 member B10		2185.248		1568.221	5861.212
IPI00426051	Q6MZU6	Hypothetical protein	1.672			2.049	1.646
IPI00298828	P02749	Beta-2-glycoprotein 1 precursor	2.199	83.341		1.672	
IPI00009032	P05455	Lupus La protein	3.412	3.695	1.521	1.408	0.764
IPI00220278	P24844	Myosin regulatory light chain 2, smooth muscle isoform	7243.278	1.657		8926.424	5680.061

Table B : Significantly regulated proteins in poorly-differentiated HCC as identified by cICAT are listed below.

Acc No	Uniprot	Name	120NT	126NT	155NT	157NT	187NT	207NT	215NT
IPI00024993	P30084	Enoyl-CoA hydratase, mitochondrial precursor		0.011	1.392	0.693	0.000	0.000	0.001
IPI00216293	Q16762	Thiosulfate sulfurtransferase	0.002		1.381	0.535	0.285	0.212	0.119
IPI00013860	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor		0.374	1.859	0.543	0.561	0.389	0.664
IPI00298547	Q99497	Protein DJ-1	0.566	0.450	1.726		0.578	0.047	0.692
IPI00788848	P07148	14 kDa protein		0.601		0.673	0.617		0.629
IPI00783862	P30043	Flavin reductase	0.671				0.694	0.432	0.311
IPI00216057	Q00796	Sorbitol dehydrogenase		0.324			0.682	0.000	0.184
IPI00513830	P05062	Fructose-bisphosphate aldolase	0.104				0.279	0.000	0.000
IPI00291560	P05089	Isoform 1 of Arginase-1				0.341	0.659	0.434	0.524
IPI00654755	P68871	Hemoglobin subunit beta	3.994	0.245	0.776	0.776	0.046	0.013	0.673
IPI00852596	Q86WI9	Ferritin light chain	0.172	0.549		0.737	0.000	0.000	7712.681
IPI00783680	P00441	Superoxide dismutase		0.421		0.391	3.905	0.000	0.230
IPI00218568	P61457	Pterin-4-alpha-carbinolamine dehydratase		0.314		0.417	1.814	0.345	0.632
IPI00022434	A6NBZ8	Serum albumin	20.035	1.582	0.646	4.147	1.578		1.281
IPI00022429	P02763	Alpha-1-acid glycoprotein 1 precursor	12282.499	2141.019	0.770	5.489	1.785	0.774	
IPI00788802	Q53EM5	Transketolase variant (Fragment)		2.354		1.829	1.352	3.356	1.731
IPI00298828	P02749	Beta-2-glycoprotein 1 precursor		1.401	0.776	2.761	102.734		2.325
IPI00383164	Q8WY24	IGHA1 SNC66 protein	10539.867	1.769		11.324	1.382		1.510
IPI00472610	Q6PI81	IGHM IGHM protein		1.530		5.123		22.746	1.854
IPI00402182	O60506	Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q		2.358			1.551	1.542	3.337
IPI00022488	P02790	Hemopexin precursor	1705.294	1.688	0.651	3.153		1.465	1.499
IPI00419585	P62937	Peptidyl-prolyl cis-trans isomerase A			2.082	1.950	17.831	1.617	2.467
IPI00297579	Q13185	Chromobox protein homolog 3			2.720	1.469	1.461	2.334	3.467
IPI00789430	Q4R520	HSP90B1 Protein		1.412	1.788	1.679		1.848	1.660
IPI00009032	P05455	Lupus La protein		1.730	3.240		2.274	3.093	2.409

* Number of peptides, standard deviation, total ion score C.I.% and best ion score C.I.% of the proteins identified from each patient samples are available excel file in the disk attached behind.

Appendix III

Table A : Significantly regulated proteins in moderately-differentiated HCC as identified by iTRAQ are listed below.

Acc No	Uniprot	Name	131NT	196NT	199NT	200NT	203NT
IPI00011062	P31327	Isoform 1 of Carbamoyl-phosphate synthase	0.206	0.495	0.473	0.230	0.253
IPI00005038	P52758	Ribonuclease UK114	0.247	0.585	0.341	0.278	0.488
IPI00794900	P11586	C-1-tetrahydrofolate synthase	0.313	0.422	0.327	0.238	0.409
IPI00465436	P04040	Catalase	0.618	0.483	0.564	0.564	0.440
IPI00473031	P00325	Alcohol dehydrogenase 1B	0.116	0.126	0.407	0.300	0.299
IPI00073772	P09467	Fructose-1,6-bisphosphatase 1	0.229	0.662	0.431	0.389	0.192
IPI00797249	Q7Z4W1	L-xylulose reductase	0.302	0.374	0.490	0.324	0.255
IPI00218407	P05062	Fructose-bisphosphate aldolase B	0.092	0.594	0.289	0.253	0.198
IPI00216136	P50053	Isoform C of Ketohexokinase	0.256	0.698	0.477	0.182	0.296
IPI00009268	Q03154	Aminoacylase-1	0.304	1.045	0.636	0.190	0.474
IPI00009532	P80404	4-aminobutyrate aminotransferase, mitochondrial precursor	0.199	0.497	0.786	0.411	0.304
IPI00004101	Q93088	Betaine--homocysteine S-methyltransferase 1	0.274	0.755	0.605	0.317	0.316
IPI00218899	P08319	Alcohol dehydrogenase 4	0.176	0.145	0.835	0.296	0.195
IPI00433347	P22307	Sterol carrier protein 2 isoform 2	0.324	0.569	0.786	0.624	0.594
IPI00026932	O75795	UDP-glucuronosyltransferase 2B17 precursor	0.344	0.425	0.859	0.421	0.443
IPI00844159	P36871	Phosphoglucomutase 1	0.295	0.718	0.703	0.678	0.465
IPI00009367	P21549	Serine--pyruvate aminotransferase	0.293	0.470	0.783	0.429	0.686
IPI00024990	Q02252	Methylmalonate-semialdehyde dehydrogenase mitochondria	0.405	0.520	1.003	0.527	0.391
IPI00647328	P30038	Aldehyde dehydrogenase 4 family, member A1	0.429	0.589	1.031	0.372	0.580
IPI00640430	P00966	Argininosuccinate synthase	0.227	0.272	0.341	0.393	
IPI00792207	Q53FB6	Aldehyde dehydrogenase 2 variant (Fragment)	0.349	1.001	0.909	0.700	0.561
IPI00783862	P30043	Flavin reductase	1.047	0.509	0.656	1.035	0.634
IPI00218836	P07108	Acyl-CoA-binding protein Isoform 2	0.477	1.254	1.037	0.673	0.549
IPI00789806	P28838	Cytosol aminopeptidase Isoform 2	0.637	1.029	0.587	0.606	0.741
IPI00332828	O00748	Ccarboxylesterase 2 isoform 1	0.300	1.108	0.838	0.464	0.397
IPI00295386	P16152	Carbonyl reductase [NADPH] 1	0.360	0.741	0.732	0.447	0.521
IPI00001539	P42765	3-ketoacyl-CoA thiolase, mitochondrial	0.324	0.723	1.219	0.664	0.415
IPI00021772	Q00266	S-adenosylmethionine synthetase isoform type-1	0.449	1.040	1.250	0.343	0.607
IPI00397860	P00167	Cytochrome b5 Isoform 1	0.203	0.812	1.004	0.324	0.281
IPI00024993	P30084	Enoyl-CoA hydratase, mitochondrial precursor	0.409	0.838	0.874	0.533	0.326
IPI00030363	P24752	Acetyl-CoA acetyltransferase, mitochondrial precursor	0.212	0.405	1.225	1.270	0.598
IPI00063130	Q6UW68	Transmembrane protein 205	0.440	0.589	0.908	1.160	0.625
IPI00218914	P00352	Retinal dehydrogenase 1	0.423	0.976	0.959	0.642	0.581
IPI00294380	Q16822	Phosphoenolpyruvate carboxykinase mitochondrial precursor	0.277	0.498	0.744	0.422	
IPI00291560	P05089	Arginase-1 Isoform 1	0.217	0.659	0.905	0.078	
IPI00783680	P00441	Superoxide dismutase	0.251	0.461			0.355
IPI00024623	P45954	Short/branched chain specific acyl-CoA dehydrogenase,	0.426	0.611			0.676
IPI00514772	P04424	Argininosuccinate lyase	0.623	0.584			0.394
IPI00797038	Q16822	Phosphoenolpyruvate carboxykinase 2 isoform 1	0.263	0.493			0.344
IPI00657682	P08263	Glutathione S-transferase A1	0.118	0.524			0.567

IPI00007282	P05181	Cytochrome P450 2E1	0.549	0.458			0.403
IPI00006934	Q9UJM8	Hydroxyacid oxidase 1	0.431	0.489			0.668
IPI00787584	P16662	Similar to UDP-glucuronosyltransferase 2B7 precursor	0.350	0.399			0.369
IPI00007219	P11712	Cytochrome P450 2C9			0.644	0.472	0.323
IPI00743616	Q06278	Hypothetical protein AOX1	0.372	0.526			0.337
IPI00329331	Q16851	UTP--glucose-1-phosphate uridylyltransferase	0.330	0.395			0.349
IPI00745729	A6NML9	Selenium-binding protein 1	0.447	0.521			0.693
IPI00216057	Q00796	Sorbitol dehydrogenase	0.270	0.434			0.422
IPI00745233	P09210	Glutathione S-transferase A2			0.491	0.554	0.621
IPI00217458	P24298	Alanine aminotransferase 1			0.508	0.411	0.344
IPI00300026	P50225	Sulfotransferase 1A1	0.226	0.541			0.349
IPI00642548	O43175	Phosphoglycerate dehydrogenase	0.348	0.712			0.426
IPI00218896	P07327	Alcohol dehydrogenase 1A	0.154	0.128			0.338
IPI00012728	P33121	Isoform 1 of Long-chain-fatty-acid--CoA ligase 1	0.350	0.556			0.374
IPI00216952	P02545	Isoform C of Lamin-A/C	2.103	1.307	1.436	1.278	2.979
IPI00003865	P11142	Isoform 1 of Heat shock cognate 71 kDa protein	1.603	1.357	1.832	1.699	1.311
IPI00465365	P09651	Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	1.606	1.688	1.349	1.256	2.643
IPI00784154	P10809	60 kDa heat shock protein, mitochondrial precursor	0.970	2.102	2.404	2.978	0.948
IPI00007752	P68371	Tubulin beta-2C chain	1.869	1.543	1.178	0.962	1.809
IPI00010779	P67936	Isoform 1 of Tropomyosin alpha-4 chain	3.127	0.767	0.823	1.485	3.088
IPI00329801	P08758	Annexin A5	3.369	1.285	1.002	1.718	2.622
IPI00007765	P38646	Stress-70 protein, mitochondrial precursor	0.852	1.786	2.001	2.590	0.894
IPI00549248	P06748	Isoform 1 of Nucleophosmin	2.280	1.454	1.302	1.191	2.372
IPI00843975	P15311	Ezrin	1.509	0.762	0.821	2.698	1.551
IPI00455315	P07355	Annexin A2	3.363	2.585	1.141	0.725	3.574
IPI00011654	P07437	Tubulin beta chain	2.053	1.464	1.199	0.833	1.815
IPI00414676	P08238	Heat shock protein HSP 90-beta	1.305	1.535	1.689	1.637	1.341
IPI00298497	P02675	Fibrinogen beta chain precursor	3.536	1.317	1.254	2.326	1.664
IPI00218319	P06753	Isoform 2 of Tropomyosin alpha-3 chain	2.580	0.997	0.892	1.520	2.005
IPI00220362	P61604	10 kDa heat shock protein, mitochondrial	0.950	2.385	2.250	2.727	0.726
IPI00029717	P02671	Isoform 2 of Fibrinogen alpha chain precursor	3.336	1.255	1.300	2.266	1.492
IPI00328230	Q01082	Isoform Short of Spectrin beta chain, brain 1	1.400	1.343	1.220	1.597	1.473
IPI00749398	P35237	Serine (or cysteine) proteinase inhibitor	1.819	0.759	0.978	2.366	1.409
IPI00021842	P02649	Apolipoprotein E precursor	1.619	3.046	1.236	1.226	1.626
IPI00219365	P26038	Moesin	1.878	0.937	0.872	1.463	1.944
IPI00025512	P04792	Heat shock protein beta-1	1.846	1.161	1.455	1.040	1.608
IPI00845339	P08107	Heat shock 70kDa protein 1A	1.389	1.943	2.392	2.125	
IPI00026260	P22392	Nucleoside diphosphate kinase B	1.965	1.892	1.110	1.807	
IPI00397808	P62992	similar to ubiquitin and ribosomal protein S27a precursor	1.865	1.422	1.872	1.371	
IPI00218585	Q15063	Isoform 2 of Periostin precursor	24.739	2.857			6.707
IPI00465431	P17931	Galectin-3	2.954	1.502			1.547
IPI00400826	P10909	Clusterin isoform 1	2.437	1.794			5.288
IPI00647915	P37802	Transgelin-2	2.900	1.593			3.332
IPI00298971	P04004	Vitronectin precursor	2.748	2.429			3.067
IPI00021263	P63104	14-3-3 protein zeta/delta	2.628	1.400	1.029	1.403	2.876
IPI00759644	Q1JUQ4	FK506 binding protein12	2.831	1.328	1.492	1.671	2.144
IPI00022418	P02751	Isoform 1 of Fibronectin precursor	3.462	4.691	3.487	1.285	2.196
IPI00646055	Q12931	Heat shock protein 75 kDa, mitochondrial	1.450	1.719	1.609	1.390	1.859
IPI00339269	P17066	Heat shock 70 kDa protein 6	1.430	2.023	2.338	2.210	
IPI00414696	P22626	Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	1.674	1.431	1.432	1.554	1.965

Table B : Significantly regulated proteins in poorly-differentiated HCC as identified by iTRAQ are listed below

Acc No	Uniprot	Name	120NT	126NT	155NT	157NT	187NT	207NT	215NT
IPI00011062	P31327	Isoform 1 of Carbamoyl-phosphate synthase	0.296	0.325	1.162	0.161	0.253	0.121	0.209
IPI00402759	Q6IB77	Isoform 1 of Glycine N-acyltransferase	0.414	0.196	0.991	0.287	0.436	0.15	0.149
IPI00332828	O00748	Carboxylesterase 2 isoform 1	0.513	0.655	1.051	0.286	0.394	0.384	0.319
IPI00025341	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	0.399	0.453	1.078	0.405	0.676	0.228	0.207
IPI00216133	Q06520	Bile salt sulfotransferase	0.343	0.341	1.09	0.269	0.391	0.256	0.175
IPI00096066	Q96I99	Succinyl-CoA ligase	0.621	0.484	1.227	0.372	0.677	0.398	0.432
IPI00797038	Q16822	Mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1	0.402	0.282	0.99	0.412	0.568	0.324	0.267
IPI00218899	P08319	Alcohol dehydrogenase 4	0.224	0.222	0.974	0.358	0.225	0.178	0.142
IPI00005038	P52758	Ribonuclease UK114	0.395	0.397	1.131	0.341	0.492	0.315	0.292
IPI00218407	P05062	Fructose-bisphosphate aldolase B	0.518	0.245	0.967	0.109	0.355	0.109	0.121
IPI00024990	Q02252	Methylmalonate-semialdehyde dehydrogenase mitochondria	0.558	0.243	1.153	0.274	0.487	0.215	0.339
IPI00218896	P07327	Alcohol dehydrogenase 1A	0.26	0.232	1.142	0.223	0.419	0.133	0.206
IPI00513827	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	0.643	0.453	1.204	0.36	0.497	0.331	0.28
IPI00004101	Q93088	Betaine--homocysteine S-methyltransferase 1	0.337	0.119	0.924	0.205	0.385	0.18	0.152
IPI00293721	O95154	Aflatoxin B1 aldehyde reductase member 3	0.56	0.471	0.947	0.51	0.413	0.441	0.398
IPI00473031	P00325	Alcohol dehydrogenase 1B	0.261	0.187	1.21	0.276	0.353	0.109	0.191
IPI00465343	P00326	Alcohol dehydrogenase 1C	0.273	0.205	1.172	0.233	0.4	0.098	0.159
IPI00012828	P09110	3-ketoacyl-CoA thiolase, peroxisomal precursor	0.652	0.339	1.078	0.225	0.544	0.225	0.151
IPI00784347	P05783	Keratin, type I cytoskeletal 18	0.485	0.544	0.956	0.658	0.488	0.514	0.431
IPI00073772	P09467	Fructose-1,6-bisphosphatase 1	0.338	0.191	1.083	0.123	0.295	0.19	0.335
IPI00295363	P00480	Ornithine carbamoyltransferase, mitochondrial precursor	0.352	0.607	1.098	0.218	0.287	0.244	0.204
IPI00009367	P21549	Serine--pyruvate aminotransferase	1.029	0.274	1.101	0.259	0.463	0.382	0.337
IPI00787584	P16662	Similar to UDP-glucuronosyltransferase 2B7 precursor	0.972	0.396	0.916	0.363	0.483	0.177	0.188
IPI00433347	P22307	Sterol carrier protein 2 isoform 2	0.939	0.405	1.11	0.15	0.652	0.294	0.5
IPI00794900	P11586	C-1-tetrahydrofolate synthase	0.704	0.518	0.823	0.442	0.574	0.514	0.561
IPI00009268	Q03154	Aminoacylase-1	0.68	0.341	1.015	0.208	0.483	0.461	0.257
IPI00551024	Q3LXA3	Dihydroxyacetone kinase	0.35	0.157	0.838	0.411	2.277	0.15	0.122
IPI00298406	Q16836	Hydroxyacyl-coenzyme A dehydrogenase Isoform 2 ,	0.327	0.477	1.06	0.272	1.228	0.375	0.464
IPI00016801	P00367	Glutamate dehydrogenase 1, mitochondrial precursor	0.413	0.399	0.847	0.266	1.968	0.362	0.627
IPI00305166	P31040	Succinate dehydrogenase flavoprotein subunit	0.49	0.531	0.902	0.492	0.597	0.788	0.612
IPI00743616	Q06278	Aldehyde oxidase	0.6	0.639	1.002	0.384	0.75	0.471	0.371
IPI00789806	P28838	Cytosol aminopeptidase Isoform 2	0.859	0.647	1.046	0.5	0.638	0.645	0.544
IPI00397860	P00167	Cytochrome b5 Isoform 1	0.318	0.395	1.108	0.172	0.883	0.227	0.158
IPI00220668	P34896	Serine hydroxymethyltransferase Isoform 2	0.507	0.423	0.951	0.346	0.712	0.613	0.39
IPI00398768	P05089	Arginase-1 Isoform 2	0.342	0.577	1.032	0.517	0.73	0.602	0.617
IPI00329331	Q16851	UTP--glucose-1-phosphate uridylyltransferase Isoform 1	1.208	0.223	0.958	0.435	0.399	0.264	0.589
IPI00007282	P05181	Cytochrome P450 2E1	0.459	0.435	0.886	0.308	0.515	0.549	0.833
IPI00299402	P11498	Pyruvate carboxylase, mitochondrial precursor	0.552	0.608	1.13	0.381	0.903	0.562	0.51
IPI00797249	Q7Z4W1	L-xylulose reductase	0.34	0.238	0.935	0.451	0.911	0.415	0.334
IPI00103467	P30837	Aldehyde dehydrogenase X, mitochondrial precursor	0.476	0.379	0.928	0.282	0.78	0.423	0.631

IPI00218914	P00352	Retinal dehydrogenase 1	0.797	0.562	1.005	0.29	0.416	0.578	0.487
IPI00795913	P32754	4-hydroxyphenylpyruvate dioxygenase	0.259	0.471	1.319	0.395	0.334	0.948	0.277
IPI00303174	Q93099	Homogentisate 1,2-dioxygenase	0.51	0.335	1.1	0.299	0.369	0.756	0.282
IPI00216057	Q00796	Sorbitol dehydrogenase	0.545	0.387	1.302	0.654	0.851	0.294	0.345
IPI00009532	P80404	4-aminobutyrate aminotransferase, mitochondrial precursor	0.402	0.59	0.876	0.232	1.203	0.243	0.265
IPI00783680	P00441	Superoxide dismutase	0.653	0.491	1.152	0.179	0.99	0.443	0.383
IPI00024993	P30084	Enoyl-CoA hydratase, mitochondrial precursor	0.499	0.503	0.946	0.228	0.733	0.29	0.376
IPI00745729	A6NML9	Selenium-binding protein 1	0.812	0.461	0.955	0.671	0.634	0.466	0.545
IPI00792207	Q53FB6	Mitochondrial aldehyde dehydrogenase 2 variant (Fragment)	0.511	0.386	1.223	0.223	0.81	0.281	0.574
IPI00024623	P45954	Short/branched chain specific acyl-CoA dehydrogenase	0.323	0.486	1.047	0.332	1.665	0.495	0.295
IPI00783313	P06737	Glycogen phosphorylase, liver form	1.425	0.301	0.957	0.497	0.52	0.326	0.451
IPI00021772	Q00266	S-adenosylmethionine synthetase isoform type-1	0.649	0.538	0.805	0.584	0.916	0.674	0.439
IPI00028910	Q14117	Dihydropyrimidinase	0.705	0.414	0.938	0.426	0.625	0.326	0.402
IPI00001539	P42765	3-ketoacyl-CoA thiolase, mitochondrial	0.398	0.423	0.957	0.241	0.685	0.22	0.249
IPI00216293	Q16762	Thiosulfate sulfurtransferase	0.77	0.509	1.008	0.191	0.438	0.326	0.359
IPI00300026	P50225	Sulfotransferase 1A1	0.275			0.321	0.565	0.428	0.357
IPI00012728	P33121	Long-chain-fatty-acid--CoA ligase 1	0.268			0.293	0.649	0.306	0.564
IPI00008753	P80297	Metallothionein-1X	0.669			0.492	0.236	0.437	0.209
IPI00217458	P24298	Alanine aminotransferase 1	0.268			0.286	0.434	0.389	0.435
IPI00339373	P36269	Gamma-glutamyltransferase 5 precursor Isoform 2	0.218			0.598	0.128	0.165	0.108
IPI00007219	P11712	Cytochrome P450 2C9	0.406			0.288	0.607	0.194	0.181
IPI00216136	P50053	Isoform C of Ketohexokinase	0.823	0.32	0.823	0.339	1.512	0.406	0.491
IPI00017819	Q14032	Bile acid CoA:amino acid N-acyltransferase	0.482	0.898	1.145	0.628	0.819	0.466	0.487
IPI00375513	P21964	Isoform Soluble of Catechol O-methyltransferase	0.703	0.338	1.156	0.656	0.93	0.332	0.553
IPI00241841	Q5XKE5	Keratin 6L	0.56	0.805	1.223	0.761	0.356	0.524	0.409
IPI00793673	O75891	Formyltetrahydrofolate dehydrogenase isoform a variant	0.508	0.751	1.156	0.52	0.71	0.544	0.412
IPI00297646	P02452	Collagen alpha-1(I) chain precursor	0.435	3.827	1.224	1.998	0.31	0.205	0.074
IPI00852596	Q86WI9	Ferritin light chain	0.547	0.695	1.271	0.578	0.604	0.246	1.34
IPI00295386	P16152	Carbonyl reductase [NADPH] 1	1.09	0.552	1.075	0.545	0.869	0.527	0.36
IPI00020632	P00966	Argininosuccinate synthase	0.438	0.16	1.001	0.237	0.879	1.264	0.375
IPI00008485	P21399	Iron-responsive element-binding protein 1	0.655	0.397	1.071	0.421	0.608	1.057	0.713
IPI00218568	P61457	Pterin-4-alpha-carbinolamine dehydratase	0.532	0.327	0.893	0.416	1.56	0.602	0.931
IPI00646632	Q96KP4	Cytosolic non-specific dipeptidase	0.896	0.426	1.158	0.543	0.831	0.648	0.579
IPI00783862	P30043	Flavin reductase	0.857	0.526	0.983	0.437	0.716	0.55	0.485
IPI00216279	P50440	Isoform Cytoplasmic of Glycine amidinotransferase	0.823	0.487	0.998	0.181	1.449	0.175	0.468
IPI00022793	Q5R1W7	Trifunctional enzyme beta subunit, mitochondrial precursor	0.562	0.597	1.037	0.554	1.067	0.763	0.569
IPI00219446	P30086	Phosphatidylethanolamine-binding protein 1	0.826	0.292	1.189	0.263	1.202	0.455	0.434
IPI00554648	P05787	Keratin, type II cytoskeletal 8	0.48	0.715	1.01	0.734	0.456	0.547	0.445
IPI00216164	Q08426	Peroxisomal bifunctional enzyme	0.721	0.731	1.15	0.509	0.499	0.332	0.337
IPI00647328	P30038	Aldehyde dehydrogenase 4 family, member A1	0.455	0.503	1.033	0.245	0.714	0.398	0.68
IPI00003482	Q16698	2,4-dienoyl-CoA reductase, mitochondrial precursor	0.72	0.827	1.037	0.227	0.529	0.482	0.336
IPI00220271	P14550	Alcohol dehydrogenase	0.948	0.335	1.249	0.594	0.845	0.446	0.671
IPI00030363	P24752	Acetyl-CoA acetyltransferase, mitochondrial precursor	0.835	0.386	1.129	0.18	0.948	0.383	0.602
IPI00011107	P48735	Isocitrate dehydrogenase [NADP], mitochondrial precursor	0.717	0.494	1.044	0.341	0.802	0.567	0.589
IPI00008934	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor	0.957	0.345	1.077	0.28	1.348	0.31	0.387
IPI00291136	P12109	Collagen alpha-1(VI) chain precursor	0.49	2.029	1.122	1.746	0.596	0.492	0.23
IPI00018206	P00505	Aspartate aminotransferase, mitochondrial precursor	0.366	0.682	0.915	0.388	0.744	0.651	0.265
IPI00009896	P07099	Epoxide hydrolase 1	1.854	0.789	0.994	0.244	0.539	0.176	0.271
IPI00556451	P38117	Isoform 2 of Electron transfer flavoprotein subunit beta	0.574	0.691	1.032	0.52	0.97	0.614	0.368

IPI00465436	P04040	Catalase	0.931	0.337	0.975	0.474	0.956	0.382	0.288
IPI00024896	P30039	Phenazine biosynthesis-like domain-containing protein		0.197	1.205	0.274	0.978	0.314	0.272
IPI00003944	P11182	Lipoamide acyltransferase	0.416			0.492	0.757	0.476	0.449
IPI00745233	P09210	Glutathione S-transferase A2	0.515	0.198	1.256			0.105	0.147
IPI00843846	P10632	Cytochrome P450 2C8	0.707			0.377	0.358	0.204	0.198
IPI00012912	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial precursor	0.754			0.503	0.507	0.6	0.484
IPI00024934	P22033	Methylmalonyl-CoA mutase, mitochondrial precursor	0.528			0.309	0.987	0.38	0.365
IPI00434346	P22309	UDP-glucuronosyltransferase 1-1 precursor	0.751			0.169	0.654	0.544	0.243
IPI00384428	Q86WA6	Isoform 1 of Valacyclovir hydrolase precursor	0.486	0.518	1.004	0.257	0.466		
IPI00027681	P40261	Nicotinamide N-methyltransferase	0.272			0.496	0.448	1.547	0.462
IPI00657852	Q16743	Cytochrome P-450 II C (Fragment)				0.345	0.488	0.176	0.184
IPI00604620	P19338	Isoform 1 of Nucleolin	1.411	1.769	1.031	1.722	2.358	2.739	1.591
IPI00644079	Q00839	Heterogeneous nuclear ribonucleoprotein U isoform a	1.779	1.492	0.948	2.008	1.7	2.213	2.406
IPI00465365	P09651	Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	1.647	1.876	0.99	2.024	2.123	2.251	2.986
IPI00329801	P08758	Annexin A5	1.565	1.759	1.199	1.582	0.642	1.938	2.824
IPI00554652	P33241	Lymphocyte-specific protein 1	2.509	4.445	1.567	2.667	0.452	2.97	0.901
IPI00019038	P61626	Lysozyme C precursor	2.376	5.557	0.711	4.208	0.317	2.828	1.669
IPI00007047	P05109	Protein S100-A8	3.219	2.484	0.912	3.026	0.443	3.278	2.475
IPI00027462	P06702	Protein S100-A9	2.762	2.951	0.891	3.106	0.369	3.484	2.998
IPI00021828	P04080	Cystatin-B	1.499	1.54	1.496	0.605	1.378	1.584	1.837
IPI00021827	P59666	Neutrophil defensin 3 precursor	3.254	7.856	0.883	9.054	0.189	5.655	4.761
IPI00021842	P02649	Apolipoprotein E precursor	1.696	1.508	0.932	2.624	1.43	0.871	1.711
IPI00414676	P08238	Heat shock protein HSP 90-beta	1.423	1.204	0.912	1.731	2.105	1.834	1.839
IPI00792352	P62828	GTP-binding nuclear protein Ran	2	1.657	0.847	1.587	1.38	2.814	3.003
IPI00792677	Q6P9V9	Similar to Tubulin alpha-ubiquitous chain	1.591	1.209	1.008	1.645	1.402	1.736	2.092
IPI00433214	Q6NWZ1	CKAP4 protein (Fragment)	1.693	1.433	1.037	2.287	2.182	1.314	2.901
IPI00479191	P31943	Heterogeneous nuclear ribonucleoprotein H	1.417	1.287	0.957	2.905	1.687	1.411	1.695
IPI00555565	Q58FF6	Heat shock protein 90Bd	1.439	1.292	1.059	1.417	1.829	1.693	1.854
IPI00306383	O14828	Isoform 2 of Secretory carrier-associated membrane protein 3		1.879	0.907	1.438	1.74	1.674	3.615
IPI00216659	Q9Y5S9	Isoform 2 of RNA-binding protein 8A		1.721	0.884	2.043	1.441	1.841	2.642
IPI00013475	Q13885	Tubulin beta-2A chain	1.667			1.54	1.435	1.424	1.814
IPI00419373	P51991	Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	1.637			1.898	2.161	2.201	2.242
IPI00219713	P02679	Isoform Gamma-A of Fibrinogen gamma chain precursor	1.439	2.3	0.567	9.31	0.882	1.977	1.11
IPI00298497	P02675	Fibrinogen beta chain precursor	1.993	3.463	0.461	12.417	1.016	2.672	1.205
IPI00027444	P30740	Leukocyte elastase inhibitor	2.27	2.072	0.998	3.313	0.624	2.04	1.29
IPI00789477	P02788	Lactotransferrin		3.909	0.939	5.324	0.364	1.953	2.255
IPI00472724	P68105	Elongation factor 1-alpha	1.657	0.982	1.078	1.43	1.199	1.684	1.688
IPI00022429	P02763	Alpha-1-acid glycoprotein 1 precursor	0.802	4.019	1.151	2.804	1.518	0.818	1.501
IPI00021263	P63104	14-3-3 protein zeta/delta	1.635	2.119	0.981	2.43	0.872	1.804	1.1
IPI00016513	P61026	Ras-related protein Rab-10	1.44	1.688	0.857	1.192	1.187	2.946	1.659
IPI00007752	P68371	Tubulin beta-2C chain	1.478	1.241	0.908	1.524	1.388	1.553	1.632
IPI00642256	P47756	Capping protein (Actin filament) muscle Z-line, beta	1.633	1.445	0.95	1.355	0.935	1.416	1.423
IPI00553177	P01009	Alpha-1-antitrypsin precursor	1.233	3.036	1.032	6.157	0.805	1.515	1.492
IPI00455383	Q00610	Isoform 2 of Clathrin heavy chain 1	1.463	1.031	0.992	1.674	1.251	1.533	2.106
IPI00013683	Q13509	Tubulin beta-3 chain	1.498	1.202	0.9	1.517	1.392	1.473	1.596
IPI00399142	O15260	Surfeit 4	0.847	1.684	1.061	0.896	2.231	1.698	1.54
IPI00465248	P06733	Isoform alpha-enolase of Alpha-enolase	1.663	1.297	1.316	1.13	1.593	1.837	1.9
IPI00383296	P52272	Isoform 2 of Heterogeneous nuclear ribonucleoprotein M	1.478	1.258	0.871	2.165	1.973	1.38	2.119
IPI00011654	P07437	Tubulin beta chain	1.6	1.262	0.903	1.659	1.369	1.448	1.873
IPI00465439	P04075	Fructose-bisphosphate aldolase A	0.968	1.654	0.979	1.693	1.416	1.754	1.337

IPI00844578	Q08211	ATP-dependent RNA helicase A	1.21	1.113	0.817	1.755	1.427	1.693	2.022
IPI00010471	P13796	Plastin-2	1.948	2.034	1.255	1.655	0.721	1.53	1.119
IPI00236554	P05164	Isoform H14 of Myeloperoxidase precursor		2.741	0.795	6.095	0.725	2.273	2.51
IPI00555812	P02774	Vitamin D-binding protein precursor		1.817	0.873	5.527	1.467	1.16	1.627
IPI00789029	P55209	Nucleosome assembly protein 1-like 1		1.047	0.909	2.488	2.161	4.64	5.354
IPI00376215	P78527	Isoform 2 of DNA-dependent protein kinase catalytic subunit		1.779	0.924	2.6	1.602	1.31	1.479
IPI00010740	P23246	Isoform Long of Splicing factor, proline- and glutamine-rich	1.279			1.834	1.513	2.056	2.592
IPI00105407	O60218	Aldo-keto reductase family 1 member B10	7.123	7.773	0.771			1.515	4.072
IPI00018146	P27348	14-3-3 protein theta	1.419			1.808	0.974	1.596	1.561
IPI00639931	Q01518	Adenylyl cyclase-associated protein	1.432	1.986	1.075			1.689	1.598
IPI00555602	Q59F68	CD68 antigen variant (Fragment)	1.439	1.439	0.876			2.439	2.12
IPI00017526	P25815	Protein S100-P				7.213	5.408	40.236	5.317
IPI00219301	P29966	Myristoylated alanine-rich C-kinase substrate	1.761			1.994	1.786		1.78

* Number of peptides, standard deviation, total ion score C.I.% and best ion score C.I.% of the proteins identified from each patient samples are available excel file in the disk attached behind.

List of Publications

I. Publications in International Peer-reviewed Journals :

1. Zubaidah R.M., Tan G.S., Tan S.B., Lim S.G., Lin Q., Chung M.C., (2008) 2-D DIGE profiling of hepatocellular carcinoma tissues identified isoforms of far upstream binding protein (FUBP) as novel candidates in liver carcinogenesis. *Proteomics.* 8: 5086-5096.

II. Poster presentations at International Scientific Conferences :

1. Zubaidah Bte Mohd. Ramdzan, Gek San Tan, Sandra B.E. Tan, Seng Gee Lim, Qingsong Lin, and Maxey C.M. Chung. 2-D DIGE profiling of Hepatocellular Carcinoma Tissues identified isoforms of Far Upstream Binding Protein (FUBP) as novel candidates in liver carcinogenesis. US Human Proteome Organization (US HUPO) Fifth Annual Conference February 22nd – 25th, 2009, San Diego, California, USA.

2. Zubaidah Bte Mohd. Ramdzan, Seng Gee Lim, Gek San Tan, Qingsong Lin, and Maxey C.M. Chung. Quantitative profiling of Hepatocellular Carcinoma (HCC) Tissues using 2-D DIGE, cICAT and iTRAQ. Human Proteome Organization (HUPO) Sixth Annual Congress. October 6th – 10th 2007, Seoul, South Korea.

III. Presentations at Local Scientific Conferences :

1. Zubaidah Mohamed Ramdzan 2-D DIGE Profiling of Hepatocellular Carcinoma Tissues - Isoforms of Far Upstream Binding Protein (FUBP) as Novel Candidates in Liver Carcinogenesis. Singapore Proteomics Forum 2009. May 15th, 2009, Oral presentation Centre of Life Science, Singapore (co-organised with Agilent Technologies)

2. Zubaidah Mohamed Ramdzan, Gek San Tan, Sandra B.E. Tan , Seng Gee Lim, Qingsong Lin, Maxey Chung. 2-D DIGE profiling of Hepatocellular Carcinoma Tissues identified isoforms of Far Upstream Binding Protein (FUBP) as novel candidates in liver carcinogenesis. Joint Fifth Structural Biology and Functional Genomics & first Biological Physics International Conference. December 9th – 11th, 2008, Poster presentation, National University of Singapore.

3. Zubaidah Mohamed Ramdzan, Seng Gee Lim, Gek San Tan, Teck Kwang Lim, Qingsong Lin, Siaw Ling Lo, Liu Yi, Hew Choy Leong and Maxey Chung. Proteome analysis of hepatocellular carcinoma (HCC) using the cleavable isotope-coded affinity tag (cICAT) approach. Joint Third AOHUPO and Fourth Structural Biology and Functional Genomics Conference, December 4^{th} – 7^{th}, 2006, Poster presentation, National University of Singapore.

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	39448.06	8	3	360.67	100	134.99	100	0	0	3
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	31367.13	8.34	2	176.13	100	93.57	100	0	0	2
SELENBP1 53 kDa protein	IPI00745729	53027.94	6.03	2	151.25	100	113.29	100	0	0	2
BLVRB Flavin reductase	IPI00783862	22105.43	7.13	2	123.74	100	67.84	99.99721	0	0	2
SOD1 Superoxide dismutase	IPI00783680	15925.9	5.7	1	124.11	100	124.11	100	0	0	1
ACAT2 Acetyl-CoA acetyltransferase, cytosolic	IPI00291419	41324.39	6.47	1	123.18	100	124.6	100	0	0	1
DAK Dihydroxyacetone kinase	IPI00551024	58940.04	7.12	1	99.61	100	99.61	100	0	0	1
PNPO 19 kDa protein	IPI00793232	19465.84	6.92	1	92.37	100	92.37	100	0	0	1
UQCRH Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondria	IPI00296022	10731.94	4.39	1	84.22	99.99994	84.22	99.99994	0	0	1
PAH Phenylalanine-4-hydroxylase	IPI00017579	51829.46	6.15	1	84.01	99.99993	84.01	99.99993	0	0	1
DCXR 26 kDa protein	IPI00797249	25726.45	8.33	1	83.80005	99.99993	85.22	99.99995	0	0	1
ASS1 Argininosuccinate synthetase 1	IPI00514341	19035.86	7.26	1	81.77	99.99989	81.77	99.99989	0	0	1
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	44854.47	6.61	1	80.56	99.99985	80.56	99.99985	0	0	1
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	35305.76	8.38	1	79.13	99.99979	79.13	99.99979	0	0	1
ERP29 Endoplasmic reticulum protein ERp29 precursor	IPI00024911	28975.15	6.77	1	78.67	99.99977	78.67	99.99977	0	0	1
FTL Ferritin light chain	IPI00852596	20007.1	5.51	1	75.6	99.99953	75.6	99.99953	0	0	1
FTH1 Ferritin heavy chain	IPI00554521	21212.29	5.3	1	69.13	99.99792	69.13	99.99792	0	0	1

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ARG1 Isoform 1 of Arginase-1	IPI00291560	34713.3	6.72	1	65.85	99.99558	65.85	99.99558	0	0	1
C21orf33 Isoform Short of ES1 protein homolog, mitochondrial precursor	IPI00218482	24741.95	8.29	1	53.53	99.92466	53.53	99.92466	0	0	1
GALM Aldose 1-epimerase	IPI00060200	37742.13	6.18	1	52.97	99.91429	52.97	99.91429	0	0	1
AK2 Isoform 1 of Adenylate kinase isoenzyme 2, mitochondrial	IPI00215901	26460.77	7.67	1	48.86	99.77918	48.86	99.77918	0	0	1
EPHX1 Epoxide hydrolase 1, microsomal	IPI00640017	16373.31	5.85	1	48.33	99.75052	48.33	99.75052	0	0	1
NQO2 NAD(P)H dehydrogenase, quinone 2	IPI00515016	21523.83	6.07	1	46.44004	99.61449	47.86	99.722	0	0	1
GPT Alanine aminotransferase 1	IPI00217458	54602.15	6.77	1	45.96	99.56943	45.96	99.56943	0	0	1
AKR1C1 Aldo-keto reductase family 1 member C1	IPI00029733	36765.02	8.02	1	44.09	99.33772	44.09	99.33772	0	0	1
AOX1 Hypothetical protein AOX1	IPI00743616	147543.6	6.78	1	44.02	99.32696	44.02	99.32696	0	0	1
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	24433.38	5.15	1	42.5	99.04491	42.5	99.04491	0	0	1
AKR1D1 CDNA FLJ25413 fis, clone TST03402, highly similar to 3-OXO-5-BETA- S	IPI00065073	30242.66	8.11	1	39.83	98.23379	39.83	98.23379	0	0	1
OAT Ornithine aminotransferase, mitochondrial precursor	IPI00022334	48504.2	6.57	1	32.28	89.95286	32.28	89.95286	0	0	1
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	56402.59	8.17	1	31.65	88.38438	31.65	88.38438	0	0	1
CRYZ 32 kDa protein	IPI00647366	31508.5	8.59	1	31.22	87.17544	31.22	87.17544	0	0	1
YSK4 132 kDa protein	IPI00798105	131531.9	6.64	1	29.02	78.71654	29.02	78.71654	0	0	0
BHMT2 Betaine--homocysteine S-methyltransferase 2	IPI00014363	40328.18	5.61	1	28.43	75.61952	28.43	75.61952	0	0	1
GRHPR GRHPR protein (Fragment)	IPI00550682	36801.01	5.95	2	77.61	99.99971	43.41	99.22546	0.003	0.218	2
P4HB Protein disulfide-isomerase precursor	IPI00010796	57080.67	4.76	2	79.33	99.9998	40.77	98.57753	0.006	0.556	2
SORD Sorbitol dehydrogenase	IPI00216057	38271.84	8.23	1	94.62	100	94.62	100	0.068	0	1

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CAT Catalase	IPI00465436	59718.75	6.9	1	55.03004	99.94666	56.45	99.96154	0.111	0	1
FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	36790.79	6.54	1	42.25004	98.98833	43.67	99.27047	0.167	0	1
AKR1C3 Aldo-keto reductase family 1 member C3	IPI00291483	36820.84	8.05	1	28.95	78.37071	28.95	78.37071	0.238	0	1
TST Thiosulfate sulfurtransferase	IPI00216293	33407.84	6.77	1	58.43	99.97562	58.43	99.97562	0.261	0	1
SAR1B GTP-binding protein SAR1b	IPI00002149	22395.51	5.76	1	40.01	98.3055	40.01	98.3055	0.263	0	1
- 12 kDa protein	IPI00797738	12027.62	6.81	2	162.55	100	100.11	100	0.285	0.197	2
PRDX1 11 kDa protein	IPI00641244	10669.51	8.79	1	46.09	99.58213	46.09	99.58213	0.309	0	1
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	11992.02	6.28	1	58.95	99.97837	58.95	99.97837	0.316	0	1
C6orf115 similar to Protein C6orf115	IPI00740277	20388.71	6.38	1	47.62	99.70621	47.62	99.70621	0.342	0	1
FAM10A4 Protein FAM10A4	IPI00218038	27389.69	5.01	1	44.77	99.43371	44.77	99.43371	0.35	0	1
HBA2;HBA1 Alpha 2 globin variant (Fragment)	IPI00853068	15270.94	8.72	1	95.46	100	95.46	100	0.387	0	1
GLUD2 Glutamate dehydrogenase 2, mitochondrial precursor	IPI00027146	61395.43	8.63	1	43.7	99.27549	43.7	99.27549	0.408	0	1
CHDH Choline dehydrogenase, mitochondrial precursor	IPI00168603	65360.13	8.67	1	31.34004	87.52507	32.76	91.00414	0.433	0	1
PARK7 Protein DJ-1	IPI00298547	19878.49	6.33	3	210.93	100	102.57	100	0.44	0.194	3
C11orf54 Isoform 4 of Ester hydrolase C11orf54	IPI00760666	23158.41	6.3	1	91.71	100	91.71	100	0.469	0	1
HBB Hemoglobin subunit beta	IPI00654755	15988.29	6.75	4	318.67	100	110.57	100	0.473	0.093	4
MPST 3-mercaptopyruvate sulfurtransferase variant (Fragment)	IPI00746782	34729.5	6.83	1	47.79	99.71748	47.79	99.71748	0.474	0	1
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	61016.38	5.7	1	76.21	99.99959	76.21	99.99959	0.503	0	1
HBD;HBB 15 kDa protein	IPI00657660	15409.88	7.74	1	47.53	99.70005	47.53	99.70005	0.541	0	1

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GPX1 16 kDa protein	IPI00784231	16180.13	5.39	1	60.63	99.98531	60.63	99.98531	0.544	0	1
CALR 37 kDa protein	IPI00793605	36679.71	4.55	1	96.61	100	96.61	100	0.565	0	1
CTSD 21 kDa protein	IPI00658053	21476.66	5.48	2	108.95	100	66.3	99.99602	0.578	0.022	2
PDIA3 Protein disulfide-isomerase A3 precursor	IPI00025252	56746.75	5.98	1	55.76	99.95491	55.76	99.95491	0.583	0	1
SAR1A SAR1 gene homolog A	IPI00644667	13653.07	6.49	1	32.91	91.30955	32.91	91.30955	0.595	0	1
LASP1 Isoform 2 of LIM and SH3 domain protein 1	IPI00386803	35990.71	8.92	1	26.7	63.68866	26.7	63.68866	0.616	0	1
B2M B2M protein	IPI00796379	13687.95	6.06	1	70.68	99.99855	70.68	99.99855	0.622	0	1
HINT1 Histidine triad nucleotide-binding protein 1	IPI00239077	13793.09	6.43	1	65.97	99.9957	65.97	99.9957	0.622	0	1
ORM2 Alpha-1-acid glycoprotein 2 precursor	IPI00020091	23587.63	5.03	1	49.45004	99.80723	50.87	99.86099	0.639	0	1
PGAM1;hCG_2015138;hCG_2015269 Phosphoglycerate mutase 1	IPI00549725	28785.83	6.67	1	59.36	99.98032	59.36	99.98032	0.674	0	1
FGG Isoform Gamma-A of Fibrinogen gamma chain precursor	IPI00219713	49464.97	5.7	1	61.9	99.98903	61.9	99.98903	0.678	0	1
- Similar to Glyceraldehyde-3-phosphate dehydrogenase	IPI00747273	12564.45	8.74	1	67.32	99.99685	67.32	99.99685	0.694	0	1
HCLS1 Hematopoietic lineage cell-specific protein	IPI00026156	53964.98	4.74	1	76.87	99.99965	76.87	99.99965	0.716	0	1
HMGB1 High-mobility group box 1	IPI00644653	18299.33	9.72	1	44.49	99.39599	44.49	99.39599	1.495	0	1
IGLV4-3 IGLV4-3 protein	IPI00382938	25960.7	6.3	1	76.17	99.99959	76.17	99.99959	1.504	0	1
ORM1 Alpha-1-acid glycoprotein 1 precursor	IPI00022429	23496.76	4.93	1	26.95	65.71988	26.95	65.71988	1.515	0	1
IGKC IGKC protein	IPI00430808	25629.86	6.15	2	122.17	100	96.48	100	1.518	0.263	2
HPX Hemopexin precursor	IPI00022488	51643.27	6.55	3	284.41	100	135.36	100	1.564	0.079	3
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	18000.88	7.68	2	181.79	100	127.21	100	1.57	0.31	2

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ALB Serum albumin	IPI00022434	71529.53	6.33	18	1405.569	100	136.74	100	1.575	0.336	18
PDIA6 Isoform 1 of Protein disulfide-isomerase A6 precursor	IPI00644989	48091.26	4.95	1	88.05	100	88.05	100	1.582	0	1
DCPS Scavenger mRNA-decapping enzyme DcpS	IPI00335385	38585.02	5.93	1	35.18	94.84721	35.18	94.84721	1.59	0	1
- Hypothetical protein DKFZp686C15213	IPI00426051	51066.19	7.85	2	136.92	100	98.93	100	1.672	0.059	2
FHL1 Four and a half LIM domains 1	IPI00029028	23685.15	8.94	1	27.6	70.48503	27.6	70.48503	1.698	0	1
UFC1 Ufm1-conjugating enzyme 1	IPI00294495	19446.02	6.9	1	45.85	99.55839	45.85	99.55839	1.803	0	1
RAD23B UV excision repair protein RAD23 homolog B	IPI00008223	43144.62	4.79	1	98.65	100	98.65	100	1.9	0	1
LOC730278;LOC729659 similar to Putative S100 calcium-binding protein A11 ps	IPI00790691	11279.74	7.77	1	56.16	99.95888	56.16	99.95888	1.904	0	1
ACTN4 Alpha-actinin-4	IPI00013808	104788.5	5.27	2	117.39	100	86.08	100	1.934	0.251	2
VIM 50 kDa protein	IPI00827679	49623.11	5.19	1	54.01	99.93254	54.01	99.93254	2.003	0	1
GC vitamin D-binding protein precursor	IPI00742696	52882.94	5.32	1	81.19	99.99987	81.19	99.99987	2.072	0	1
CANX Calnexin precursor	IPI00020984	67525.85	4.47	2	75.16	99.99948	39.68	98.17172	2.12	0.01	2
APOH Beta-2-glycoprotein 1 precursor	IPI00298828	38272.66	8.34	1	46.94	99.65641	46.94	99.65641	2.199	0	1
RNH1 Ribonuclease/angiogenin inhibitor	IPI00783491	49839.99	4.68	1	46.99	99.66034	46.99	99.66034	2.422	0	1
EEF1G;LOC729998 similar to Elongation factor 1-gamma	IPI00738381	50270.31	7.09	1	40.69	98.55109	40.69	98.55109	2.477	0	1
RPSA Ribosomal protein SA	IPI00413108	33292.65	4.79	1	130.15	100	130.15	100	2.542	0	1
SSB Lupus La protein	IPI00009032	46808.16	6.68	1	100.16	100	100.16	100	3.412	0	1
RPS4X 14 kDa protein	IPI00646114	14010.58	10.06	1	27.8	71.81342	27.8	71.81342	3.594	0	1
TES Isoform 2 of Testin	IPI00216425	46878.3	7.82	1	29.44	80.67843	29.44	80.67843	3.934	0	1

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TAGLN Transgelin	IPI00216138	22596.43	8.87	1	54.29	99.93675	54.29	99.93675	4.626	0	1
HP Haptoglobin precursor	IPI00641737	46693.35	6.28	3	135.73	100	82.56	99.99991	17.625	1936.574	3
- Hypothetical protein DKFZp686M24218	IPI00784998	52387.11	7.89	3	98.18001	100	37.99	97.302	29.941	2049.335	3
IGHG1 IGHG1 protein	IPI00448938	51362.63	8.69	2	175.85	100	98.93	100	152.493	13283.795	2
HSP90AA1 Hsp89-alpha-delta-N	IPI00604607	63211.62	5.03	2	132.14	100	93.38	100	159.32	8863.38	2
EFEMP1 Isoform 2 of EGF-containing fibulin-like extracellular matrix protei	IPI00220813	53686.69	4.9	1	34.62	94.13805	34.62	94.13805	4717.485	0	1
IGHA1 SNC66 protein	IPI00383164	53631.38	6.22	1	85.34	100	85.34	100	5126.801	0	1
PPP2R1A Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A	IPI00554737	65266.91	5	1	31.85	88.90717	31.85	88.90717	6165.208	0	1
FLNA Filamin-A	IPI00333541	280563.9	5.7	2	139.03	100	84.87	99.99994	6478.319	1890.214	2
MYL9 Myosin regulatory light chain 2, smooth muscle isoform	IPI00220278	19814.45	4.8	1	96.5	100	96.5	100	7243.278	0	1
- PHAPI protein (Fragment)	IPI00394706	15315.69	4.5	2	92.22	100	66.68	99.99635	8686.613	126.571	2
FN1 Isoform 3 of Fibronectin precursor	IPI00339223	259035.4	5.47	3	142.0295	100	68.71	99.99771	8730.836	3271.841	3
VCP 89 kDa protein	IPI00843748	89270.64	5.11	1	52.99004	99.91468	54.41	99.93848	9994.004	0	1
TUBB Tubulin beta chain	IPI00011654	49638.97	4.78	1	167.9	100	167.9	100	10062.12	0	1
RNF113A RING finger protein 113A	IPI00007343	38762.6	5.51	1	33.97	93.19164	33.97	93.19164	10245.76	0	1
BAT1 Isoform 2 of Spliceosome RNA helicase BAT1	IPI00641829	50646.91	5.59	1	33.6	92.58617	33.6	92.58617	10364.71	0	1
HSPG2 365 kDa protein	IPI00747758	364402.6	6.07	2	143.98	100	74.25	99.99936	10654.38	702.065	2
TRIM28 Isoform 2 of Transcription intermediary factor 1-beta	IPI00438230	79423.48	5.67	1	54.04	99.93301	54.04	99.93301	10936.02	0	1
SERPINA1 Alpha 1-antitrypsin	IPI00790784	40237.62	5.26	1	41.64	98.83576	41.64	98.83576	11205.49	0	1

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ACTR2 actin-related protein 2 isoform a	IPI00470573	45347.55	6.73	1	34.31	93.70433	34.31	93.70433	12043.56	0	1
CD59 CD59 glycoprotein precursor	IPI00011302	14167.79	6.02	1	51.29	99.8738	51.29	99.8738	14766.27	0	1
LAMC1 Laminin subunit gamma-1 precursor	IPI00298281	177492.5	5.01	1	28.85	77.8669	28.85	77.8669	32204.27	0	1
FHL2 FHL2 isoform 5	IPI00396967	44147.85	8.51	1	54.79	99.94363	54.79	99.94363	38693.42	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
AKR1D1 CDNA FLJ25413 fis, clone TST03402, highly similar to 3-OXO-5-BETA- S	IPI00065073	30242.66	8.11	2	132.08	100	93.09	100	0	0	2
AGXT Serine--pyruvate aminotransferase	IPI00009367	42982.44	8.61	2	120.34	100	75.38	99.99953	0	0	2
HLA-DRA major histocompatibility complex, class II, DR alpha precursor	IPI00464948	28602.71	4.91	2	99.73	100	54.73	99.94494	0	0	2
CMBL carboxymethylenebutenolidase-like	IPI00383046	28030.17	6.71	2	74.52	99.99942	40.81	98.64219	0	0	2
FTL Ferritin light chain	IPI00852596	20007.1	5.51	1	110.02	100	110.02	100	0	0	1
FTH1 Ferritin heavy chain	IPI00554521	21212.29	5.3	1	109.55	100	109.55	100	0	0	1
PAH Phenylalanine-4-hydroxylase	IPI00017579	51829.46	6.15	1	107.39	100	107.39	100	0	0	1
AOX1 Hypothetical protein AOX1	IPI00743616	147543.6	6.78	1	102.15	100	102.15	100	0	0	1
ASS1 Argininosuccinate synthetase 1	IPI00514341	19035.86	7.26	1	85.21	100	85.21	100	0	0	1
GPT Alanine aminotransferase 1	IPI00217458	54602.15	6.77	1	49.1	99.7987	49.1	99.7987	0	0	1
GSTZ1 glutathione transferase zeta 1 isoform 2	IPI00157928	19360.02	8.27	1	48.42	99.76458	48.42	99.76458	0	0	1
ALAD delta-aminolevulinic acid dehydratase isoform a	IPI00442121	39008.71	7.59	1	39.3	98.07762	39.3	98.07762	0	0	1
GSTM1 28 kDa protein	IPI00647885	27599.04	6.24	1	39.26	98.05983	39.26	98.05983	0	0	1
NIT2 Nitrilase family member 2	IPI00549467	30588.56	6.82	1	38.96	97.92107	38.96	97.92107	0	0	1
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	24433.38	5.15	3	191.02	100	75.89	99.99958	0.001	0.03	3
KRT1 Keratin, type II cytoskeletal 1	IPI00220327	65977.98	8.16	1	55.41	99.95292	55.41	99.95292	0.001	0	1
GLUD2 Glutamate dehydrogenase 2, mitochondrial precursor	IPI00027146	61395.43	8.63	2	162.06	100	99.29	100	0.004	0.127	2

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ALDOB Fructose-bisphosphate aldolase B	IPI00218407	39448.06	8	2	259.04	100	129.97	100	0.005	0.105	2
SORD Sorbitol dehydrogenase	IPI00216057	38271.84	8.23	2	146.27	100	101.03	100	0.008	0.274	2
SELENBP1 53 kDa protein	IPI00745729	53027.94	6.03	2	194.04	100	141.37	100	0.009	0.304	2
HBB Hemoglobin subunit beta	IPI00654755	15988.29	6.75	5	407.49	100	109.1	100	0.027	1.413	5
IGHG1 IGHG1 protein	IPI00448938	51362.63	8.69	3	186.78	100	70.95	99.99869	0.047	2.133	3
PYGL 97 kDa protein	IPI00783313	97272.1	6.71	1	36.58	96.40383	36.58	96.40383	0.128	0	1
CAT Catalase	IPI00465436	59718.75	6.9	1	72.17004	99.99901	73.59	99.99928	0.15	0	1
ALDH1L1 10-formyltetrahydrofolate dehydrogenase	IPI00290553	98766.56	5.63	1	75.61	99.99955	75.61	99.99955	0.178	0	1
SUOX 54 kDa protein	IPI00853137	53851.08	5.35	1	46.74	99.65339	46.74	99.65339	0.317	0	1
LTB4DH Leukotriene B4 12-hydroxydehydrogenase	IPI00642248	19212.93	6.34	1	35.41	95.29196	35.41	95.29196	0.321	0	1
PGM1 Isoform 1 of Phosphoglucomutase-1	IPI00219526	61410.53	6.3	1	90.75	100	90.75	100	0.333	0	1
PABPC4 Isoform 1 of Polyadenylate-binding protein 4	IPI00012726	70738.09	9.31	1	95.84	100	95.84	100	0.356	0	1
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	56402.59	8.17	3	224.56	100	94.09	100	0.363	0.049	3
DCXR 26 kDa protein	IPI00797249	25726.45	8.33	1	46.87004	99.66362	48.29	99.75743	0.407	0	1
CBR1 Carbonyl reductase [NADPH] 1	IPI00295386	30355.86	8.55	1	70.17	99.99843	70.17	99.99843	0.421	0	1
TAGLN Transgelin	IPI00216138	22596.43	8.87	1	52.4	99.90585	52.4	99.90585	0.422	0	1
ADK Isoform Long of Adenosine kinase	IPI00290279	40519.66	6.24	1	71.47	99.99883	71.47	99.99883	0.454	0	1
ARG1 Isoform 1 of Arginase-1	IPI00291560	34713.3	6.72	1	90.41	100	90.41	100	0.458	0	1
HP Haptoglobin precursor	IPI00641737	46693.35	6.28	3	220.39	100	85.59	100	0.478	0.074	3

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IGHA1 SNC66 protein	IPI00383164	53631.38	6.22	1	97.78	100	97.78	100	0.509	0	1
GRHPR Glyoxylate reductase/hydroxypyruvate reductase	IPI00514020	43565.62	7.05	2	143.5	100	99.9	100	0.517	0.008	2
BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101	44969.85	6.58	3	170.62	100	74.01	99.99935	0.534	0.173	3
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	35305.76	8.38	1	83.32	99.99992	83.32	99.99992	0.536	0	1
PPP1CA protein phosphatase 1, catalytic subunit, alpha isoform 3	IPI00027423	38606.37	6.2	1	41.66	98.88355	41.66	98.88355	0.545	0	1
HGD Homogentisate 1,2-dioxygenase	IPI00303174	49940.59	6.54	1	42.67	99.11521	42.67	99.11521	0.553	0	1
HLA-DRB1;HLA-DRB5;LOC730415;hCG_1998957;HLA-DRB4;HLA-DRB3 HLA class II hist	IPI00005182	29970.06	7.71	1	39.25	98.05536	39.25	98.05536	0.567	0	1
- 28 kDa protein	IPI00472065	27488.58	6.54	1	60.74004	99.9862	62.16	99.99005	0.583	0	1
C11orf54 Isoform 4 of Ester hydrolase C11orf54	IPI00760666	23158.41	6.3	2	172.27	100	132.36	100	0.591	0.019	2
EPHX1 Epoxide hydrolase 1, microsomal	IPI00640017	16373.31	5.85	1	60.38	99.98501	60.38	99.98501	0.597	0	1
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	52737.86	6.3	2	137.98	100	71.49	99.99884	0.599	0.03	2
ALDH1A1 Aldehyde dehydrogenase 1 family, member A1	IPI00642144	22639.55	5.76	2	137.54	100	92.1	100	0.607	0.047	2
BLVRB Flavin reductase	IPI00783862	22105.43	7.13	2	114.74	100	74.73	99.99945	0.612	0.128	2
FAH 33 kDa protein	IPI00793664	32625.4	7.12	1	38.23	97.54054	38.23	97.54054	0.614	0	1
SEC14L3 SEC14-like protein 3	IPI00025260	46018.41	5.79	1	48.48	99.76781	48.48	99.76781	0.625	0	1
HCLS1 Hematopoietic lineage cell-specific protein	IPI00026156	53964.98	4.74	1	73.97	99.99934	73.97	99.99934	0.627	0	1
SOD1 Superoxide dismutase	IPI00783680	15925.9	5.7	2	102.28	100	76.36	99.99962	0.641	0.027	2
VIM 50 kDa protein	IPI00827679	49623.11	5.19	1	45.95	99.58424	45.95	99.58424	0.648	0	1
ORM2 Alpha-1-acid glycoprotein 2 precursor	IPI00020091	23587.63	5.03	1	108.71	100	110.13	100	0.677	0	1

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TF Transferrin variant (Fragment)	IPI00798430	77029.59	6.68	3	235.8895	100	114.54	100	0.679	0.055	3
LOC730278;LOC729659 similar to Putative S100 calcium-binding protein A11 ps	IPI00790691	11279.74	7.77	1	41.14	98.74154	41.14	98.74154	0.709	0	1
SAR1B GTP-binding protein SAR1b	IPI00002149	22395.51	5.76	1	82.21	99.9999	82.21	99.9999	1.49	0	1
- 63 kDa protein	IPI00792605	62706.83	10.91	1	55.85004	99.95746	57.27	99.96932	1.506	0	1
ACAT2 Acetyl-CoA acetyltransferase, cytosolic	IPI00291419	41324.39	6.47	1	123.49	100	123.49	100	1.508	0	1
HPX Hemopexin precursor	IPI00022488	51643.27	6.55	2	183.22	100	101.14	100	1.513	0.038	2
CLGN Calmegin precursor	IPI00024776	69994.44	4.58	1	57.46	99.97063	57.46	99.97063	1.521	0	1
ALB Serum albumin	IPI00022434	71529.53	6.33	13	1021.869	100	138.38	100	1.55	0.342	12
PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904	72886.97	4.96	2	165.67	100	102.64	100	1.556	0.064	2
CTSB Cathepsin B precursor	IPI00295741	37796.83	5.88	1	117.71	100	117.71	100	1.592	0	1
BAT1 Isoform 2 of Spliceosome RNA helicase BAT1	IPI00641829	50646.91	5.59	1	42.85	99.15113	42.85	99.15113	1.608	0	1
ACY3 HCBP1	IPI00382975	30891.26	6.79	1	67.51	99.9971	67.51	99.9971	1.638	0	1
C6orf108 putative c-Myc-responsive isoform 2	IPI00395835	16177.23	6.31	1	43.34	99.2417	43.34	99.2417	1.638	0	1
MYL9 Myosin regulatory light chain 2, smooth muscle isoform	IPI00220278	19814.45	4.8	1	86.78	100	86.78	100	1.657	0	1
UFC1 Ufm1-conjugating enzyme 1	IPI00294495	19446.02	6.9	1	68.11	99.99747	68.11	99.99747	1.667	0	1
PARK7 Protein DJ-1	IPI00298547	19878.49	6.33	2	221.62	100	133.29	100	1.757	0.015	2
MTPN Myotrophin	IPI00179589	12886.6	5.27	1	53.2	99.92169	53.2	99.92169	1.767	0	1
PDIA6 Isoform 1 of Protein disulfide-isomerase A6 precursor	IPI00644989	48091.26	4.95	1	118.57	100	118.57	100	1.864	0	1
SYNCRIP Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q	IPI00402182	65641.59	8.69	1	57.55	99.97124	57.55	99.97124	1.873	0	1

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HNRPR HNRPR protein	IPI00644055	71170.32	8.23	1	57.55	99.97124	57.55	99.97124	1.873	0	1
A1BG 41 kDa protein	IPI00644018	40692.54	5.5	2	141.35	100	102.54	100	1.887	0.5	2
CTSD 21 kDa protein	IPI00658053	21476.66	5.48	2	124.25	100	71.69	99.99889	1.918	0.162	2
FIS1 Mitochondrial fission 1 protein	IPI00007052	16927.02	8.84	1	49.82	99.82945	49.82	99.82945	1.921	0	1
MBNL1 Isoform EXP42 of Muscleblind-like protein 1	IPI00021692	41789.99	9.16	1	39.67	98.23461	39.67	98.23461	1.941	0	1
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	44854.47	6.61	1	130.99	100	130.99	100	2.032	0	1
HINT1 Histidine triad nucleotide-binding protein 1	IPI00239077	13793.09	6.43	1	88.04	100	88.04	100	2.074	0	1
LYPLA1 Isoform 2 of Acyl-protein thioesterase 1	IPI00398727	22860.58	6.05	1	56.73	99.96526	56.73	99.96526	2.084	0	1
TST Thiosulfate sulfurtransferase	IPI00216293	33407.84	6.77	2	132.53	100	89.23	100	2.136	0.052	2
HINT2 Histidine triad nucleotide-binding protein 2	IPI00000335	17151.24	9.2	1	46.1	99.59836	46.1	99.59836	2.146	0	1
UGDH UDP-glucose 6-dehydrogenase	IPI00031420	54989.25	6.73	1	54.45	99.94127	54.45	99.94127	2.169	0	1
FLJ11151 Hypothetical protein FLJ11151	IPI00305010	35525.88	5.78	1	50.59	99.85716	50.59	99.85716	2.194	0	1
ANXA2 annexin A2 isoform 1	IPI00418169	40385.72	8.53	1	71.33	99.9988	71.33	99.9988	2.214	0	1
CUTA Isoform C of Protein CutA precursor	IPI00554556	16821.85	5.15	1	66.43	99.99628	66.43	99.99628	2.224	0	1
PRDX2 15 kDa protein	IPI00794777	15128.81	5.82	1	73.96004	99.99934	75.38	99.99953	2.27	0	1
UQCRH Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondria	IPI00296022	10731.94	4.39	1	98.32	100	98.32	100	2.282	0	1
PDLIM1 PDZ and LIM domain protein 1	IPI00010414	36049.04	6.56	2	115.73	100	91.07	100	2.364	0.31	2
PEPD Xaa-Pro dipeptidase	IPI00257882	54512.91	5.64	1	65	99.99483	65	99.99483	2.42	0	1
HSPA1A;HSPA1B Heat shock 70kDa protein 1A	IPI00647012	51914.69	5.35	1	36.07	95.95573	36.07	95.95573	2.496	0	1

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LASP1 Isoform 2 of LIM and SH3 domain protein 1	IPI00386803	35990.71	8.92	1	44.6	99.43266	44.6	99.43266	2.654	0	1
CBX3;LOC653972 Chromobox protein homolog 3	IPI00297579	20798.35	5.23	1	34.74004	94.50667	36.16	96.03868	2.666	0	1
TXN2 Thioredoxin, mitochondrial precursor	IPI00017799	21811.28	8.85	1	86.97	100	86.97	100	2.759	0	1
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	61016.38	5.7	3	218.29	100	103.66	100	2.945	0.75	3
TMEM4 Isoform 1 of MIR-interacting saposin-like protein precursor	IPI00443909	20639.17	4.81	1	92.87	100	92.87	100	2.981	0	1
P4HB Protein disulfide-isomerase precursor	IPI00010796	57080.67	4.76	3	190.35	100	86.11	100	3.168	3.193	3
AARS 107 kDa protein	IPI00784131	106643.1	5.33	1	95.36	100	95.36	100	3.178	0	1
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	18000.88	7.68	3	274.36	100	157.77	100	3.361	0.681	3
FUBP1 Isoform 2 of Far upstream element-binding protein 1	IPI00644386	68861.11	7.74	1	46.2	99.6075	46.2	99.6075	3.6	0	1
SSB Lupus La protein	IPI00009032	46808.16	6.68	1	101.98	100	101.98	100	3.695	0	1
LOC131691 similar to peptidylprolyl isomerase A isoform 1	IPI00741973	18098.81	6.41	1	45.27	99.51377	45.27	99.51377	4.351	0	1
- 12 kDa protein	IPI00797738	12027.62	6.81	3	230.71	100	109.64	100	29.697	1774.747	3
APOH Beta-2-glycoprotein 1 precursor	IPI00298828	38272.66	8.34	2	91.88	100	53.5	99.92691	83.341	2450.538	2
ATOX1 Copper transport protein ATOX1	IPI00010863	7396.73	6.71	2	143.19	100	76.02	99.99959	115.681	3337.859	2
HMGB1 High-mobility group box 1	IPI00644653	18299.33	9.72	2	110.68	100	76.02	99.99959	152.685	5106.955	2
AKR1B10 Aldo-keto reductase family 1 member B10	IPI00105407	35997.82	7.12	1	111.12	100	111.12	100	2185.248	0	1
C1QBP Protein	IPI00795465	20360.71	4.1	1	86.62	100	86.62	100	3140.323	0	1
GLO1 Lactoylglutathione lyase	IPI00220766	20764.25	5.12	1	73.76	99.99931	73.76	99.99931	3330.002	0	1
FN1 Isoform 12 of Fibronectin precursor	IPI00556632	221308.4	5.84	7	413.8796	100	162.75	100	3399.395	25662.17	7

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TKT Transketolase	IPI00643920	67834.72	7.58	2	146.94	100	79.7	99.99982	3850.95	1557.205	2
PPA1 Pyrophosphatase (Inorganic) 1	IPI00643288	19968.92	5.07	1	47.94	99.73707	47.94	99.73707	3991.631	0	1
NUDC 24 kDa protein	IPI00646767	23916.97	5.47	1	54.95	99.94766	54.95	99.94766	4530.008	0	1
FLJ14668 Hypothetical protein FLJ14668	IPI00303722	15630.66	7.56	1	81.85	99.99989	81.85	99.99989	4834.623	0	1
FAM10A4 Protein FAM10A4	IPI00218038	27389.69	5.01	1	98.85	100	98.85	100	5588.454	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
GSTM1 28 kDa protein	IPI00647885	27599.04	6.24	1	63.06	99.99193	63.06	99.99193	0	0	1
IGHA1 Hypothetical protein DKFZp686G21220 (Fragment)	IPI00423460	54354	6.15	1	47.09	99.68084	47.09	99.68084	0	0	0
MGC29506 hypothetical protein LOC51237	IPI00102821	20681.23	5.37	1	41.07	98.72352	41.07	98.72352	0	0	1
ALDOB Fructose-bisphosphate aldolase	IPI00513830	24113.34	6.65	2	166.2	100	140.51	100	0.003	0.112	2
SELENBP1 CDNA FLJ13813 fis, clone THYRO1000358, moderately similar to SELEN	IPI00030385	25937	6.19	1	35.85	95.75366	35.85	95.75366	0.18	0	1
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	52737.86	6.3	1	37.46	97.06901	37.46	97.06901	0.239	0	1
C6orf115 similar to Protein C6orf115	IPI00740277	20388.71	6.38	1	61.51	99.98847	61.51	99.98847	0.248	0	1
GALM Aldose 1-epimerase	IPI00060200	37742.13	6.18	1	49.28	99.80724	49.28	99.80724	0.316	0	1
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	31367.13	8.34	2	179.04	100	93.96	100	0.374	0.058	2
SOD1 Superoxide dismutase	IPI00783680	15925.9	5.7	1	75.99	99.99959	75.99	99.99959	0.39	0	1
CTSB Cathepsin B precursor	IPI00295741	37796.83	5.88	1	35.42	95.31171	35.42	95.31171	0.396	0	1
TST Thiosulfate sulfurtransferase	IPI00216293	33407.84	6.77	1	46.77	99.65643	46.77	99.65643	0.401	0	1
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	35305.76	8.38	1	73.47	99.99927	73.47	99.99927	0.444	0	1
CAT Catalase	IPI00465436	59718.75	6.9	1	32.56004	90.94246	33.98	93.46847	0.462	0	1
PEPD Xaa-Pro dipeptidase	IPI00257882	54512.91	5.64	1	36.86	96.63477	36.86	96.63477	0.487	0	1
PARK7 Protein DJ-1	IPI00298547	19878.49	6.33	1	54.78	99.94567	54.78	99.94567	0.497	0	1
B2M B2M protein	IPI00796379	13687.95	6.06	1	70.59	99.99857	70.59	99.99857	0.532	0	1
HBB Hemoglobin subunit beta	IPI00654755	15988.29	6.75	3	291.82	100	122.31	100	0.554	0.093	3
HBB Hemoglobin delta Etolia variant	IPI00830113	19482.91	8.32	2	84.55	99.99994	52.2	99.9016	0.569	0.008	2

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PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	11992.02	6.28	1	53.9	99.93347	53.9	99.93347	0.599	0	1
BLVRB Flavin reductase	IPI00783862	22105.43	7.13	1	42.38	99.05591	42.38	99.05591	0.603	0	1
TPI1 Isoform 2 of Triosephosphate isomerase	IPI00451401	27109.05	8.48	2	154.56	100	104.08	100	0.614	0.108	2
- 14 kDa protein	IPI00788848	13799	5.24	1	103.43	100	104.85	100	0.619	0	1
IGHA1 SNC66 protein	IPI00383164	53631.38	6.22	1	41.38	98.81146	41.38	98.81146	0.626	0	1
PGM1 Isoform 1 of Phosphoglucomutase-1	IPI00219526	61410.53	6.3	1	34.48	94.17877	34.48	94.17877	0.629	0	1
HCLS1 Hematopoietic lineage cell-specific protein	IPI00026156	53964.98	4.74	1	86.26	100	86.26	100	0.635	0	1
FTL Ferritin light chain	IPI00852596	20007.1	5.51	1	62.34	99.99047	62.34	99.99047	0.642	0	1
- 12 kDa protein	IPI00797738	12027.62	6.81	3	108.04	100	59.33	99.98094	0.648	0.149	3
ARG1 Isoform 1 of Arginase-1	IPI00291560	34713.3	6.72	1	36.95	96.70379	36.95	96.70379	0.661	0	1
IGHG1 Hypothetical protein DKFZp686O01196	IPI00423463	52579.41	8.46	2	101.12	100	54.84	99.94642	0.663	0.012	2
PGAM1;hCG_2015138;hCG_2015269 Phosphoglycerate mutase 1	IPI00549725	28785.83	6.67	1	75.54	99.99954	75.54	99.99954	0.665	0	1
CBR1 Carbonyl reductase [NADPH] 1	IPI00295386	30355.86	8.55	1	46.67	99.64843	46.67	99.64843	0.667	0	1
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	24433.38	5.15	1	45.28	99.51581	45.28	99.51581	0.669	0	1
NPC2 Epididymal secretory protein E1 precursor	IPI00301579	16559.48	7.56	1	85.05	99.99995	85.05	99.99995	0.671	0	1
AK2 Isoform 1 of Adenylate kinase isoenzyme 2, mitochondrial	IPI00215901	26460.77	7.67	1	47.51	99.71026	47.51	99.71026	0.672	0	1
GPX1 16 kDa protein	IPI00784231	16180.13	5.39	1	46.05	99.59448	46.05	99.59448	0.692	0	1
HLA-DRA major histocompatibility complex, class II, DR alpha precursor	IPI00464948	28602.71	4.91	1	64.19	99.99378	64.19	99.99378	0.699	0	1
PRDX1 11 kDa protein	IPI00641244	10669.51	8.79	1	65.15	99.99501	65.15	99.99501	0.703	0	1
C11orf54 Isoform 4 of Ester hydrolase C11orf54	IPI00760666	23158.41	6.3	1	107.61	100	107.61	100	0.707	0	1

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PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	18000.88	7.68	2	120.28	100	66.9	99.99667	1.494	0.076	2
SSB Lupus La protein	IPI00009032	46808.16	6.68	1	98.89	100	98.89	100	1.521	0	1
HSP90B1 Protein	IPI00789430	26539.06	8.95	1	60.2	99.9844	60.2	99.9844	1.539	0	1
GLO1 Lactoylglutathione lyase	IPI00220766	20764.25	5.12	1	52.37	99.90537	52.37	99.90537	1.549	0	1
P4HB Protein disulfide-isomerase precursor	IPI00010796	57080.67	4.76	1	43.85	99.327	43.85	99.327	1.647	0	1
LASP1 Isoform 2 of LIM and SH3 domain protein 1	IPI00386803	35990.71	8.92	1	37.62	97.17502	37.62	97.17502	1.724	0	1
CES1 Isoform 1 of Liver carboxylesterase 1 precursor	IPI00010180	62481.15	6.15	1	37.19	96.881	37.19	96.881	1.785	0	1
FAM10A4 Protein FAM10A4	IPI00218038	27389.69	5.01	1	95.14	100	95.14	100	1.906	0	1
TXNDC5;MUTED thioredoxin domain containing 5 isoform 2	IPI00395646	43641.51	5.77	1	39.21	98.04109	39.21	98.04109	1.956	0	1
LOC440055 similar to ribosomal protein S12	IPI00456898	14588.54	6.43	1	62.41	99.99062	62.41	99.99062	2.036	0	1
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	61016.38	5.7	3	180.71	100	84.67	99.99994	2.36	0.814	3
UQCRH Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondria	IPI00296022	10731.94	4.39	1	116.19	100	116.19	100	2.542	0	1
PDIA3 Protein disulfide-isomerase A3 precursor	IPI00025252	56746.75	5.98	1	60.36	99.98497	60.36	99.98497	2.695	0	1
TKT Transketolase variant (Fragment)	IPI00788802	67862.77	7.9	1	41.13	98.74103	41.13	98.74103	2.814	0	1
FUBP1 Isoform 2 of Far upstream element-binding protein 1	IPI00644386	68861.11	7.74	1	38.26	97.56211	38.26	97.56211	3.8	0	1
HSPA1A;HSPA1B Heat shock 70kDa protein 1A	IPI00647012	51914.69	5.35	2	71.75	99.99891	45.19	99.50567	345.665	36059.63	2
FN1 Isoform 12 of Fibronectin precursor	IPI00556632	221308.4	5.84	3	151.2795	100	66.93	99.99669	3225.625	165571.7	3
C1QBP Protein	IPI00795465	20360.71	4.1	1	96.03	100	96.03	100	24539.93	0	1
FLNB Isoform 2 of Filamin-B	IPI00382696	275526.9	5.53	1	66.19	99.99607	66.19	99.99607	27210.4	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	44854.47	6.61	1	96.18	100	96.18	100	0	0	1
KRT9 Keratin, type I cytoskeletal 9	IPI00019359	62091.91	5.19	1	75.02	99.99947	75.02	99.99947	0	0	1
DCXR 26 kDa protein	IPI00797249	25726.45	8.33	1	72.63005	99.99909	74.05	99.99934	0	0	1
DSG1 Desmoglein-1 precursor	IPI00025753	113643.9	4.9	1	71.94	99.99893	71.94	99.99893	0	0	1
PAH Phenylalanine-4-hydroxylase	IPI00017579	51829.46	6.15	1	68.64	99.99772	68.64	99.99772	0	0	1
SERPINB12 SERPINB12 protein	IPI00643202	48415.18	5.25	1	62.72	99.99107	62.72	99.99107	0	0	1
KRT10 57 kDa protein	IPI00383111	56527.82	5.09	1	49.4	99.8083	49.4	99.8083	0	0	1
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	56402.59	8.17	2	156.5	100	81.66	99.99989	0.006	0.25	2
KRT1 Keratin, type II cytoskeletal 1	IPI00220327	65977.98	8.16	2	277.83	100	161.16	100	0.034	0.011	2
FTH1 Ferritin heavy chain	IPI00554521	21212.29	5.3	1	124.95	100	124.95	100	0.181	0	1
ALDOB Fructose-bisphosphate aldolase	IPI00513830	24113.34	6.65	1	140.6	100	140.6	100	0.261	0	1
CAT Catalase	IPI00465436	59718.75	6.9	1	62.69004	99.99101	64.11	99.99352	0.268	0	1
AK2 Isoform 1 of Adenylate kinase isoenzyme 2, mitochondrial	IPI00215901	26460.77	7.67	1	64.64	99.99426	64.64	99.99426	0.273	0	1
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	39909.67	8.75	1	56.36	99.9614	56.36	99.9614	0.273	0	1
ACAT2 Acetyl-CoA acetyltransferase, cytosolic	IPI00291419	41324.39	6.47	1	42.54004	99.06973	43.96	99.32917	0.283	0	1
FTL Ferritin light chain	IPI00852596	20007.1	5.51	1	94.28	100	94.28	100	0.292	0	1
PGM1 Isoform 1 of Phosphoglucomutase-1	IPI00219526	61410.53	6.3	1	46.49	99.62536	46.49	99.62536	0.309	0	1
ARG1 Isoform 1 of Arginase-1	IPI00291560	34713.3	6.72	1	51.76	99.88867	51.76	99.88867	0.326	0	1
TST Thiosulfate sulfurtransferase	IPI00216293	33407.84	6.77	1	59.77	99.9824	59.77	99.9824	0.36	0	1

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HINT2 Histidine triad nucleotide-binding protein 2	IPI00000335	17151.24	9.2	1	44.64	99.4264	44.64	99.4264	0.377	0	1
GLUD2 Glutamate dehydrogenase 2, mitochondrial precursor	IPI00027146	61395.43	8.63	1	57.25	99.96855	57.25	99.96855	0.443	0	1
HGD Homogentisate 1,2-dioxygenase	IPI00303174	49940.59	6.54	1	59.1	99.97946	59.1	99.97946	0.451	0	1
TPI1 Isoform 2 of Triosephosphate isomerase	IPI00451401	27109.05	8.48	2	157.12	100	85.45	100	0.461	0.204	2
- 11 kDa protein	IPI00382841	11283.54	5.82	2	53.03	99.9169	29.41	80.87456	0.462	0.087	2
C11orf54 Isoform 4 of Ester hydrolase C11orf54	IPI00760666	23158.41	6.3	2	152.86	100	113.44	100	0.486	0.058	2
FAM10A4 Protein FAM10A4	IPI00218038	27389.69	5.01	1	89.44	100	89.44	100	0.493	0	1
RAD23B UV excision repair protein RAD23 homolog B	IPI00008223	43144.62	4.79	1	63.37	99.99232	63.37	99.99232	0.527	0	1
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	31367.13	8.34	2	122.61	100	88.21	100	0.531	0.09	2
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	35305.76	8.38	1	82.35	99.9999	82.35	99.9999	0.536	0	1
PNPO 19 kDa protein	IPI00793232	19465.84	6.92	1	48.71	99.7753	48.71	99.7753	0.551	0	1
BLVRB Flavin reductase	IPI00783862	22105.43	7.13	1	57.41	99.96969	57.41	99.96969	0.553	0	1
GPX1 16 kDa protein	IPI00784231	16180.13	5.39	1	63.26	99.99212	63.26	99.99212	0.554	0	1
GALM Aldose 1-epimerase	IPI00060200	37742.13	6.18	1	49.83	99.82638	49.83	99.82638	0.559	0	1
- 12 kDa protein	IPI00797738	12027.62	6.81	3	244.08	100	107.84	100	0.578	0.059	3
MPST 3-mercaptopyruvate sulfurtransferase variant (Fragment)	IPI00746782	34729.5	6.83	1	75.07	99.99948	75.07	99.99948	0.614	0	1
PGAM1;hCG_2015138;hCG_2015269 Phosphoglycerate mutase 1	IPI00549725	28785.83	6.67	1	65.63	99.99543	65.63	99.99543	0.625	0	1
SOD1 Superoxide dismutase	IPI00783680	15925.9	5.7	1	62.18	99.98989	62.18	99.98989	0.629	0	1
CALR 37 kDa protein	IPI00793605	36679.71	4.55	1	63.99	99.99334	63.99	99.99334	0.643	0	1
AKR1A1 Aldo-keto reductase family 1, member A1	IPI00647702	16506.3	5.84	1	42.93	99.14962	42.93	99.14962	0.644	0	1

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PRDM10 CDNA FLJ20227 fis, clone COLF5152	IPI00386081	105524.9	8.83	1	43.80005	99.304	45.22	99.49811	0.668	0	1
SELENBP1 53 kDa protein	IPI00745729	53027.94	6.03	1	43.38	99.23332	43.38	99.23332	0.695	0	1
RBP4 Retinol binding protein 4, plasma	IPI00480192	22929.13	5.77	1	50.34	99.84561	50.34	99.84561	0.704	0	1
SYNCRIP Isoform 1 of Heterogeneous nuclear ribonucleoprotein Q	IPI00018140	69559.59	8.68	1	54.18	99.93623	54.18	99.93623	1.497	0	1
TKT Transketolase variant (Fragment)	IPI00788802	67862.77	7.9	1	55.44	99.95229	55.44	99.95229	1.525	0	1
LOC730278;LOC729659 similar to Putative S100 calcium-binding protein A11 ps	IPI00790691	11279.74	7.77	1	71.72	99.99888	71.72	99.99888	1.608	0	1
AMBP AMBP protein precursor	IPI00022426	38973.98	5.95	1	42.71004	99.10545	44.13	99.35492	1.627	0	1
TF Transferrin variant (Fragment)	IPI00798430	77029.59	6.68	5	256.61	100	110.59	100	1.631	0.426	5
A1BG 41 kDa protein	IPI00644018	40692.54	5.5	2	103.92	100	57.29	99.96884	1.635	0.203	2
PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904	72886.97	4.96	1	71.75	99.99888	71.75	99.99888	1.66	0	1
IGKC IGKC protein	IPI00430808	25629.86	6.15	3	240.96	100	129.33	100	1.663	0.231	3
ANXA2 annexin A2 isoform 1	IPI00418169	40385.72	8.53	1	52.2	99.8994	52.2	99.8994	1.67	0	1
APOH Beta-2-glycoprotein 1 precursor	IPI00298828	38272.66	8.34	3	118.14	100	55.69	99.95496	1.672	0.373	3
FGB Fibrinogen beta chain precursor	IPI00298497	55892.26	8.54	1	65.12	99.99486	65.12	99.99486	1.676	0	1
UFC1 Ufm1-conjugating enzyme 1	IPI00294495	19446.02	6.9	2	80.88	99.99986	41.31	98.76516	1.824	0.198	2
IGHA1 SNC66 protein	IPI00383164	53631.38	6.22	1	73.52	99.99926	73.52	99.99926	1.84	0	1
CTSD 21 kDa protein	IPI00658053	21476.66	5.48	2	110.31	100	56.04	99.95845	1.851	0.128	2
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	61016.38	5.7	1	50.52	99.85188	50.52	99.85188	1.859	0	1
HPX Hemopexin precursor	IPI00022488	51643.27	6.55	5	320.7	100	98.52	100	1.873	0.164	5
LGALS1 Galectin-1	IPI00219219	14706.2	5.34	3	193.45	100	67.63	99.99712	1.906	0.099	3

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APOA2 Apolipoprotein A-II precursor	IPI00021854	11167.9	6.26	1	68.16	99.99745	68.16	99.99745	1.95	0	1
FHL1 Four and a half LIM domains 1	IPI00029028	23685.15	8.94	2	71.95	99.99893	40.25	98.4238	1.96	0.029	2
- Hypothetical protein DKFZp686C15213	IPI00426051	51066.19	7.85	2	128.73	100	92.81	100	2.049	0.637	2
IGHM IGHM protein	IPI00472610	52633.11	7.5	3	200.34	100	92.81	100	2.065	0.586	3
SERPINB6 Serpin peptidase inhibitor, clade B (Ovalbumin), member 6	IPI00513699	21231.33	6.89	1	42.54	99.06973	42.54	99.06973	2.14	0	1
LYPLA1 Isoform 2 of Acyl-protein thioesterase 1	IPI00398727	22860.58	6.05	1	63.61	99.99273	63.61	99.99273	2.143	0	1
IGHM Hypothetical protein DKFZp686I15212	IPI00418153	56983.02	8.39	2	66.11	99.99591	35.92	95.72819	2.238	0.447	2
- 29 kDa protein	IPI00791859	28830.89	5.65	1	49.49	99.81224	49.49	99.81224	2.269	0	1
F2 70 kDa protein	IPI00784409	69916.09	5.64	1	77.87	99.99973	77.87	99.99973	2.277	0	1
CTSB Cathepsin B precursor	IPI00295741	37796.83	5.88	1	93.1	100	93.1	100	2.291	0	1
EEF1G;LOC729998 similar to Elongation factor 1-gamma	IPI00738381	50270.31	7.09	1	45.21	99.49695	45.21	99.49695	2.326	0	1
PGLYRP2 Isoform 2 of N-acetylmuramoyl-L-alanine amidase precursor	IPI00394992	67957.49	7.62	1	67.82	99.99724	67.82	99.99724	2.472	0	1
TAGLN Transgelin	IPI00216138	22596.43	8.87	1	52.57	99.90761	52.57	99.90761	2.57	0	1
- Hypothetical protein DKFZp686M24218	IPI00784998	52387.11	7.89	3	103.64	100	37.35	96.92665	2.583	0.789	3
CP 20 kDa protein	IPI00793108	20180.8	5.27	1	49.14	99.79648	49.14	99.79648	2.612	0	1
ALB Serum albumin	IPI00022434	71529.53	6.33	16	1299.41	100	131	100	2.648	14.824	15
B2M B2M protein	IPI00796379	13687.95	6.06	1	84.75	99.99994	84.75	99.99994	2.732	0	1
GRN Isoform 1 of Granulins precursor	IPI00296713	63499.84	6.43	1	48.4	99.75867	48.4	99.75867	2.796	0	1
HLA-DRA major histocompatibility complex, class II, DR alpha precursor	IPI00464948	28602.71	4.91	2	137.77	100	103.75	100	3.362	0.101	2
CD59 CD59 glycoprotein precursor	IPI00011302	14167.79	6.02	1	55.07	99.94805	55.07	99.94805	3.983	0	1

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VTN Vitronectin precursor	IPI00298971	54271.17	5.55	1	82.44	99.9999	82.44	99.9999	4.404	0	1
UQCRC1 24 kDa protein	IPI00792890	24089.1	5.51	1	61.58	99.9884	61.58	99.9884	4.479	0	1
LUM Lumican precursor	IPI00020986	38404.79	6.16	1	54.35	99.93868	54.35	99.93868	6.147	0	1
ORM2 Alpha-1-acid glycoprotein 2 precursor	IPI00020091	23587.63	5.03	1	64.58	99.99418	64.58	99.99418	6.199	0	1
P4HB Protein disulfide-isomerase precursor	IPI00010796	57080.67	4.76	2	143.8	100	79.48	99.99981	77.276	6099.774	2
RNH1 Ribonuclease/angiogenin inhibitor	IPI00783491	49839.99	4.68	2	127.09	100	68.45	99.99761	135.005	5964.038	2
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472138	40312.04	5.9	2	69.97	99.99832	42.88	99.13978	168.042	4725.628	2
EPHX1 Epoxide hydrolase 1	IPI00009896	52914.96	6.77	3	126.44	100	55.28	99.9505	567.814	20945.161	3
AKR1B10 Aldo-keto reductase family 1 member B10	IPI00105407	35997.82	7.12	1	58.79	99.97794	58.79	99.97794	1568.221	0	1
- CDNA FLJ41483 fis, clone BRTHA2002808, highly similar to GAMMA- INTERFERO	IPI00446576	16995.2	4.57	1	53.24	99.92082	53.24	99.92082	2879.897	0	1
TUBA1B Tubulin alpha-1B chain	IPI00387144	50119.6	4.94	1	55.28	99.9505	55.28	99.9505	3088.856	0	1
VIM 50 kDa protein	IPI00827679	49623.11	5.19	1	93.62	100	93.62	100	3355.97	0	1
ENO3 Beta-enolase	IPI00218474	46957.32	7.59	1	53.5	99.92542	53.5	99.92542	4406.242	0	1
FN1 Isoform 12 of Fibronectin precursor	IPI00556632	221308.4	5.84	3	121.81	100	73.35	99.99923	4732.048	1377.937	3
EFEMP1 Isoform 2 of EGF-containing fibulin-like extracellular matrix protei	IPI00220813	53686.69	4.9	3	117.64	100	43.1	99.18227	5360.354	2518.163	3
LGALS3BP 16 kDa protein	IPI00794873	16452.93	5.74	1	66.18	99.99598	66.18	99.99598	6538.959	0	1
RTN3 Isoform 5 of Reticulon-3	IPI00394896	26435.07	9.08	1	58.69	99.97743	58.69	99.97743	6823.166	0	1
- 29 kDa protein	IPI00177423	28641.2	8.34	1	58.69	99.97743	58.69	99.97743	6823.166	0	1
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472057	40336.98	5.67	2	52.56	99.9074	27.09	67.37043	6963.845	2945.924	2
PRELP Prolargin precursor	IPI00020987	43782.15	9.47	1	46.26	99.60499	46.26	99.60499	7718.268	0	1

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MYL9 Myosin regulatory light chain 2, smooth muscle isoform	IPI00220278	19814.45	4.8	1	70.32	99.99845	70.32	99.99845	8926.424	0	1
UCHL1 16 kDa protein	IPI00657702	15680.62	5.19	1	79.18	99.9998	79.18	99.9998	12476.04	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	39448.06	8	2	188.78	100	137.28	100	0	0	2
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	56402.59	8.17	2	169.32	100	84.69	99.99994	0	0	2
C11orf54 Isoform 4 of Ester hydrolase C11orf54	IPI00760666	23158.41	6.3	2	118.84	100	87.61	100	0	0	2
PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904	72886.97	4.96	2	86.85	100	58.45	99.97596	0	0	2
SOD1 Superoxide dismutase	IPI00783680	15925.9	5.7	2	79.21	99.9998	43.44	99.23808	0	0	2
PGM1 Isoform 1 of Phosphoglucomutase-1	IPI00219526	61410.53	6.3	1	83.76	99.99993	83.76	99.99993	0	0	1
PGAM1;hCG_2015138;hCG_2015269 Phosphoglycerate mutase 1	IPI00549725	28785.83	6.67	1	72.96	99.99915	72.96	99.99915	0	0	1
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	11992.02	6.28	1	71.12	99.9987	71.12	99.9987	0	0	1
TXNDC5;MUTED thioredoxin domain containing 5 isoform 2	IPI00395646	43641.51	5.77	1	64.99005	99.99467	66.41	99.99615	0	0	1
AKR1C1 Aldo-keto reductase family 1 member C1	IPI00029733	36765.02	8.02	1	59.3	99.98023	59.3	99.98023	0	0	1
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	24433.38	5.15	1	58.91	99.97838	58.91	99.97838	0	0	1
PAH Phenylalanine-4-hydroxylase	IPI00017579	51829.46	6.15	1	57.7	99.97143	57.7	99.97143	0	0	1
P4HB Protein disulfide-isomerase precursor	IPI00010796	57080.67	4.76	1	49.05	99.79063	49.05	99.79063	0	0	1
PBLD 28 kDa protein	IPI00396138	28133.41	6.55	1	45.79	99.55649	45.79	99.55649	0	0	1
GSTZ1 glutathione transferase zeta 1 isoform 2	IPI00157928	19360.02	8.27	1	43.73	99.2873	43.73	99.2873	0	0	1
CBR1 Carbonyl reductase [NADPH] 1	IPI00295386	30355.86	8.55	1	43.53	99.25371	43.53	99.25371	0	0	1
BHMT2 Betaine--homocysteine S-methyltransferase 2	IPI00014363	40328.18	5.61	1	43.03	99.16265	43.03	99.16265	0	0	1
CHDH Choline dehydrogenase, mitochondrial precursor	IPI00168603	65360.13	8.67	1	38.67004	97.71491	40.09	98.35219	0	0	1
DCXR 26 kDa protein	IPI00797249	25726.45	8.33	1	40.07005	98.3446	41.49	98.80627	0	0	1

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PDIA6 Isoform 1 of Protein disulfide-isomerase A6 precursor	IPI00644989	48091.26	4.95	1	39.34	98.04157	39.34	98.04157	0	0	1
PEBP1 22 kDa protein	IPI00795288	21730.87	8.33	1	39.28	98.01433	39.28	98.01433	0	0	0
ALDH1A1 Aldehyde dehydrogenase 1 family, member A1	IPI00642144	22639.55	5.76	1	38.43	97.58506	38.43	97.58506	0	0	1
AKR1D1 CDNA FLJ25413 fis, clone TST03402, highly similar to 3-OXO-5-BETA- S	IPI00065073	30242.66	8.11	1	34.67	94.26006	34.67	94.26006	0	0	1
GSTM1 glutathione S-transferase M1 isoform 2	IPI00152326	21238.76	7.67	1	31.76	88.78221	31.76	88.78221	0	0	1
GFER Augmenter of liver regeneration	IPI00472356	23463.22	8.01	1	30.99	86.60609	30.99	86.60609	0	0	1
ALDH1L1 10-formyltetrahydrofolate dehydrogenase	IPI00290553	98766.56	5.63	1	30.78	85.94253	30.78	85.94253	0	0	1
IFIT3 Interferon-induced protein with tetratricopeptide repeats 3	IPI00024254	55949.51	5.12	1	29.83	82.50527	29.83	82.50527	0	0	1
NDUFV2 28 kDa protein	IPI00646556	27889.3	8.15	1	28.5	76.23667	28.5	76.23667	0	0	1
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	31367.13	8.34	2	136.28	100	70.46	99.99849	0.002	0.103	2
PARK7 Protein DJ-1	IPI00298547	19878.49	6.33	3	151.98	100	82.84	99.99991	0.003	0.067	3
SELENBP1 53 kDa protein	IPI00745729	53027.94	6.03	2	130.17	100	93.82	100	0.003	0.081	2
HP Haptoglobin precursor	IPI00641737	46693.35	6.28	3	166.83	100	67.37	99.99692	0.004	0.135	3
GALM Aldose 1-epimerase	IPI00060200	37742.13	6.18	2	138.82	100	73.29	99.99921	0.004	0.177	2
BLVRB Flavin reductase	IPI00783862	22105.43	7.13	2	85.69	100	59.93	99.9829	0.006	0.098	2
DAK Dihydroxyacetone kinase	IPI00551024	58940.04	7.12	2	160.59	100	81.09	99.99987	0.007	0.237	2
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	44854.47	6.61	2	104.62	100	79.89	99.99983	0.008	0.329	2
TST Thiosulfate sulfurtransferase	IPI00216293	33407.84	6.77	1	85.95	100	85.95	100	0.045	0	1
ATOX1 Copper transport protein ATOX1	IPI00010863	7396.73	6.71	1	117.87	100	117.87	100	0.054	0	1
HINT1 Histidine triad nucleotide-binding protein 1	IPI00239077	13793.09	6.43	1	61.61	99.98839	61.61	99.98839	0.069	0	1

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ALB Serum albumin	IPI00022434	71529.53	6.33	13	831.752	100	148.84	100	0.073	2.434	12
ORM2 Alpha-1-acid glycoprotein 2 precursor	IPI00020091	23587.63	5.03	1	91.33005	100	92.75	100	0.099	0	1
FAH Fumarylacetoacetase	IPI00031708	46344.21	6.46	1	38.77	97.76691	38.77	97.76691	0.111	0	1
- 12 kDa protein	IPI00797738	12027.62	6.81	3	233.93	100	119.64	100	0.113	0.01	3
HGD Homogentisate 1,2-dioxygenase	IPI00303174	49940.59	6.54	1	45.24	99.49661	45.24	99.49661	0.138	0	1
CAT Catalase	IPI00465436	59718.75	6.9	1	55.70004	99.95472	57.12	99.96735	0.147	0	1
MPST 3-mercaptopyruvate sulfurtransferase variant (Fragment)	IPI00746782	34729.5	6.83	1	70.92	99.99864	70.92	99.99864	0.156	0	1
SORD Sorbitol dehydrogenase	IPI00216057	38271.84	8.23	1	57.23	99.96816	57.23	99.96816	0.164	0	1
PNPO 19 kDa protein	IPI00793232	19465.84	6.92	1	61.7	99.98863	61.7	99.98863	0.165	0	1
AK2 Isoform 1 of Adenylate kinase isoenzyme 2, mitochondrial	IPI00215901	26460.77	7.67	1	41.89	98.9113	41.89	98.9113	0.173	0	1
UQCRH Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondria	IPI00296022	10731.94	4.39	1	121.32	100	121.32	100	0.193	0	1
C6orf108 putative c-Myc-responsive isoform 2	IPI00395835	16177.23	6.31	1	42.33	99.0162	42.33	99.0162	0.202	0	1
TMEM4 Isoform 1 of MIR-interacting saposin-like protein precursor	IPI00443909	20639.17	4.81	1	63.78	99.99295	63.78	99.99295	0.22	0	1
ASGR2 Isoform 3 of Asialoglycoprotein receptor 2	IPI00150200	32529.64	5.46	1	39.7	98.19737	39.7	98.19737	0.231	0	1
ACY1 15 kDa protein	IPI00792542	15083.28	5.77	1	48.88	99.78228	48.88	99.78228	0.238	0	1
GPX1 16 kDa protein	IPI00784231	16180.13	5.39	1	83.63	99.99993	83.63	99.99993	0.24	0	1
CALR 37 kDa protein	IPI00793605	36679.71	4.55	1	75.05	99.99947	75.05	99.99947	0.241	0	1
FAM10A4 Protein FAM10A4	IPI00218038	27389.69	5.01	1	97.99	100	97.99	100	0.246	0	1
TPI1 Isoform 1 of Triosephosphate isomerase	IPI00465028	30771.7	5.65	4	324.78	100	92.69	100	0.268	0.049	4
HINT2 Histidine triad nucleotide-binding protein 2	IPI00000335	17151.24	9.2	1	54.06	99.93394	54.06	99.93394	0.284	0	1

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HBB Hemoglobin delta Etolia variant	IPI00830113	19482.91	8.32	2	102.19	100	65.42	99.99517	0.294	0.005	2
- 11 kDa protein	IPI00382841	11283.54	5.82	1	29.38	80.59528	29.38	80.59528	0.313	0	1
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	35305.76	8.38	1	78.35	99.99975	78.35	99.99975	0.327	0	1
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	39909.67	8.75	1	46.32	99.60744	46.32	99.60744	0.337	0	1
ORM1 Alpha-1-acid glycoprotein 1 precursor	IPI00022429	23496.76	4.93	1	105.65	100	105.65	100	0.347	0	1
- 18 kDa protein	IPI00745933	17925.71	6.21	3	166.5	100	74.6	99.99942	0.349	0.018	3
CTSD 21 kDa protein	IPI00658053	21476.66	5.48	2	91.28	100	46.14	99.59083	0.351	0.023	2
ACAT2 Acetyl-CoA acetyltransferase, cytosolic	IPI00291419	41324.39	6.47	1	116.01	100	117.43	100	0.355	0	1
B2M B2M protein	IPI00796379	13687.95	6.06	1	67.66	99.99712	67.66	99.99712	0.381	0	1
EEF1G;LOC729998 similar to Elongation factor 1-gamma	IPI00738381	50270.31	7.09	1	43.34	99.22034	43.34	99.22034	0.391	0	1
LGALS1 Galectin-1	IPI00219219	14706.2	5.34	2	114.67	100	59.66	99.98181	0.396	0.182	2
ARG1 Isoform 1 of Arginase-1	IPI00291560	34713.3	6.72	1	49.93	99.82904	49.93	99.82904	0.396	0	1
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	52737.86	6.3	1	52.3	99.90094	52.3	99.90094	0.406	0	1
- 63 kDa protein	IPI00792605	62706.83	10.91	1	45.43	99.51816	45.43	99.51816	0.406	0	1
GCSH;LOC730107 Glycine cleavage system H protein, mitochondrial precursor	IPI00011604	18898.67	4.91	1	30.19	83.89699	30.19	83.89699	0.412	0	1
PDLIM1 PDZ and LIM domain protein 1	IPI00010414	36049.04	6.56	1	75.55	99.99953	75.55	99.99953	0.442	0	1
HBB Hemoglobin subunit beta	IPI00654755	15988.29	6.75	3	248.49	100	98.34	100	0.446	0.27	3
KRT1 Keratin, type II cytoskeletal 1	IPI00220327	65977.98	8.16	1	61.46	99.98798	61.46	99.98798	0.447	0	1
HPX Hemopexin precursor	IPI00022488	51643.27	6.55	2	89.65	100	45.82	99.55954	0.457	0.151	2
AGXT Serine--pyruvate aminotransferase	IPI00009367	42982.44	8.61	1	29.23	79.91336	29.23	79.91336	0.478	0	1

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HNRPR HNRPR protein	IPI00644055	71170.4	8.23	2	76.47	99.99962	44.34	99.38069	0.485	0.131	2
SYNCRIP Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q	IPI00402182	65641.59	8.69	2	76.47	99.99962	44.34	99.38069	0.485	0.131	2
HMGB1 High-mobility group box 1	IPI00644653	18299.33	9.72	1	39.36	98.05057	39.36	98.05057	0.485	0	1
UFC1 Ufm1-conjugating enzyme 1	IPI00294495	19446.02	6.9	1	31.90942	89.16161	34.16	93.54484	0.522	0	1
RAD23B UV excision repair protein RAD23 homolog B	IPI00008223	43144.62	4.79	1	90.4	100	90.4	100	0.543	0	1
TXNDC4 Thioredoxin domain-containing protein 4 precursor	IPI00401264	46941.4	5.09	1	39.63	98.16808	39.63	98.16808	0.547	0	1
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	61016.38	5.7	2	100.55	100	59.26	99.98005	0.55	0.374	2
EPHX1 Epoxide hydrolase 1, microsomal	IPI00640017	16373.31	5.85	1	30.03	83.29267	30.03	83.29267	0.559	0	1
PRDX6 Peroxiredoxin-6	IPI00220301	25019.19	6	1	29.15	79.53992	29.15	79.53992	0.578	0	1
FHL1 Four and a half LIM domains 1	IPI00029028	23685.15	8.94	1	29.41	80.72887	29.41	80.72887	0.617	0	1
FGG Isoform Gamma-A of Fibrinogen gamma chain precursor	IPI00219713	49464.97	5.7	1	40.77	98.59101	40.77	98.59101	0.631	0	1
A1BG 41 kDa protein	IPI00644018	40692.54	5.5	2	63.48	99.99245	34.65	94.23357	0.638	0.087	2
TF Transferrin variant (Fragment)	IPI00798430	77029.59	6.68	4	218.5901	100	103.56	100	0.645	0.249	4
HCLS1 Hematopoietic lineage cell-specific protein	IPI00026156	53964.98	4.74	1	46.95	99.66045	46.95	99.66045	0.682	0	1
- Hypothetical protein DKFZp686C15213	IPI00426051	51066.19	7.85	1	26.94	65.96646	26.94	65.96646	1.646	0	1
CLGN Calmegin precursor	IPI00024776	69994.44	4.58	1	63.4	99.99231	63.4	99.99231	1.658	0	1
HLA-DRA major histocompatibility complex, class II, DR alpha precursor	IPI00464948	28602.71	4.91	1	64.2	99.9936	64.2	99.9936	2.221	0	1
APOA2 Apolipoprotein A-II precursor	IPI00021854	11167.9	6.26	1	86.81	100	86.81	100	2.97	0	1
CMBL carboxymethylenebutenolidase-like	IPI00383046	28030.17	6.71	1	36.07	95.84178	36.07	95.84178	3.047	0	1
VIM 50 kDa protein	IPI00827679	49623.11	5.19	1	86.17	100	86.17	100	3.133	0	1

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TAGLN Transgelin	IPI00216138	22596.43	8.87	1	36.58	96.30251	36.58	96.30251	4.751	0	1
FN1 fibronectin 1 isoform 4 preproprotein	IPI00414283	256351.1	5.53	1	44.62004	99.41937	46.04	99.5813	7.383	0	1
MYL9 Myosin regulatory light chain 2, smooth muscle isoform	IPI00220278	19814.45	4.8	1	27.73	71.62687	27.73	71.62687	5680.061	0	1
AKR1B10 Aldo-keto reductase family 1 member B10	IPI00105407	35997.82	7.12	1	64.68	99.99427	64.68	99.99427	5861.212	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
CPS1 Isoform 2 of Carbamoyl-phosphate synthase [ammonia], mitochondrial pre	IPI00397498	115964.1	5.67	5	194.44	100	61.38	99.98784	0	0	5
UQCRC1 18 kDa protein	IPI00792217	18454.07	7.66	1	52.86	99.91355	52.86	99.91355	0	0	1
ADH1C Alcohol dehydrogenase 1C	IPI00465343	39841.67	8.63	1	33.58004	92.67568	35	94.71832	0	0	1
ADH4 Alcohol dehydrogenase 4	IPI00218899	40195.71	8.25	1	29.53	81.38891	29.53	81.38891	0	0	1
TST Thiosulfate sulfurtransferase	IPI00216293	33407.84	6.77	2	56.73004	99.96454	35.21	94.96764	0.002	0.185	2
GAPDH 39 kDa protein	IPI00788737	38766.83	8.76	2	66.36	99.99614	33.81	93.05341	0.005	0.28	2
ASS1 Argininosuccinate synthetase 1	IPI00514341	19035.86	7.26	1	32.11	89.72524	32.11	89.72524	0.103	0	1
ALDOB Fructose-bisphosphate aldolase	IPI00513830	24113.34	6.65	1	102.93	100	102.93	100	0.104	0	1
FTL Ferritin light chain	IPI00852596	20007.1	5.51	1	47.82	99.72409	47.82	99.72409	0.172	0	1
AK2 Isoform 1 of Adenylate kinase isoenzyme 2, mitochondrial	IPI00215901	26460.77	7.67	1	36.28	96.06656	36.28	96.06656	0.242	0	1
- 11 kDa protein	IPI00382841	11283.54	5.82	1	37.3	96.88992	37.3	96.88992	0.283	0	1
PNPO 19 kDa protein	IPI00793232	19465.84	6.92	1	67.52	99.99704	67.52	99.99704	0.295	0	1
CBR1 Carbonyl reductase [NADPH] 1	IPI00295386	30355.86	8.55	1	37.77	97.20892	37.77	97.20892	0.304	0	1
- 12 kDa protein	IPI00797738	12027.62	6.81	1	40.71	98.58169	40.71	98.58169	0.344	0	1
PGAM1;hCG_2015138;hCG_2015269 Phosphoglycerate mutase 1	IPI00549725	28785.83	6.67	1	70.12	99.99838	70.12	99.99838	0.375	0	1
UQCRH Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondria	IPI00296022	10731.94	4.39	1	61.72	99.98876	61.72	99.98876	0.38	0	1
CTSD 21 kDa protein	IPI00658053	21476.66	5.48	2	73.09	99.99918	37.59	97.09081	0.399	0.014	2
TUBB4 Tubulin beta-4 chain	IPI00023598	49553.9	4.78	2	60.29	99.98438	36.54	96.29514	0.421	0.022	2
TUBB2A Tubulin beta-2A chain	IPI00013475	49874.96	4.78	2	60.29	99.98438	36.54	96.29514	0.421	0.022	2

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HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	61016.38	5.7	2	69.22005	99.998	39.93	98.30265	0.423	0.019	2
TXNDC5;MUTED thioredoxin domain containing 5 isoform 2	IPI00395646	43641.51	5.77	2	95.38005	100	69.55	99.99815	0.451	0.02	2
CAT Catalase	IPI00465436	59718.75	6.9	1	36.25004	96.03934	37.67	97.14391	0.484	0	1
SELENBP1 CDNA FLJ13813 fis, clone THYRO1000358, moderately similar to SELEN	IPI00030385	25937	6.19	1	31.08	86.97517	31.08	86.97517	0.508	0	1
MDH2 Malate dehydrogenase, mitochondrial precursor	IPI00291006	35508.76	8.92	1	42.12	98.97489	42.12	98.97489	0.52	0	1
TPI1 Isoform 1 of Triosephosphate isomerase	IPI00465028	30771.7	5.65	2	122.56	100	63.32	99.99222	0.545	0.051	2
CTSB Cathepsin B precursor	IPI00295741	37796.83	5.88	1	107.42	100	107.42	100	0.561	0	1
PARK7 Protein DJ-1	IPI00298547	19878.49	6.33	3	108.73	100	39.94	98.30655	0.566	0.217	3
CLGN Calmegin precursor	IPI00024776	69994.44	4.58	1	33.93	93.24272	33.93	93.24272	0.57	0	1
AKR1C3 Aldo-keto reductase family 1 member C3	IPI00291483	36820.84	8.05	1	31.26	87.50398	31.26	87.50398	0.616	0	1
BLVRB Flavin reductase	IPI00783862	22105.43	7.13	1	38.02	97.36505	38.02	97.36505	0.671	0	1
HLA-DRA major histocompatibility complex, class II, DR alpha precursor	IPI00464948	28602.71	4.91	1	35.26	95.02524	35.26	95.02524	0.707	0	1
FGG Isoform Gamma-A of Fibrinogen gamma chain precursor	IPI00219713	49464.97	5.7	1	44.44	99.39914	44.44	99.39914	1.545	0	1
LGALS1 Galectin-1	IPI00219219	14706.2	5.34	2	67.24	99.99685	43.93	99.32427	1.654	0.145	2
VIM 50 kDa protein	IPI00827679	49623.11	5.19	1	84.06	99.99993	84.06	99.99993	1.881	0	1
HP Haptoglobin precursor	IPI00641737	46693.35	6.28	4	188.82	100	72.93	99.99915	2.024	0.275	4
FLNA filamin A, alpha	IPI00302592	279843.5	5.69	1	36.13	95.92834	36.13	95.92834	2.068	0	1
SERPINB6 Serpin peptidase inhibitor, clade B (Ovalbumin), member 6	IPI00513699	21231.33	6.89	1	58.6	99.97694	58.6	99.97694	2.234	0	1
FHL1 Isoform 1 of Four and a half LIM domains protein 1	IPI00647207	31872.84	8.72	1	34.41	93.94977	34.41	93.94977	2.632	0	1
IGHG1 Hypothetical protein DKFZp686K03196	IPI00423464	52327.11	8.84	4	209.7701	100	94.69	100	2.783	0.331	4
HBA2;HBA1 Alpha 2 globin variant (Fragment)	IPI00853068	15270.94	8.72	1	43.41	99.23832	43.41	99.23832	3.069	0	1

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- Hypothetical protein DKFZp686C15213	IPI00426051	51066.19	7.85	2	76.74001	99.99965	40.5	98.51142	3.09	0.155	2
IGLV4-3 IGLV4-3 protein	IPI00382938	25960.7	6.3	2	138.6	100	75.32	99.99951	3.51	0.544	2
HBB Hemoglobin delta Etolia variant	IPI00830113	19482.91	8.32	2	91.4	100	54.33	99.93837	3.625	0.103	2
ORM2 Alpha-1-acid glycoprotein 2 precursor	IPI00020091	23587.63	5.03	1	62.83	99.99129	62.83	99.99129	3.629	0	1
IGKC IGKC protein	IPI00430808	25629.86	6.15	1	79.96	99.99983	79.96	99.99983	3.633	0	1
TAGLN Transgelin	IPI00216138	22596.43	8.87	1	37.12	96.75831	37.12	96.75831	3.702	0	1
HBB Hemoglobin subunit beta	IPI00654755	15988.29	6.75	3	271.53	100	108.66	100	3.994	0.221	3
A1BG 41 kDa protein	IPI00644018	40692.54	5.5	1	35.89	95.69699	35.89	95.69699	6.382	0	1
TF Transferrin variant (Fragment)	IPI00798430	77029.59	6.68	8	421.3802	100	92.64	100	8.548	143.573	8
ALB Serum albumin	IPI00022434	71529.53	6.33	18	1058.079	100	109.61	100	20.035	818.215	18
HPX Hemopexin precursor	IPI00022488	51643.27	6.55	3	152.32	100	74.4	99.99939	1705.294	93062.586	3
IGHA1 SNC66 protein	IPI00383164	53631.38	6.22	1	34.65	94.27505	34.65	94.27505	10539.87	0	1
ORM1 Alpha-1-acid glycoprotein 1 precursor	IPI00022429	23496.76	4.93	1	42.1	98.97015	42.1	98.97015	12282.5	0	1
SERPINA1 Alpha 1-antitrypsin	IPI00790784	40237.62	5.26	1	57.26	99.96861	57.26	99.96861	15093.25	0	1

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Poor Diff 126NT

Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
GSTM1 28 kDa protein	IPI00647885	27599.04	6.24	1	29.62	81.89189	29.62	81.89189	0	0	1
FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	36790.79	6.54	1	28.71004	77.67102	30.13	83.89825	0	0	1
HBB Hemoglobin delta Etolia variant	IPI00830113	19482.91	8.32	2	82.24	99.9999	56.23	99.96047	0.006	0.149	2
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	31367.13	8.34	2	176.51	100	93.23	100	0.011	0.455	2
EPHX1 Epoxide hydrolase 1	IPI00009896	52914.96	6.77	2	93.37	100	69.48	99.99813	0.011	0.316	2
SPTA1 Spectrin, alpha, erythrocytic 1	IPI00641363	279501.7	4.95	1	33.51004	92.60618	34.93	94.66821	0.19	0	1
HBB Hemoglobin subunit beta	IPI00654755	15988.29	6.75	3	285.2	100	103.01	100	0.245	0.135	3
PABPC4 Isoform 1 of Polyadenylate-binding protein 4	IPI00012726	70738.09	9.31	1	78.5	99.99977	78.5	99.99977	0.283	0	1
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	11992.02	6.28	1	47.46	99.70224	47.46	99.70224	0.314	0	1
SORD Sorbitol dehydrogenase	IPI00216057	38271.84	8.23	1	42.79	99.12728	42.79	99.12728	0.324	0	1
C11orf54 Isoform 4 of Ester hydrolase C11orf54	IPI00760666	23158.41	6.3	1	62.78	99.99125	62.78	99.99125	0.333	0	1
GOT2 Aspartate aminotransferase, mitochondrial precursor	IPI00018206	47445.27	9.14	2	56.5	99.96286	29.9	83.02252	0.369	0.01	2
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	35305.76	8.38	1	102.95	100	102.95	100	0.374	0	1
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	39448.06	8	2	273.7	100	140.17	100	0.398	0.004	2
SOD1 Superoxide dismutase	IPI00783680	15925.9	5.7	2	175.47	100	111.51	100	0.421	0.016	2
PRDX2 15 kDa protein	IPI00794777	15128.81	5.82	2	52.58004	99.90841	31.17	87.32719	0.441	0.02	2
GFER Augmenter of liver regeneration	IPI00472356	23463.22	8.01	1	28.16	74.65612	28.16	74.65612	0.442	0	1

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PARK7 Protein DJ-1	IPI00298547	19878.49	6.33	1	111.67	100	111.67	100	0.45	0	1
FTH1 Ferritin heavy chain	IPI00554521	21212.29	5.3	1	105.74	100	105.74	100	0.46	0	1
FTL Ferritin light chain	IPI00852596	20007.1	5.51	1	95.55	100	95.55	100	0.549	0	1
RAD23B UV excision repair protein RAD23 homolog B	IPI00008223	43144.62	4.79	1	36	95.83252	36	95.83252	0.57	0	1
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	44854.47	6.61	1	66.35	99.99616	66.35	99.99616	0.577	0	1
RAD23A UV excision repair protein RAD23 homolog A	IPI00008219	39584.65	4.56	1	40.96	98.66993	40.96	98.66993	0.589	0	1
- 14 kDa protein	IPI00788848	13799	5.24	1	77.37005	99.9997	78.79	99.99978	0.601	0	1
SPTAN1 283 kDa protein	IPI00744706	283049.5	5.24	1	44.98	99.47292	44.98	99.47292	0.619	0	1
HLA-DPA1 Major histocompatibility complex, class II, DP alpha 1	IPI00644713	24043.96	5.09	1	35.65	95.48276	35.65	95.48276	0.65	0	1
CUTA Isoform C of Protein CutA precursor	IPI00554556	16821.85	5.15	1	37.52004	97.06324	38.94	97.88226	0.67	0	1
MYL9 Myosin regulatory light chain 2, smooth muscle isoform	IPI00220278	19814.45	4.8	1	50.84	99.86327	50.84	99.86327	0.682	0	1
ATOX1 Copper transport protein ATOX1	IPI00010863	7396.73	6.71	1	30.90004	86.51445	32.32	90.27537	0.688	0	1
PYCARD Isoform 2 of Apoptosis-associated speck-like protein containing a CA	IPI00221360	19956.4	5.66	1	59.7	99.98222	59.7	99.98222	0.691	0	1
FAM10A4 Protein FAM10A4	IPI00218038	27389.69	5.01	1	83.07	99.99992	83.07	99.99992	0.693	0	1
HLA-DRA major histocompatibility complex, class II, DR alpha precursor	IPI00464948	28602.71	4.91	1	57.03	99.96712	57.03	99.96712	0.835	0	1
ORM2 Alpha-1-acid glycoprotein 2 precursor	IPI00020091	23587.63	5.03	1	55.59	99.9542	55.59	99.9542	1.486	0	1
HCLS1 Hematopoietic lineage cell-specific protein	IPI00026156	53964.98	4.74	1	70.3	99.99845	70.3	99.99845	1.5	0	1
PLS3 Plastin-3	IPI00848312	70391.1	5.52	1	57.06	99.96735	57.06	99.96735	1.515	0	1
IGHM IGHM protein	IPI00472610	52633.11	7.5	3	190.54	100	83.13	99.99992	1.53	0.153	3

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APOA2 Apolipoprotein A-II precursor	IPI00021854	11167.9	6.26	1	87.43	100	87.43	100	1.55	0	1
B2M B2M protein	IPI00796379	13687.95	6.06	1	82.7	99.99991	82.7	99.99991	1.581	0	1
ALB Serum albumin	IPI00022434	71529.53	6.33	12	1148.64	100	158	100	1.582	0.2	10
UFC1 Ufm1-conjugating enzyme 1	IPI00294495	19446.02	6.9	2	58.85	99.97838	32.77	91.23255	1.634	0.235	2
HPX Hemopexin precursor	IPI00022488	51643.27	6.55	2	180.51	100	107.47	100	1.688	0.098	2
EEF1G;LOC729998 similar to Elongation factor 1-gamma	IPI00738381	50270.31	7.09	1	45.18	99.49665	45.18	99.49665	1.699	0	1
LOC653879 similar to Complement C3 precursor	IPI00739237	44900.89	4.94	1	38.63	97.72557	38.63	97.72557	1.706	0	1
SSB Lupus La protein	IPI00009032	46808.16	6.68	1	84.57	99.99994	84.57	99.99994	1.73	0	1
IGHA1 SNC66 protein	IPI00383164	53631.38	6.22	1	103.26	100	103.26	100	1.769	0	1
PAH Phenylalanine-4-hydroxylase	IPI00017579	51829.46	6.15	1	79.66	99.99982	79.66	99.99982	1.93	0	1
TKT Transketolase variant (Fragment)	IPI00788802	67862.77	7.9	1	67.56	99.99709	67.56	99.99709	2.354	0	1
SYNCRIP Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q	IPI00402182	65641.59	8.69	1	40.19004	98.41193	41.61	98.85482	2.358	0	1
HSP90AA1 Hsp89-alpha-delta-N	IPI00604607	63211.62	5.03	2	153.92	100	114.41	100	2.362	0.576	2
VCP 89 kDa protein	IPI00843748	89270.64	5.11	1	46.28004	99.60928	47.7	99.71824	2.549	0	1
FLNA Filamin-A	IPI00333541	280563.9	5.7	1	36.1	95.92739	36.1	95.92739	2.637	0	1
FGB Fibrinogen beta chain precursor	IPI00298497	55892.26	8.54	1	53.29	99.92222	53.29	99.92222	3.143	0	1
UQCRC1 24 kDa protein	IPI00792890	24089.1	5.51	1	40.77	98.61045	40.77	98.61045	3.182	0	1
PML promyelocytic leukemia protein isoform 10	IPI00181058	64995.65	5.19	1	32.46004	90.58395	33.88	93.20995	3.533	0	1
CYC1 Cytochrome c1 heme protein, mitochondrial precursor	IPI00029264	35367	9.15	1	45.22	99.50126	45.22	99.50126	4.023	0	1

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HSPG2 365 kDa protein	IPI00747758	364402.6	6.07	1	34.09	93.53046	34.09	93.53046	4.093	0	1
AKR1B10 Aldo-keto reductase family 1 member B10	IPI00105407	35997.82	7.12	1	107.22	100	107.22	100	5.923	0	1
FN1 Isoform 12 of Fibronectin precursor	IPI00556632	221308.4	5.84	3	162.0301	100	77.76	99.99972	48.526	876.844	3
HSPA4 Heat shock 70 kDa protein 4	IPI00002966	94240.29	5.18	2	63.02004	99.99172	39.07	97.94471	60.506	2978.441	2
PGK1 Phosphoglycerate kinase 1	IPI00169383	44586.13	8.3	2	94.39	100	69.26	99.99803	79.731	1564.507	2
- Hypothetical protein DKFZp686C15213	IPI00426051	51066.19	7.85	2	124.88	100	83.13	99.99992	90.973	5392.506	2
NNMT Nicotinamide N-methyltransferase	IPI00027681	29555.06	5.56	2	112.33	100	88.99	100	129.08	3325.475	2
ORM1 Alpha-1-acid glycoprotein 1 precursor	IPI00022429	23496.76	4.93	1	85.03	99.99995	85.03	99.99995	2141.019	0	1
ACSL4 Isoform Short of Long-chain-fatty-acid--CoA ligase 4	IPI00219897	74387.9	8.33	1	30.3	84.51636	30.3	84.51636	2771.111	0	1
TXN2 Thioredoxin, mitochondrial precursor	IPI00017799	21811.28	8.85	1	70.13	99.99839	70.13	99.99839	3984.918	0	1
ACTG1;PSPHL Actin, cytoplasmic 2	IPI00021440	41765.79	5.31	1	61.67	99.98871	61.67	99.98871	8330.845	0	1
TUBB Tubulin beta chain	IPI00011654	49638.97	4.78	1	47.42	99.69948	47.42	99.69948	9648.022	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
- CDNA FLJ46317 fis, clone TESTI4041832	IPI00443413	49623.29	10.33	1	29.97	83.27398	29.97	83.27398	0	0	0
IGHG1 IGHG1 protein	IPI00448938	51362.63	8.69	2	125.85	100	79.09	99.9998	0.012	0.751	2
HLA-DRA major histocompatibility complex, class II, DR alpha precursor	IPI00464948	28602.71	4.91	2	70.14	99.99839	38.84	97.83034	0.018	1.369	2
FGG Isoform Gamma-A of Fibrinogen gamma chain precursor	IPI00219713	49464.97	5.7	1	64.96	99.9947	64.96	99.9947	0.488	0	1
ORM2 Alpha-1-acid glycoprotein 2 precursor	IPI00020091	23587.63	5.03	1	86.51005	100	87.93	100	0.55	0	1
ASS1 Argininosuccinate synthetase 1	IPI00514341	19035.86	7.26	1	82.81	99.99991	82.81	99.99991	0.556	0	1
STOM Erythrocyte band 7 integral membrane protein	IPI00219682	31710.74	7.71	1	41	98.68055	41	98.68055	0.596	0	1
FGB Fibrinogen beta chain precursor	IPI00298497	55892.26	8.54	1	45.05	99.48073	45.05	99.48073	0.637	0	1
ALB Serum albumin	IPI00022434	71529.53	6.33	10	645.8195	100	111.37	100	0.646	0.236	7
HPX Hemopexin precursor	IPI00022488	51643.27	6.55	1	29.46	81.18983	29.46	81.18983	0.651	0	1
CP 20 kDa protein	IPI00793108	20180.8	5.27	1	29.13	79.70483	29.13	79.70483	0.653	0	1
BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101	44969.85	6.58	1	58.13	99.97445	58.13	99.97445	0.661	0	1
A1BG 41 kDa protein	IPI00644018	40692.54	5.5	1	34.97	94.71077	34.97	94.71077	0.662	0	1
IGKC IGKC protein	IPI00430808	25629.86	6.15	1	79.94	99.99983	79.94	99.99983	0.677	0	1
HBA2;HBA1 Alpha 2 globin variant (Fragment)	IPI00853068	15270.94	8.72	1	64.41	99.99398	64.41	99.99398	0.695	0	1
- Hypothetical protein DKFZp686M24218	IPI00784998	52387.11	7.89	3	113.97	100	47.39	99.69703	0.704	0.054	3
CTSB Cathepsin B precursor	IPI00295741	37796.83	5.88	1	52.65	99.90976	52.65	99.90976	1.465	0	1
HINT1 Histidine triad nucleotide-binding protein 1	IPI00239077	13793.09	6.43	1	50.37	99.84746	50.37	99.84746	1.487	0	1
CUTA Isoform C of Protein CutA precursor	IPI00554556	16821.85	5.15	1	26.17	59.87707	26.17	59.87707	1.501	0	1
- 14 kDa protein	IPI00455040	14347.57	8.86	1	34.27	93.78569	34.27	93.78569	1.51	0	1

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RAD23B UV excision repair protein RAD23 homolog B	IPI00008223	43144.62	4.79	1	67.25	99.99687	67.25	99.99687	1.559	0	1
B2M B2M protein	IPI00796379	13687.95	6.06	1	75.48	99.99953	75.48	99.99953	1.618	0	1
SAR1A SAR1 gene homolog A	IPI00644667	13653.07	6.49	1	33.33	92.284	33.33	92.284	1.642	0	1
- 12 kDa protein	IPI00797738	12027.62	6.81	2	71.97	99.99894	41.11	98.71355	1.662	0.255	2
RAB21 Ras-related protein Rab-21	IPI00007755	24332.25	8.11	1	29.22	80.12108	29.22	80.12108	1.664	0	1
IFIT3 Interferon-induced protein with tetratricopeptide repeats 3	IPI00024254	55949.51	5.12	1	41.31	98.77145	41.31	98.77145	1.673	0	1
HMGB1 High-mobility group box 1	IPI00644653	18299.33	9.72	1	26.16	59.78458	26.16	59.78458	1.686	0	1
RAD23A UV excision repair protein RAD23 homolog A	IPI00008219	39584.65	4.56	1	54.96	99.94699	54.96	99.94699	1.718	0	1
PARK7 Protein DJ-1	IPI00298547	19878.49	6.33	3	171.16	100	101.59	100	1.726	0.052	3
PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904	72886.97	4.96	2	99.8	100	56.77	99.96505	1.73	0.033	2
SERPINB6 Serpin peptidase inhibitor, clade B (Ovalbumin), member 6	IPI00513699	21231.33	6.89	1	38.59	97.70177	38.59	97.70177	1.773	0	1
ETFB Isoform 2 of Electron transfer flavoprotein subunit beta	IPI00556451	37411	6.78	1	27.25	68.71093	27.25	68.71093	1.773	0	1
HSP90B1 Protein	IPI00789430	26539.06	8.95	1	74.12	99.99936	74.12	99.99936	1.788	0	1
LOC389842 similar to Ran-specific GTPase-activating protein	IPI00399212	35001.84	8.76	1	24.03942	34.46849	26.29	60.97054	1.806	0	1
- Actinin alpha4 isoform	IPI00845465	59542.11	4.82	1	69.07	99.99794	69.07	99.99794	1.807	0	1
LASP1 Isoform 2 of LIM and SH3 domain protein 1	IPI00386803	35990.71	8.92	1	31.64	88.61344	31.64	88.61344	1.822	0	1
CTSD 21 kDa protein	IPI00658053	21476.66	5.48	2	88.87	100	50.24	99.84282	1.858	0.219	2
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	35305.76	8.38	1	59.97	99.98327	59.97	99.98327	1.859	0	1
TES Isoform 2 of Testin	IPI00216425	46878.3	7.82	1	28.6	77.0706	28.6	77.0706	1.864	0	1
HSP90AA1 Hsp89-alpha-delta-N	IPI00604607	63211.62	5.03	2	122.82	100	79.13	99.9998	1.969	0.19	2
CDC42 Isoform 2 of Cell division control protein 42 homolog precursor	IPI00016786	21245.02	6.15	1	43.29	99.22126	43.29	99.22126	1.977	0	1
CLGN Calmegin precursor	IPI00024776	69994.44	4.58	1	40.3	98.44978	40.3	98.44978	2.006	0	1

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ACAT2 Acetyl-CoA acetyltransferase, cytosolic	IPI00291419	41324.39	6.47	1	78.69	99.99978	78.69	99.99978	2.025	0	1
C6orf115 similar to Protein C6orf115	IPI00740277	20388.71	6.38	1	41.92	98.93244	41.92	98.93244	2.034	0	1
VCP 89 kDa protein	IPI00843748	89270.64	5.11	1	37.19004	96.8276	38.61	97.71233	2.046	0	1
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	18000.88	7.68	3	151.52	100	61.03	99.9869	2.082	0.551	3
LYPLA1 Isoform 2 of Acyl-protein thioesterase 1	IPI00398727	22860.58	6.05	1	46.76	99.64974	46.76	99.64974	2.169	0	1
LGALS1 Galectin-1	IPI00219219	14706.2	5.34	1	35.59	95.41444	35.59	95.41444	2.195	0	1
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	61016.38	5.7	1	77.99	99.99974	77.99	99.99974	2.206	0	1
CALR 37 kDa protein	IPI00793605	36679.71	4.55	1	54.75	99.94436	54.75	99.94436	2.215	0	1
AARS 107 kDa protein	IPI00784131	106643.1	5.33	1	48.86	99.78403	48.86	99.78403	2.256	0	1
GALM Aldose 1-epimerase	IPI00060200	37742.13	6.18	1	57.9	99.97306	57.9	99.97306	2.291	0	1
HCLS1 Hematopoietic lineage cell-specific protein	IPI00026156	53964.98	4.74	1	70.22	99.99842	70.22	99.99842	2.293	0	1
ERP29 Endoplasmic reticulum protein ERp29 precursor	IPI00024911	28975.15	6.77	1	86.64	100	86.64	100	2.305	0	1
PPP2CB Serine/threonine-protein phosphatase 2A catalytic subunit beta isofo	IPI00429689	35552.33	5.21	1	40.94	98.6622	40.94	98.6622	2.486	0	1
DCPS Scavenger mRNA-decapping enzyme DcpS	IPI00335385	38585.02	5.93	1	32.26	90.12828	32.26	90.12828	2.616	0	1
PYCARD Isoform 2 of Apoptosis-associated speck-like protein containing a CA	IPI00221360	19956.4	5.66	1	34.12	93.56731	34.12	93.56731	2.647	0	1
- CDNA FLJ41483 fis, clone BRTHA2002808, highly similar to GAMMA- INTERFERO	IPI00446576	16995.2	4.57	1	55.96	99.95789	55.96	99.95789	2.653	0	1
NPM1 Isoform 1 of Nucleophosmin	IPI00549248	32554.84	4.64	1	31.5	88.2404	31.5	88.2404	2.684	0	1
PEPD Xaa-Pro dipeptidase	IPI00257882	54512.91	5.64	1	45.58	99.54039	45.58	99.54039	2.711	0	1
CBX3;LOC653972 Chromobox protein homolog 3	IPI00297579	20798.35	5.23	1	54.07005	99.93493	55.49	99.95308	2.72	0	1
CPOX Coproporphyrinogen III oxidase, mitochondrial precursor	IPI00093057	50119.97	8.59	1	38.65004	97.73333	40.07	98.36547	2.883	0	1
SSB Lupus La protein	IPI00009032	46808.16	6.68	1	93.81	100	93.81	100	3.24	0	1
- Similar to Glyceraldehyde-3-phosphate dehydrogenase	IPI00747273	12564.45	8.74	1	45.06	99.48193	45.06	99.48193	3.874	0	1

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CNBP Isoform 3 of Cellular nucleic acid-binding protein	IPI00430814	18400.04	8	1	48.69004	99.77541	50.11	99.83805	7.744	0	1
TPI1 Isoform 1 of Triosephosphate isomerase	IPI00465028	30771.7	5.65	3	154.12	100	59.12	99.97966	23.12	1066.058	3
FAM10A4 Protein FAM10A4	IPI00218038	27389.69	5.01	1	84.68	99.99994	84.68	99.99994	3863.983	0	1
ANP32A Acidic leucine-rich nuclear phosphoprotein 32 family member A	IPI00025849	28568.28	3.99	1	54.61	99.94254	54.61	99.94254	4214.713	0	1
P4HB Protein disulfide-isomerase precursor	IPI00010796	57080.67	4.76	1	41.31	98.77145	41.31	98.77145	4728.755	0	1
VIM 50 kDa protein	IPI00827679	49623.11	5.19	1	92.83	100	92.83	100	6591.874	0	1
ACP1 Isoform 1 of Low molecular weight phosphotyrosine protein phosphatase	IPI00219861	18030.77	6.3	1	41.88	98.92256	41.88	98.92256	6934.492	0	1
HSP90AB1 Heat shock protein HSP 90-beta	IPI00414676	83212.1	4.97	1	29.37	80.79596	29.37	80.79596	9725.499	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
ARG1 Isoform 1 of Arginase-1	IPI00291560	34713.3	6.72	1	36.01	95.70457	36.01	95.70457	0.341	0	1
SOD1 Superoxide dismutase	IPI00783680	15925.9	5.7	1	87.27	100	87.27	100	0.391	0	1
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	11992.02	6.28	1	61.72	99.98847	61.72	99.98847	0.417	0	1
- 12 kDa protein	IPI00797738	12027.62	6.81	1	62.62	99.99062	62.62	99.99062	0.447	0	1
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	61016.38	5.7	3	158.04	100	63.16	99.99172	0.515	0.128	3
AGPS Alkyldihydroxyacetonephosphate synthase, peroxisomal p	IPI00010349	72865.75	6.99	1	29.45	80.54613	29.45	80.54613	0.525	0	1
TST Thiosulfate sulfurtransferase	IPI00216293	33407.84	6.77	1	43.67	99.26378	43.67	99.26378	0.535	0	1
SPTA1 Spectrin, alpha, erythrocytic 1	IPI00641363	279501.7	4.95	1	29.80004	82.05259	31.22	87.05786	0.539	0	1
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial pre	IPI00013860	35305.76	8.38	1	55.69	99.95376	55.69	99.95376	0.543	0	1
RAD23B UV excision repair protein RAD23 homolog B	IPI00008223	43144.62	4.79	1	67.48	99.99694	67.48	99.99694	0.545	0	1
UQCRH Ubiquinol-cytochrome c reductase complex 11 kDa prot	IPI00296022	10731.94	4.39	1	107.15	100	107.15	100	0.572	0	1
TPI1 Isoform 2 of Triosephosphate isomerase	IPI00451401	27109.05	8.48	2	131.33	100	73.91	99.9993	0.586	0.016	2
CUTA Isoform C of Protein CutA precursor	IPI00554556	16821.85	5.15	1	46.27004	99.59542	47.69	99.70825	0.628	0	1
TMEM4 Isoform 1 of MIR-interacting saposin-like protein precurs	IPI00443909	20639.17	4.81	1	46.74	99.63692	46.74	99.63692	0.669	0	1
- 14 kDa protein	IPI00788848	13799	5.24	1	108.14	100	109.56	100	0.673	0	1
HINT1 Histidine triad nucleotide-binding protein 1	IPI00239077	13793.09	6.43	1	63.21	99.99182	63.21	99.99182	0.673	0	1
FAM10A4 Protein FAM10A4	IPI00218038	27389.69	5.01	1	81.22	99.99987	81.22	99.99987	0.677	0	1
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	31367.13	8.34	1	81.79	99.99989	81.79	99.99989	0.693	0	1
TXNDC4 Thioredoxin domain-containing protein 4 precursor	IPI00401264	46941.4	5.09	1	79.73	99.99982	79.73	99.99982	0.698	0	1

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FTL Ferritin light chain	IPI00852596	20007.1	5.51	1	91.31	100	91.31	100	0.737	0	1
PGM1 Isoform 1 of Phosphoglucomutase-1	IPI00219526	61410.53	6.3	1	64.58	99.99403	64.58	99.99403	1.513	0	1
SERPINB6 Serpin peptidase inhibitor, clade B (Ovalbumin), mer	IPI00513699	21231.33	6.89	1	51.66	99.88305	51.66	99.88305	1.55	0	1
HPR Isoform 1 of Haptoglobin-related protein precursor	IPI00477597	38982.65	6.42	1	53.67	99.92638	53.67	99.92638	1.559	0	1
HBB Hemoglobin delta Etolia variant	IPI00830113	19482.91	8.32	2	91.72	100	52.96	99.9133	1.565	0.164	2
GPX1 16 kDa protein	IPI00784231	16180.13	5.39	1	45.89	99.55842	45.89	99.55842	1.666	0	1
HSP90B1 Protein	IPI00789430	26539.06	8.95	1	53.06	99.91528	53.06	99.91528	1.679	0	1
CLGN Calmegin precursor	IPI00024776	69994.44	4.58	1	43	99.14097	43	99.14097	1.711	0	1
TKT Transketolase variant (Fragment)	IPI00788802	67862.77	7.9	1	43.84	99.29204	43.84	99.29204	1.829	0	1
HCLS1 Hematopoietic lineage cell-specific protein	IPI00026156	53964.98	4.74	1	36.75	96.37752	36.75	96.37752	1.87	0	1
CDC42 Isoform 2 of Cell division control protein 42 homolog pre	IPI00016786	21245.02	6.15	1	30.69	85.37803	30.69	85.37803	1.923	0	1
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	18000.88	7.68	1	49.19	99.79346	49.19	99.79346	1.95	0	1
FLNA Filamin-A	IPI00333541	280563.9	5.7	1	41.56	98.80324	41.56	98.80324	1.961	0	1
GOT2 Aspartate aminotransferase, mitochondrial precursor	IPI00018206	47445.27	9.14	1	76.51	99.99962	76.51	99.99962	2.049	0	1
ACTN1 Actinin alpha 1 isoform b	IPI00759776	105501.7	5.25	1	31.24	87.11732	31.24	87.11732	2.076	0	1
APOA2 Apolipoprotein A-II precursor	IPI00021854	11167.9	6.26	1	108.2	100	108.2	100	2.25	0	1
ALDH1A1 Aldehyde dehydrogenase 1 family, member A1	IPI00642144	22639.55	5.76	1	61.83	99.98875	61.83	99.98875	2.385	0	1
CTSD 21 kDa protein	IPI00658053	21476.66	5.48	2	107.42	100	54.79	99.94311	2.437	0.167	2
ORM2 Alpha-1-acid glycoprotein 2 precursor	IPI00020091	23587.63	5.03	1	94.8	100	94.8	100	2.606	0	1
A1BG 41 kDa protein	IPI00644018	40692.54	5.5	2	119.93	100	78.47	99.99976	2.626	0.569	2

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AMBP AMBP protein precursor	IPI00022426	38973.98	5.95	1	63.46004	99.99227	64.88	99.99443	2.714	0	1
NNMT Nicotinamide N-methyltransferase	IPI00027681	29555.06	5.56	1	77.62	99.9997	77.62	99.9997	2.743	0	1
APOH Beta-2-glycoprotein 1 precursor	IPI00298828	38272.66	8.34	1	44.36	99.37193	44.36	99.37193	2.761	0	1
TXNDC5;MUTED thioredoxin domain containing 5 isoform 2	IPI00395646	43641.51	5.77	1	30.39	84.33227	30.39	84.33227	2.779	0	1
CTSB Cathepsin B precursor	IPI00295741	37796.83	5.88	1	68.95	99.99782	68.95	99.99782	2.824	0	1
HPX Hemopexin precursor	IPI00022488	51643.27	6.55	5	404.4301	100	131.08	100	3.153	1.208	5
FGG Isoform Gamma-A of Fibrinogen gamma chain precursor	IPI00219713	49464.97	5.7	1	83.22	99.99992	83.22	99.99992	3.287	0	1
SULT2A1 Bile salt sulfotransferase	IPI00216133	33757.96	5.71	1	55.29	99.9493	55.29	99.9493	3.287	0	1
STOM Erythrocyte band 7 integral membrane protein	IPI00219682	31710.74	7.71	1	42.65	99.06888	42.65	99.06888	3.435	0	1
TF Transferrin variant (Fragment)	IPI00798430	77029.59	6.68	3	209.84	100	101.29	100	3.58	1.754	3
GC vitamin D-binding protein precursor	IPI00742696	52882.94	5.32	2	122.68	100	67.15	99.9967	4.145	0.547	2
ALB Serum albumin	IPI00022434	71529.53	6.33	14	1275.52	100	175.28	100	4.147	3.729	12
LOC653879 similar to Complement C3 precursor	IPI00739237	44900.89	4.94	1	45.08	99.46788	45.08	99.46788	4.278	0	1
PDIA3 Protein disulfide-isomerase A3 precursor	IPI00025252	56746.75	5.98	1	57.55	99.96987	57.55	99.96987	4.298	0	1
FGB Fibrinogen beta chain precursor	IPI00298497	55892.26	8.54	2	142.11	100	91.46	100	4.826	3.793	2
IGKC IGKC protein	IPI00430808	25629.86	6.15	2	174.84	100	105.13	100	4.902	2.918	2
IGHM IGHM protein	IPI00472610	52633.11	7.5	3	252.62	100	92.23	100	5.123	4.386	3
ORM1 Alpha-1-acid glycoprotein 1 precursor	IPI00022429	23496.76	4.93	1	110.22	100	110.22	100	5.489	0	1
A2M Alpha-2-macroglobulin precursor	IPI00478003	163174.8	6	1	47.45004	99.69168	48.87	99.77767	6.543	0	1
IGHA1 SNC66 protein	IPI00383164	53631.38	6.22	1	105.21	100	105.21	100	11.324	0	1

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FN1 fibronectin 1 isoform 4 preproprotein	IPI00414283	256351.1	5.53	1	43.60004	99.25183	45.02	99.46048	21005.85	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
FTL Ferritin light chain	IPI00852596	20007.1	5.51	1	92.59	100	92.59	100	0	0	1
CAST calpastatin isoform c	IPI00302047	47014.15	4.72	1	54.82	99.94605	54.82	99.94605	0	0	1
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	31367.13	8.34	1	52.52	99.90839	52.52	99.90839	0	0	1
NNMT Nicotinamide N-methyltransferase	IPI00027681	29555.06	5.56	1	48.01	99.7412	48.01	99.7412	0	0	1
- ABC1 protein	IPI00784697	99637.02	8.07	1	38.22	97.53419	38.22	97.53419	0	0	0
SELENBP1 53 kDa protein	IPI00745729	53027.94	6.03	2	113.07	100	68.12	99.99748	0.008	0.256	2
IFIT3 Interferon-induced protein with tetratricopeptide repeats 3	IPI00024254	55949.51	5.12	2	74.04	99.99935	51.32	99.87923	0.009	0.666	2
HLA-DRA major histocompatibility complex, class II, DR alpha precursor	IPI00464948	28602.71	4.91	2	104.59	100	61.35	99.98801	0.022	1.417	2
HBB Hemoglobin subunit beta	IPI00654755	15988.29	6.75	3	263.16	100	108.96	100	0.046	2.072	3
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	39909.67	8.75	1	54.04	99.93544	54.04	99.93544	0.165	0	1
HGD Homogentisate 1,2-dioxygenase	IPI00303174	49940.59	6.54	1	49.38	99.81122	49.38	99.81122	0.228	0	1
TAGLN Transgelin	IPI00216138	22596.43	8.87	1	49.44	99.81381	49.44	99.81381	0.276	0	1
ALDOB Fructose-bisphosphate aldolase	IPI00513830	24113.34	6.65	1	104.23	100	104.23	100	0.279	0	1
TST Thiosulfate sulfurtransferase	IPI00216293	33407.84	6.77	1	60.92	99.98676	60.92	99.98676	0.285	0	1
- 63 kDa protein	IPI00792605	62706.83	10.91	1	77.75	99.99973	77.75	99.99973	0.308	0	1
TPI1 Isoform 1 of Triosephosphate isomerase	IPI00465028	30771.7	5.65	5	391.53	100	117.53	100	0.336	8.167	5
FTH1 Ferritin heavy chain	IPI00554521	21212.29	5.3	1	94.4	100	94.4	100	0.36	0	1

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PABPC4 Isoform 1 of Polyadenylate-binding protein 4	IPI00012726	70738.09	9.31	1	86.28	100	86.28	100	0.362	0	1
MGC29506 hypothetical protein LOC51237	IPI00102821	20681.23	5.37	1	122.93	100	122.93	100	0.376	0	1
SCP2 sterol carrier protein 2 isoform 2	IPI00433347	54380.39	6.25	1	66.31	99.99617	66.31	99.99617	0.439	0	1
C6orf115 similar to Protein C6orf115	IPI00740277	20388.71	6.38	1	73.62	99.99929	73.62	99.99929	0.44	0	1
HCLS1 Hematopoietic lineage cell-specific protein	IPI00026156	53964.98	4.74	1	84.01	99.99993	84.01	99.99993	0.442	0	1
GPX1 16 kDa protein	IPI00784231	16180.13	5.39	1	89.86	100	89.86	100	0.478	0	1
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	52737.86	6.3	1	74.55	99.99943	74.55	99.99943	0.488	0	1
FABP3 Fatty acid-binding protein, heart	IPI00219684	14848.73	6.29	1	47.25004	99.69171	48.67	99.77769	0.501	0	1
B2M B2M protein	IPI00796379	13687.95	6.06	1	107.28	100	107.28	100	0.55	0	1
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	35305.76	8.38	1	102.82	100	102.82	100	0.561	0	1
FIS1 Mitochondrial fission 1 protein	IPI00007052	16927.02	8.84	1	56.64	99.96452	56.64	99.96452	0.561	0	1
LOC730278;LOC729659 similar to Putative S100 calcium-binding protein A11 ps	IPI00790691	11279.74	7.77	1	83.07	99.99992	83.07	99.99992	0.565	0	1
PDLIM1 PDZ and LIM domain protein 1	IPI00010414	36049.04	6.56	1	90.06	100	90.06	100	0.571	0	1
PARK7 Protein DJ-1	IPI00298547	19878.49	6.33	1	99.26	100	99.26	100	0.578	0	1
IQGAP1 Ras GTPase-activating-like protein IQGAP1	IPI00009342	189133.8	6.08	1	48.66005	99.77718	50.08	99.83932	0.595	0	1
ACTN1 Actinin alpha 1 isoform b	IPI00759776	105501.7	5.25	1	43.61004	99.28722	45.03	99.486	0.597	0	1
- 14 kDa protein	IPI00788848	13799	5.24	2	190.51	100	129.76	100	0.617	0.107	2
IGKC IGKC protein	IPI00430808	25629.86	6.15	3	226.49	100	93.77	100	0.648	0.077	3
ARG1 Isoform 1 of Arginase-1	IPI00291560	34713.3	6.72	1	42.91	99.16255	42.91	99.16255	0.659	0	1

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PGAM1;hCG_2015138;hCG_2015269 Phosphoglycerate mutase 1	IPI00549725	28785.83	6.67	1	96.41	100	96.41	100	0.662	0	1
VIM 50 kDa protein	IPI00827679	49623.11	5.19	1	107.69	100	107.69	100	0.666	0	1
SORD Sorbitol dehydrogenase	IPI00216057	38271.84	8.23	1	59.93	99.98337	59.93	99.98337	0.682	0	1
HBB Hemoglobin delta Etolia variant	IPI00830113	19482.91	8.32	2	65.67	99.99556	37.49	97.08284	0.688	0.007	2
BLVRB Flavin reductase	IPI00783862	22105.43	7.13	2	128.62	100	69.01	99.99794	0.694	0.015	2
DDTL D-dopachrome tautomerase-like	IPI00472043	14186.27	5.89	1	41.44	98.82521	41.44	98.82521	0.698	0	1
HP Haptoglobin precursor	IPI00641737	46693.35	6.28	1	63.32	99.99238	63.32	99.99238	0.703	0	1
CBX3;LOC653972 Chromobox protein homolog 3	IPI00297579	20798.35	5.23	1	70.28004	99.99847	71.7	99.99889	1.461	0	1
NPC2 Epididymal secretory protein E1 precursor	IPI00301579	16559.48	7.56	1	80.12	99.99984	80.12	99.99984	1.482	0	1
PPP1CB Serine/threonine-protein phosphatase PP1-beta catalytic subunit	IPI00218236	37162.62	5.84	1	45.96	99.58508	45.96	99.58508	1.506	0	1
LOC131691 similar to peptidylprolyl isomerase A isoform 1	IPI00741973	18098.81	6.41	1	39.15	98.00951	39.15	98.00951	1.506	0	1
GLG1 79 kDa protein	IPI00647145	79265.84	6.13	1	39.69004	98.24226	41.11	98.73246	1.543	0	1
HNRPR HNRPR protein	IPI00644055	71170.4	8.23	2	100.87	100	53.56	99.9279	1.551	0.145	2
SYNCRIP Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q	IPI00402182	65641.59	8.69	2	100.87	100	53.56	99.9279	1.551	0.145	2
ALB Serum albumin	IPI00022434	71529.53	6.33	14	839.7489	100	122.78	100	1.578	0.565	12
MTPN Myotrophin	IPI00179589	12886.6	5.27	1	105.3	100	105.3	100	1.599	0	1
TF Transferrin variant (Fragment)	IPI00798430	77029.59	6.68	6	332.8101	100	109.12	100	1.618	0.446	6
FLJ11286 FLJ11286 protein	IPI00383563	28987.22	6.47	2	72.21	99.99902	44.92	99.47282	1.633	0.169	2
HNRPF Heterogeneous nuclear ribonucleoprotein F	IPI00003881	45642.85	5.38	1	61.8	99.98919	61.8	99.98919	1.634	0	1

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PEPD Xaa-Pro dipeptidase	IPI00257882	54512.91	5.64	1	60.85	99.98654	60.85	99.98654	1.646	0	1
PTER Phosphotriesterase-related protein	IPI00100933	38993.01	6.07	1	37.19	96.87421	37.19	96.87421	1.658	0	1
APOD Apolipoprotein D precursor	IPI00006662	21261.76	5.06	1	75.34	99.99952	75.34	99.99952	1.698	0	1
- 11 kDa protein	IPI00382841	11283.54	5.82	2	57.39	99.97015	32.66	91.12926	1.71	0.152	2
- 12 kDa protein	IPI00797738	12027.62	6.81	3	261.62	100	118.76	100	1.728	0.278	3
CANX Calnexin precursor	IPI00020984	67525.85	4.47	2	101.3	100	60.62	99.98581	1.756	0.088	2
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	24433.38	5.15	2	149.32	100	86.62	100	1.77	0.31	2
ORM1 Alpha-1-acid glycoprotein 1 precursor	IPI00022429	23496.76	4.93	2	176.62	100	104.11	100	1.785	0.182	2
- 29 kDa protein	IPI00411329	29377.25	9.14	2	108	100	70.74	99.99862	1.799	0.052	2
DCPS Scavenger mRNA-decapping enzyme DcpS	IPI00335385	38585.02	5.93	1	58.5	99.97688	58.5	99.97688	1.802	0	1
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	11992.02	6.28	1	72.84	99.99915	72.84	99.99915	1.814	0	1
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	56402.59	8.17	2	162.2101	100	120.05	100	1.873	0.738	2
PPP1CA protein phosphatase 1, catalytic subunit, alpha isoform 3	IPI00027423	38606.37	6.2	2	150.06	100	87.25	100	1.914	0.029	2
HINT1 Histidine triad nucleotide-binding protein 1	IPI00239077	13793.09	6.43	1	87.67	100	87.67	100	2.044	0	1
ACAT2 Acetyl-CoA acetyltransferase, cytosolic	IPI00291419	41324.39	6.47	1	71.56	99.99886	71.56	99.99886	2.071	0	1
HNRPH2 Heterogeneous nuclear ribonucleoprotein H'	IPI00026230	49232.29	5.89	1	61.04	99.98712	61.04	99.98712	2.095	0	1
HSPA1A;HSPA1B Heat shock 70kDa protein 1A	IPI00647012	51914.69	5.35	3	161.12	100	83.21	99.99992	2.097	0.513	3
RBP4 Retinol binding protein 4, plasma	IPI00480192	22929.13	5.77	1	65.87005	99.99576	67.29	99.99695	2.188	0	1
- 14 kDa protein	IPI00455040	14347.57	8.86	1	109.44	100	109.44	100	2.198	0	1

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OS9 33 kDa protein	IPI00793206	32504.35	7.63	1	52.72	99.91251	52.72	99.91251	2.215	0	1
SSB Lupus La protein	IPI00009032	46808.16	6.68	1	108.34	100	108.34	100	2.274	0	1
VCP 89 kDa protein	IPI00843748	89270.64	5.11	1	72.53004	99.99909	73.95	99.99934	2.312	0	1
CD59 CD59 glycoprotein precursor	IPI00011302	14167.79	6.02	1	74.82	99.99946	74.82	99.99946	2.33	0	1
PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904	72886.97	4.96	2	165.46	100	84.08	99.99994	2.331	0.925	2
EEF1G;LOC729998 similar to Elongation factor 1-gamma	IPI00738381	50270.31	7.09	1	57.24	99.9691	57.24	99.9691	2.374	0	1
ALDOA 45 kDa protein	IPI00796333	45232.14	8.48	1	74.09	99.99936	74.09	99.99936	2.433	0	1
ATOX1 Copper transport protein ATOX1	IPI00010863	7396.73	6.71	2	115.5	100	78.21	99.99975	2.484	0.684	2
CUTA Isoform C of Protein CutA precursor	IPI00554556	16821.85	5.15	1	62.19	99.99012	62.19	99.99012	2.492	0	1
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	61016.38	5.7	2	179.01	100	103.17	100	2.566	0.018	2
PML promyelocytic leukemia protein isoform 10	IPI00181058	64995.65	5.19	1	42.53004	99.08598	43.95	99.34089	2.611	0	1
FAM10A4 Protein FAM10A4	IPI00218038	27389.69	5.01	1	106.29	100	106.29	100	2.795	0	1
GLUD2 Glutamate dehydrogenase 2, mitochondrial precursor	IPI00027146	61395.43	8.63	1	72.87942	99.99916	75.13	99.9995	2.96	0	1
CPOX Coproporphyrinogen III oxidase, mitochondrial precursor	IPI00093057	50119.97	8.59	1	60.34004	99.98487	61.76	99.98909	3.025	0	1
TMEM4 Isoform 1 of MIR-interacting saposin-like protein precursor	IPI00443909	20639.17	4.81	2	149.64	100	117.8	100	3.244	0.273	2
SFRS6 Isoform SRP55-3 of Splicing factor, arginine/serine-rich 6	IPI00215879	38395.63	11.01	1	40.4	98.50734	40.4	98.50734	3.525	0	1
SOD1 Superoxide dismutase	IPI00783680	15925.9	5.7	1	58.47	99.97672	58.47	99.97672	3.905	0	1
HMGB3 Non-histone chromosomal protein	IPI00411540	17511	9.8	2	104.31	100	63.55	99.99277	4.124	1.707	2
PLA2G12B Group XIIB secretory phospholipase A2-like protein precursor	IPI00000240	21644.24	5.75	1	42.84	99.14894	42.84	99.14894	4.392	0	1

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HMGB1 High-mobility group box 1	IPI00644653	18299.33	9.72	2	140.49	100	75.11	99.9995	4.43	1.401	2
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	18000.88	7.68	3	268.27	100	129.9	100	17.831	593.948	3
CTSZ CTSZ protein (Fragment)	IPI00448792	33540.65	9.43	2	66.7	99.9965	39.59	98.20129	52.63	1454.771	2
APOH Beta-2-glycoprotein 1 precursor	IPI00298828	38272.66	8.34	2	61.35	99.98801	37.96	97.38206	102.734	4470.551	2
RNH1 Ribonuclease/angiogenin inhibitor	IPI00783491	49839.99	4.68	2	105.98	100	56.18	99.96056	104.433	3151.618	2
FN1 fibronectin 1 isoform 4 preproprotein	IPI00414283	256351.1	5.53	2	147.98	100	80.38	99.99985	116.699	5205.885	2
CTSD 33 kDa protein	IPI00852597	32543.31	5.88	4	335.28	100	107.84	100	120.467	3899.161	4
FLJ11151 Hypothetical protein FLJ11151	IPI00305010	35525.88	5.78	2	209.39	100	124.35	100	153.946	6667.232	2
GALM Aldose 1-epimerase	IPI00060200	37742.13	6.18	1	95.05	100	95.05	100	2111.703	0	1
SFRS4 Splicing factor, arginine/serine-rich 4	IPI00000015	56645.27	11.52	1	39.4	98.12086	39.4	98.12086	2593.756	0	1
TXN2 Thioredoxin, mitochondrial precursor	IPI00017799	21811.28	8.85	1	44.86	99.46548	44.86	99.46548	3108.837	0	1
TRIM28 Isoform 2 of Transcription intermediary factor 1-beta	IPI00438230	79423.48	5.67	1	48.71	99.77973	48.71	99.77973	3132.645	0	1
PPA1 Pyrophosphatase (Inorganic) 1	IPI00643288	19968.92	5.07	1	56.62	99.96436	56.62	99.96436	3643.519	0	1
ITGB4BP Eukaryotic translation initiation factor 6	IPI00010105	26582.19	4.56	1	69.75	99.99827	69.75	99.99827	4020.212	0	1
TIMM8B Mitochondrial import inner membrane translocase subunit Tim8 B	IPI00001546	9337.54	5.02	1	108.12	100	108.12	100	4266.774	0	1
LOC641827;LOC649440 Similar to eukaryotic translation elongation factor 1 b	IPI00397392	24875.39	4.66	1	81.33	99.99988	81.33	99.99988	4544.575	0	1
LGALS3BP 16 kDa protein	IPI00794873	16452.93	5.74	1	60.52	99.98548	60.52	99.98548	4677.497	0	1
PSAP Prosaposin	IPI00219825	61651.56	5.11	1	75.9	99.99958	75.9	99.99958	5529.873	0	1
PDIA6 Isoform 1 of Protein disulfide-isomerase A6 precursor	IPI00644989	48091.26	4.95	1	120.75	100	120.75	100	7249.579	0	1

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GRN Isoform 1 of Granulins precursor	IPI00296713	63499.84	6.43	1	54.04	99.93544	54.04	99.93544	8801.206	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio* (H/L)	ICAT Standard Deviation*	ICAT Peptides
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	56402.59	8.17	3	277.44	100	101.41	100	0	0	3
SOD1 Superoxide dismutase	IPI00783680	15925.9	5.7	2	126	100	82.1	99.9999	0	0	2
ALDOB Fructose-bisphosphate aldolase	IPI00513830	24113.34	6.65	1	147	100	147	100	0	0	1
FTL Ferritin light chain	IPI00852596	20007.1	5.51	1	99.97	100	99.97	100	0	0	1
PNPO 19 kDa protein	IPI00793232	19465.84	6.92	1	86.91	100	86.91	100	0	0	1
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	31367.13	8.34	1	84.42	99.99994	84.42	99.99994	0	0	1
- 63 kDa protein	IPI00792605	62706.83	10.91	1	76.76	99.99967	76.76	99.99967	0	0	1
FTH1 Ferritin heavy chain	IPI00554521	21212.29	5.3	1	62.72	99.99159	62.72	99.99159	0	0	1
SHMT1 14 kDa protein	IPI00008665	14332.98	5.62	1	50.16	99.84839	50.16	99.84839	0	0	1
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	44854.47	6.61	1	46.2	99.62267	46.2	99.62267	0	0	1
PRDX6 Peroxiredoxin-6	IPI00220301	25019.19	6	1	40.65	98.6457	40.65	98.6457	0	0	1
SORD Sorbitol dehydrogenase	IPI00216057	38271.84	8.23	1	40.38	98.55883	40.38	98.55883	0	0	1
GSTZ1 glutathione transferase zeta 1 isoform 2	IPI00157928	19360.02	8.27	1	36.56	96.52691	36.56	96.52691	0	0	1
C6orf115 similar to Protein C6orf115	IPI00740277	20388.71	6.38	1	53.51	99.9299	53.51	99.9299	0.001	0	1
GRHPR GRHPR protein (Fragment)	IPI00550682	36801.01	5.95	2	117.23	100	78.4	99.99977	0.005	0.089	2
SELENBP1 53 kDa protein	IPI00745729	53027.94	6.03	2	155.88	100	124.13	100	0.006	0.099	2
HBB Hemoglobin subunit beta	IPI00654755	15988.29	6.75	2	188.14	100	106.58	100	0.013	1.085	2
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	24433.38	5.15	3	178.11	100	80.78	99.99987	0.02	0.526	3
PARK7 Protein DJ-1	IPI00298547	19878.49	6.33	3	194.71	100	98.65	100	0.047	1.822	3

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BHMT2 Betaine--homocysteine S-methyltransferase 2	IPI00014363	40328.18	5.61	1	68.72	99.99789	68.72	99.99789	0.06	0	1
DAK Dihydroxyacetone kinase	IPI00551024	58940.04	7.12	1	43.23	99.25232	43.23	99.25232	0.113	0	1
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	39909.67	8.75	1	44.73	99.47068	44.73	99.47068	0.148	0	1
TST Thiosulfate sulfurtransferase	IPI00216293	33407.84	6.77	1	74.49	99.99944	74.49	99.99944	0.212	0	1
CAT Catalase	IPI00465436	59718.75	6.9	1	55.09004	99.95128	56.51	99.96487	0.261	0	1
GLUD2 Glutamate dehydrogenase 2, mitochondrial precursor	IPI00027146	61395.43	8.63	1	52.18	99.90478	52.18	99.90478	0.293	0	1
DDTL D-dopachrome tautomerase-like	IPI00472043	14186.27	5.89	1	45.59	99.56577	45.59	99.56577	0.306	0	1
C11orf54 Isoform 4 of Ester hydrolase C11orf54	IPI00760666	23158.41	6.3	1	133.14	100	133.14	100	0.312	0	1
PGM1 Isoform 1 of Phosphoglucomutase-1	IPI00219526	61410.53	6.3	1	92.43	100	92.43	100	0.317	0	1
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	11992.02	6.28	1	68.46	99.99776	68.46	99.99776	0.345	0	1
HP Haptoglobin precursor	IPI00641737	46693.35	6.28	2	155.35	100	79.87	99.99984	0.349	0.022	2
P4HB Protein disulfide-isomerase precursor	IPI00010796	57080.67	4.76	2	138.1	100	71.71	99.99894	0.354	0.284	2
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	35305.76	8.38	1	88.1	100	88.1	100	0.389	0	1
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	52737.86	6.3	1	63.84	99.9935	63.84	99.9935	0.412	0	1
BLVRB Flavin reductase	IPI00783862	22105.43	7.13	1	71.31	99.99884	71.31	99.99884	0.432	0	1
ARG1 Isoform 1 of Arginase-1	IPI00291560	34713.3	6.72	1	110.42	100	110.42	100	0.434	0	1
ATOX1 Copper transport protein ATOX1	IPI00010863	7396.73	6.71	1	39.63	98.28716	39.63	98.28716	0.482	0	1
C6orf108 putative c-Myc-responsive isoform 2	IPI00395835	16177.23	6.31	1	47.23	99.70234	47.23	99.70234	0.506	0	1
FIS1 Mitochondrial fission 1 protein	IPI00007052	16927.02	8.84	1	49.61	99.82793	49.61	99.82793	0.513	0	1
GALM Aldose 1-epimerase	IPI00060200	37742.13	6.18	1	95.3	100	95.3	100	0.523	0	1

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AKR1C3 Aldo-keto reductase family 1 member C3	IPI00291483	36820.84	8.05	1	36.95	96.8252	36.95	96.8252	0.534	0	1
SAR1B GTP-binding protein SAR1b	IPI00002149	22395.51	5.76	1	36.37	96.37159	36.37	96.37159	0.565	0	1
- 29 kDa protein	IPI00791859	28830.89	5.65	1	44.18	99.39922	44.18	99.39922	0.596	0	1
CRYZ 32 kDa protein	IPI00647366	31508.5	8.59	2	99.84	100	64.46	99.99437	0.597	0.032	2
PDLIM1 PDZ and LIM domain protein 1	IPI00010414	36049.04	6.56	1	82.8	99.99992	82.8	99.99992	0.597	0	1
- 12 kDa protein	IPI00797738	12027.62	6.81	2	97.3	100	70.59	99.99863	0.628	0.084	2
CTSD 21 kDa protein	IPI00658053	21476.66	5.48	2	132.96	100	73.11	99.99923	0.643	0.141	2
HINT1 Histidine triad nucleotide-binding protein 1	IPI00239077	13793.09	6.43	1	81.29	99.99988	81.29	99.99988	0.651	0	1
GPX1 16 kDa protein	IPI00784231	16180.13	5.39	1	74.49	99.99944	74.49	99.99944	0.651	0	1
NDUFS5 NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	IPI00220063	12509.39	9.27	1	41.5	98.88643	41.5	98.88643	0.657	0	1
B2M B2M protein	IPI00796379	13687.95	6.06	1	76.28	99.99963	76.28	99.99963	0.666	0	1
UQCRH Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondria	IPI00296022	10731.94	4.39	1	106.17	100	106.17	100	0.667	0	1
C1orf123 Uncharacterized protein C1orf123	IPI00016605	18036.81	4.93	1	39.25	98.13054	39.25	98.13054	0.668	0	1
PRDM10 CDNA FLJ20227 fis, clone COLF5152	IPI00386081	105524.9	8.83	2	162.31	100	91.81	100	0.7	0.06	2
PXN Isoform Beta of Paxillin	IPI00335634	64491.84	5.73	1	57.06004	99.96905	58.48	99.97768	0.701	0	1
CTSB Cathepsin B precursor	IPI00295741	37796.83	5.88	1	98.13	100	98.13	100	0.707	0	1
HPX Hemopexin precursor	IPI00022488	51643.27	6.55	1	35.58	95.64773	35.58	95.64773	1.465	0	1
GC vitamin D-binding protein precursor	IPI00742696	52882.94	5.32	1	56.04	99.96085	56.04	99.96085	1.499	0	1
HGD Homogentisate 1,2-dioxygenase	IPI00303174	49940.59	6.54	1	46.57	99.65349	46.57	99.65349	1.539	0	1
RHOA Transforming protein RhoA precursor	IPI00027500	21754.07	5.83	1	54.66	99.94621	54.66	99.94621	1.541	0	1

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HNRPR HNRPR protein	IPI00644055	71170.4	8.23	2	86.74	100	51.17	99.87985	1.542	0.057	2
SYNCRIP Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q	IPI00402182	65641.59	8.69	2	86.74	100	51.17	99.87985	1.542	0.057	2
TXNDC5;MUTED thioredoxin domain containing 5 isoform 2	IPI00395646	43641.51	5.77	1	41.55	98.89918	41.55	98.89918	1.548	0	1
GRN Isoform 1 of Granulins precursor	IPI00296713	63499.84	6.43	1	75.54	99.99956	75.54	99.99956	1.612	0	1
PGAM1;hCG_2015138;hCG_2015269 Phosphoglycerate mutase 1	IPI00549725	28785.83	6.67	1	93.11	100	93.11	100	1.615	0	1
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	18000.88	7.68	2	119.5	100	60.64	99.98643	1.617	0.028	2
SAR1A SAR1 gene homolog A	IPI00644667	13653.07	6.49	1	60.44	99.98579	60.44	99.98579	1.675	0	1
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	61016.38	5.7	2	162.23	100	100.16	100	1.742	0.149	2
FUBP1 Isoform 2 of Far upstream element-binding protein 1	IPI00644386	68861.11	7.74	1	70.28	99.99853	70.28	99.99853	1.841	0	1
HSP90B1 Protein	IPI00789430	26539.06	8.95	1	122.38	100	122.38	100	1.848	0	1
RAD23A UV excision repair protein RAD23 homolog A	IPI00008219	39584.65	4.56	1	65.12	99.99516	65.12	99.99516	1.95	0	1
LYPLA1 Isoform 2 of Acyl-protein thioesterase 1	IPI00398727	22860.58	6.05	1	36.43	96.42137	36.43	96.42137	2.001	0	1
CLGN Calmegin precursor	IPI00024776	69994.44	4.58	1	70.82	99.9987	70.82	99.9987	2.065	0	1
FLJ14668 Hypothetical protein FLJ14668	IPI00303722	15630.66	7.56	1	48.94	99.79922	48.94	99.79922	2.229	0	1
CBX3;LOC653972 Chromobox protein homolog 3	IPI00297579	20798.35	5.23	1	38.62004	97.83872	40.04	98.44147	2.334	0	1
AKR1C1 Aldo-keto reductase family 1 member C1	IPI00029733	36765.02	8.02	1	50.99	99.87477	50.99	99.87477	2.383	0	1
HMGB2 High mobility group protein B2	IPI00219097	24018.73	7.62	1	80.39	99.99986	80.39	99.99986	2.912	0	1
SSB Lupus La protein	IPI00009032	46808.16	6.68	1	102.7	100	102.7	100	3.093	0	1
PAH Phenylalanine-4-hydroxylase	IPI00017579	51829.46	6.15	1	87.09	100	87.09	100	3.104	0	1
PDIA6 Isoform 1 of Protein disulfide-isomerase A6 precursor	IPI00644989	48091.26	4.95	1	144.36	100	144.36	100	3.283	0	1

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TKT Transketolase variant (Fragment)	IPI00788802	67862.77	7.9	1	52.64	99.91435	52.64	99.91435	3.356	0	1
LOC646993 similar to high-mobility group box 3	IPI00376756	23728.83	8.94	1	66.36	99.99636	66.36	99.99636	4.214	0	1
ALDOA 45 kDa protein	IPI00796333	45232.14	8.48	1	52.41	99.90969	52.41	99.90969	5.64	0	1
ORM2 Alpha-1-acid glycoprotein 2 precursor	IPI00020091	23587.63	5.03	1	70.34005	99.99855	71.76	99.99895	8.625	0	1
IGHM IGHM protein	IPI00472610	52633.11	7.5	3	198.07	100	87.67	100	22.746	838.009	3
F2 70 kDa protein	IPI00784409	69916.09	5.64	2	104.61	100	60.55	99.98614	135.449	5127.253	2
UCHL1 16 kDa protein	IPI00657702	15680.62	5.19	1	72.6	99.99914	72.6	99.99914	3093.871	0	1
OAT Ornithine aminotransferase, mitochondrial precursor	IPI00022334	48504.2	6.57	2	97.7	100	67.63	99.99729	3138.444	187.339	2
BCAT2 Isoform A of Branched-chain-amino-acid aminotransferase, mitochondria	IPI00396258	44259.06	8.88	1	41.45	98.87354	41.45	98.87354	3273.891	0	1
C1QBP Protein	IPI00795465	20360.71	4.1	1	113.88	100	113.88	100	4788.718	0	1
LTF 73 kDa protein	IPI00789477	73114.24	8.2	2	58.93005	99.97988	35.22	95.27158	4837.229	1249.721	2
- Hypothetical protein DKFZp686M24218	IPI00784998	52387.11	7.89	1	82.47	99.99991	82.47	99.99991	5866.472	0	1
FN1 Isoform 12 of Fibronectin precursor	IPI00556632	221308.4	5.84	3	245.1195	100	106.7	100	6050.422	4977.344	3
MMP9 Matrix metalloproteinase-9 precursor	IPI00027509	78377.35	5.69	1	62.44	99.99103	62.44	99.99103	7784.208	0	1
PRTN3 Myeloblastin precursor	IPI00027409	27789.27	8.72	1	124.76	100	124.76	100	19980.05	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg ICAT Ratio (H/L)	ICAT Standard Deviation	ICAT Peptides
ALDOB Fructose-bisphosphate aldolase	IPI00513830	24113.34	6.65	1	139.09	100	139.09	100	0	0	1
DCXR 26 kDa protein	IPI00797249	25726.45	8.33	1	83.54005	99.99993	84.96	99.99995	0	0	1
PGM1 Isoform 1 of Phosphoglucomutase-1	IPI00219526	61410.53	6.3	1	79.15	99.9998	79.15	99.9998	0	0	1
AKR1D1 CDNA FLJ25413 fis, clone TST03402, highly similar to 3-OXO-5-BETA- S	IPI00065073	30242.66	8.11	1	79.1	99.9998	79.1	99.9998	0	0	1
CBR1 Carbonyl reductase [NADPH] 1	IPI00295386	30355.86	8.55	1	55.56	99.955	55.56	99.955	0	0	1
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	44854.47	6.61	1	53.98	99.93526	53.98	99.93526	0	0	1
CHDH Choline dehydrogenase, mitochondrial precursor	IPI00168603	65360.13	8.67	1	43.95004	99.34808	45.37	99.52989	0	0	1
SUOX 54 kDa protein	IPI00853137	53851.08	5.35	1	37.61	97.19329	37.61	97.19329	0	0	1
CAT Catalase	IPI00465436	59718.75	6.9	1	36.01004	95.9431	37.43	97.07451	0	0	1
COQ9 36 kDa protein	IPI00746245	35945.65	5.42	1	31.98	89.7388	31.98	89.7388	0	0	1
TAGLN Transgelin	IPI00216138	22596.43	8.87	1	30.26	84.75251	30.26	84.75251	0	0	1
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	31367.13	8.34	1	68.45	99.99769	68.45	99.99769	0.001	0	1
GSTZ1 glutathione transferase zeta 1 isoform 2	IPI00157928	19360.02	8.27	1	44.92	99.47857	44.92	99.47857	0.001	0	1
TST Thiosulfate sulfurtransferase	IPI00216293	33407.84	6.77	1	53.61	99.9295	53.61	99.9295	0.119	0	1
PNPO 19 kDa protein	IPI00793232	19465.84	6.92	1	79.31	99.99981	79.31	99.99981	0.125	0	1
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	56402.59	8.17	1	100.91	100	100.91	100	0.14	0	1
GALM Aldose 1-epimerase	IPI00060200	37742.13	6.18	1	51.67	99.8898	51.67	99.8898	0.151	0	1
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	24433.38	5.15	1	62.41	99.99071	62.41	99.99071	0.178	0	1
SORD Sorbitol dehydrogenase	IPI00216057	38271.84	8.23	1	67.71	99.99726	67.71	99.99726	0.184	0	1

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SOD1 Superoxide dismutase	IPI00783680	15925.9	5.7	1	119.95	100	119.95	100	0.23	0	1
GOT2 Aspartate aminotransferase, mitochondrial precursor	IPI00018206	47445.27	9.14	1	90.98	100	90.98	100	0.288	0	1
BLVRB Flavin reductase	IPI00783862	22105.43	7.13	1	35.68	95.62278	35.68	95.62278	0.311	0	1
HPR Isoform 1 of Haptoglobin-related protein precursor	IPI00477597	38982.65	6.42	1	40.28	98.48226	40.28	98.48226	0.362	0	1
AKR1A1 Aldo-keto reductase family 1, member A1	IPI00647702	16506.3	5.84	1	83.06	99.99992	83.06	99.99992	0.423	0	1
C6orf115 similar to Protein C6orf115	IPI00740277	20388.71	6.38	1	40.23	98.46468	40.23	98.46468	0.45	0	1
SCP2 sterol carrier protein 2 isoform 2	IPI00433347	54380.39	6.25	1	78.04	99.99975	78.04	99.99975	0.464	0	1
AK2 Isoform 1 of Adenylate kinase isoenzyme 2, mitochondrial	IPI00215901	26460.77	7.67	1	48.78	99.78561	48.78	99.78561	0.465	0	1
SHMT1 14 kDa protein	IPI00008665	14332.98	5.62	1	79.84	99.99983	79.84	99.99983	0.482	0	1
C11orf54 Isoform 4 of Ester hydrolase C11orf54	IPI00760666	23158.41	6.3	1	106.56	100	106.56	100	0.511	0	1
ORM2 Alpha-1-acid glycoprotein 2 precursor	IPI00020091	23587.63	5.03	1	51.92004	99.89596	53.34	99.92498	0.512	0	1
ARG1 Isoform 1 of Arginase-1	IPI00291560	34713.3	6.72	1	54.35	99.94054	54.35	99.94054	0.524	0	1
B2M B2M protein	IPI00796379	13687.95	6.06	1	86.21	100	86.21	100	0.547	0	1
PGAM1;hCG_2015138;hCG_2015269 Phosphoglycerate mutase 1	IPI00549725	28785.83	6.67	1	46.22	99.61346	46.22	99.61346	0.58	0	1
HCLS1 Hematopoietic lineage cell-specific protein	IPI00026156	53964.98	4.74	1	75.49	99.99954	75.49	99.99954	0.589	0	1
ACAT2 Acetyl-CoA acetyltransferase, cytosolic	IPI00291419	41324.39	6.47	1	103.96	100	105.38	100	0.625	0	1
- 14 kDa protein	IPI00788848	13799	5.24	1	122.62	100	124.04	100	0.629	0	1
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	11992.02	6.28	1	35.87	95.81015	35.87	95.81015	0.632	0	1
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	35305.76	8.38	1	65.78	99.99572	65.78	99.99572	0.664	0	1
HBB Hemoglobin subunit beta	IPI00654755	15988.29	6.75	3	287.9	100	118.13	100	0.673	0.051	3
PARK7 Protein DJ-1	IPI00298547	19878.49	6.33	1	97.9	100	97.9	100	0.692	0	1

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ATOX1 Copper transport protein ATOX1	IPI00010863	7396.73	6.71	1	41.46004	98.84337	42.88	99.16594	0.694	0	1
P4HB Protein disulfide-isomerase precursor	IPI00010796	57080.67	4.76	1	65.66	99.9956	65.66	99.9956	1.462	0	1
LOC389842 similar to Ran-specific GTPase-activating protein	IPI00399212	35001.84	8.76	1	45.09942	99.49967	47.35	99.70201	1.479	0	1
HPX Hemopexin precursor	IPI00022488	51643.27	6.55	3	125.66	100	58.71	99.97821	1.499	0.251	3
IGHA1 SNC66 protein	IPI00383164	53631.38	6.22	1	90.46	100	90.46	100	1.51	0	1
METAP2 CDNA FLJ34411 fis, clone HEART2002220, highly similar to METHIONINE	IPI00300763	50477.81	5.2	1	31.22	87.77642	31.22	87.77642	1.611	0	1
HSP90B1 Protein	IPI00789430	26539.06	8.95	1	105.19	100	105.19	100	1.66	0	1
TXNDC4 Thioredoxin domain-containing protein 4 precursor	IPI00401264	46941.4	5.09	1	83.69005	99.99993	85.11	100	1.678	0	1
CTSD 21 kDa protein	IPI00658053	21476.66	5.48	2	115.58	100	66.13	99.99605	1.7	0.153	2
TKT Transketolase variant (Fragment)	IPI00788802	67862.77	7.9	1	50.18	99.84469	50.18	99.84469	1.731	0	1
CALR 37 kDa protein	IPI00793605	36679.71	4.55	2	155.73	100	80.11	99.99984	1.754	0.429	2
CUTA Isoform C of Protein CutA precursor	IPI00554556	16821.85	5.15	1	35.64	95.58228	35.64	95.58228	1.778	0	1
LOC440055 similar to ribosomal protein S12	IPI00456898	14588.54	6.43	1	78.31	99.99976	78.31	99.99976	1.793	0	1
IGHM IGHM protein	IPI00472610	52633.11	7.5	3	225.59	100	85.19	100	1.854	0.656	3
PDIA6 Isoform 1 of Protein disulfide-isomerase A6 precursor	IPI00644989	48091.26	4.95	1	125.06	100	125.06	100	1.864	0	1
SPTBN1 275 kDa protein	IPI00794135	274658.8	5.39	1	42.8	99.15043	42.8	99.15043	1.871	0	1
RAD23A UV excision repair protein RAD23 homolog A	IPI00008219	39584.65	4.56	1	45.24	99.51561	45.24	99.51561	1.888	0	1
RNF113A RING finger protein 113A	IPI00007343	38762.6	5.51	1	31.13	87.52047	31.13	87.52047	1.908	0	1
EIF1 Eukaryotic translation initiation factor 1	IPI00015077	12724.56	6.89	1	32.68	91.2663	32.68	91.2663	1.922	0	1
HSP90AA1 Hsp89-alpha-delta-N	IPI00604607	63211.62	5.03	1	58.22	99.97561	58.22	99.97561	1.95	0	1
GPX1 16 kDa protein	IPI00784231	16180.13	5.39	1	39.36	98.12415	39.36	98.12415	2.112	0	1

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FAM10A4 Protein FAM10A4	IPI00218038	27389.69	5.01	1	91.75	100	91.75	100	2.209	0	1
HNRPF Heterogeneous nuclear ribonucleoprotein F	IPI00003881	45642.85	5.38	1	66.74	99.99657	66.74	99.99657	2.249	0	1
- 14 kDa protein	IPI00455040	14347.57	8.86	1	105.49	100	105.49	100	2.273	0	1
LOC131691 similar to peptidylprolyl isomerase A isoform 1	IPI00741973	18098.81	6.41	1	47.8	99.73134	47.8	99.73134	2.311	0	1
APOH Beta-2-glycoprotein 1 precursor	IPI00298828	38272.66	8.34	2	91.37	100	48.84	99.78855	2.325	1.014	2
SSB Lupus La protein	IPI00009032	46808.16	6.68	1	111.45	100	111.45	100	2.409	0	1
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	18000.88	7.68	3	228.89	100	131.94	100	2.467	0.131	3
SPTAN1 283 kDa protein	IPI00744706	283049.5	5.24	1	31.77	89.23043	31.77	89.23043	2.501	0	1
RAB21 Ras-related protein Rab-21	IPI00007755	24332.25	8.11	1	47.75	99.72823	47.75	99.72823	2.551	0	1
PPP1CA protein phosphatase 1, catalytic subunit, alpha isoform 3	IPI00027423	38606.37	6.2	1	31.64	88.90318	31.64	88.90318	2.689	0	1
- Glucose phosphate isomerase	IPI00848316	63079.21	8.43	1	42.5	99.08967	42.5	99.08967	2.987	0	1
GRN Isoform 1 of Granulins precursor	IPI00296713	63499.84	6.43	1	34.64	94.43842	34.64	94.43842	2.987	0	1
ERH Enhancer of rudimentary homolog	IPI00029631	12251	5.63	1	91.13	100	91.13	100	3.077	0	1
SYNCRIP Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q	IPI00402182	65641.59	8.69	1	38.4	97.6601	38.4	97.6601	3.337	0	1
HNRPR HNRPR protein	IPI00644055	71170.32	8.23	1	38.4	97.6601	38.4	97.6601	3.337	0	1
CBX3;LOC653972 Chromobox protein homolog 3	IPI00297579	20798.35	5.23	1	41.42004	98.83267	42.84	99.15822	3.467	0	1
TES Isoform 2 of Testin	IPI00216425	46878.3	7.82	1	33.35	92.51489	33.35	92.51489	3.676	0	1
QSOX1 Isoform 2 of Sulfhydryl oxidase 1 precursor	IPI00465016	66818.34	8.85	1	36.91	96.7024	36.91	96.7024	4.003	0	1
NPC2 Epididymal secretory protein E1 precursor	IPI00301579	16559.48	7.56	1	103.07	100	103.07	100	4.042	0	1
- Actinin alpha4 isoform	IPI00845465	59542.11	4.82	2	100.85	100	55.89	99.95829	78.278	2818.645	2
GC vitamin D-binding protein precursor	IPI00742696	52882.94	5.32	2	132.76	100	75.71	99.99957	79.725	2672.351	2

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UFC1 Ufm1-conjugating enzyme 1	IPI00294495	19446.02	6.9	2	75.37	99.99953	38.45	97.68688	86.823	1482.113	2
FN1 fibronectin 1 isoform 4 preproprotein	IPI00414283	256351.1	5.53	2	119.8	100	75.17	99.99951	114.055	1540.07	2
AFP Alpha-fetoprotein precursor	IPI00022443	68632.99	5.48	1	56.98	99.96755	56.98	99.96755	1259.6	0	1
- 29 kDa protein	IPI00411329	29377.25	9.14	1	41.79	98.92799	41.79	98.92799	2161.134	0	1
F2 70 kDa protein	IPI00784409	69916.09	5.64	1	75.09005	99.9995	76.51	99.99964	2389.757	0	1
BCAT2 Isoform A of Branched-chain-amino-acid aminotransferase, mitochondria	IPI00396258	44259.06	8.88	1	75.13	99.9995	75.13	99.9995	4244.754	0	1
UCHL1 16 kDa protein	IPI00657702	15680.62	5.19	1	114.95	100	114.95	100	7205.28	0	1
FTL Ferritin light chain	IPI00852596	20007.1	5.51	1	72.98	99.99918	72.98	99.99918	7712.681	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio * (115/114)	iTRAQ Standard Deviation * (115/114)	iTRAQ Peptides (115/114)
POSTN Isoform 2 of Periostin precursor	IPI00218585	96544.46875	7.87	1	72.84999847	99.99949111	72.84999847	99.99949111	24.73917341	0	1
COL1A2 Collagen alpha-2(I) chain precursor	IPI00304962	136968.0469	9.08	1	94.27999878	100	94.27999878	100	13.94230409	0	1
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1406	5.6	3	199.3300018	100	85.90000153	100	8.586292956	5.86325591	3
PRELP Prolargin precursor	IPI00020987	46264.33984	9.47	4	194.1799927	100	52.11999893	99.93979572	7.653537067	1.69200739	4
LUM 23 kDa protein	IPI00794403	25919.60938	8.52	2	117.8000031	100	83.20999908	100	6.796665649	1.2258881	2
BGN CDNA FLJ35635 fis, clone SPLEN2011805, highly similar to	IPI00385748	39528	6.31	3	209.9899902	100	95.19999695	100	6.215801838	1.66310797	3
TAGLN Transgelin	IPI00216138	25234.73047	8.87	3	131.3200073	100	52.47000122	99.94445728	5.633770241	0.56875397	3
SERPINA1 Alpha-1-antitrypsin precursor	IPI00553177	51885.51172	5.37	5	290.7799988	100	92.73999786	100	5.39849275	2.35972142	5
HBB Hemoglobin subunit beta	IPI00654755	17808.5	6.75	12	1000.98999	100	138.6000061	100	5.232844264	1.52721961	21
HBD;HBB Hemoglobin subunit delta	IPI00473011	17865.5	7.85	9	700.250061	100	122.2799988	100	5.137607915	1.35573786	15
ANXA4 annexin IV	IPI00793199	39558.51953	5.84	5	271.6499939	100	80.65000153	99.99991554	5.111776365	0.5293396	5
HBG2;HBE1;HBG1 Hemoglobin subunit gamma-2	IPI00554676	18034.5293	6.64	2	84.23000336	100	42.65000153	99.46712281	4.735193958	0.50201534	4
IGHM Hypothetical protein DKFZp686I15212	IPI00418153	62655.28125	8.39	6	272.8399963	100	61.43999863	99.99295911	4.691345142	1.06612521	6
ALB Isoform 1 of Serum albumin precursor	IPI00745872	79715.90625	5.92	27	1632.174438	100	114.9700012	100	4.62106406	1.5109062	32
IGHM IGHM protein	IPI00761159	57955.55078	7.53	5	298.8899841	100	84.55000305	100	4.40607813	1.10746392	5
IGLV4-3 IGLV4-3 protein	IPI00382938	28252.89063	6.3	2	185.9199982	100	102.6100006	100	4.403126611	0.24181286	2
IGHG1 Hypothetical protein DKFZp686O01196	IPI00423463	58171.78906	8.46	5	327.5700073	100	90.12000275	100	4.191251943	0.85220869	5
VIM Vimentin	IPI00418471	56977.44141	5.06	18	1041.103394	100	88.40000153	100	4.021581911	1.67800105	19
HBA2;HBA1 Alpha 2 globin variant (Fragment)	IPI00853068	17045.16992	8.72	6	448.1199951	100	115.8700027	100	3.979262515	1.24917404	17

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IGHA1 IGHA1 protein	IPI00166866	57142.32031	6.26	5	299.2399902	100	90.12000275	100	3.6498017	0.50412413	6
FGB Fibrinogen beta chain precursor	IPI00298497	61772.66016	8.54	3	124.1999969	100	50.40999985	99.91074608	3.536530728	0.91573108	3
FN1 Isoform 1 of Fibronectin precursor	IPI00022418	276716.375	5.45	13	709.7888184	100	86.59999847	100	3.462952784	2.30017338	13
APOA1 Apolipoprotein A-I precursor	IPI00021841	34071.30859	5.56	1	73.94999695	99.99960497	73.94999695	99.99960497	3.403968799	0	1
TPM1 Isoform 1 of Tropomyosin alpha-1 chain	IPI00014581	38351.23828	4.69	3	143.8999939	100	52.59000015	99.94597096	3.398269777	0.56957008	3
ANXA5 Annexin A5	IPI00329801	39272.76172	4.94	4	236.8000031	100	78.11000061	99.99984843	3.369572778	1.19881208	5
ANXA2 Annexin A2	IPI00455315	43516.26953	7.57	10	572.848938	100	98.91999817	100	3.363958056	2.4820809	10
FGA Isoform 2 of Fibrinogen alpha chain precursor	IPI00029717	76032.28906	8.23	4	250.3699951	100	77.08999634	99.9998083	3.336872651	0.63220092	4
HP HP protein	IPI00478493	43017.64844	6.13	4	237.230011	100	65.5	99.99723543	3.325875204	4.97E-02	4
FLNA Filamin-A	IPI00333541	305957.375	5.7	7	399.6499939	100	66.12999725	99.99760874	3.228230673	1.51878973	7
ACTC1 Actin, alpha cardiac muscle 1	IPI00023006	45148.14063	5.23	11	690.1700439	100	89.95999908	100	3.184060246	1.02347845	16
TPM4 Isoform 1 of Tropomyosin alpha-4 chain	IPI00010779	32340.88086	4.67	3	139.1000061	100	52.59000015	99.94597096	3.127817741	0.15999281	3
DKFZp686D0972 hypothetical protein LOC345651	IPI00003269	44988.21875	5.39	3	188.4899902	100	85.37000275	100	3.059748262	0.6669657	5
KRT19 Keratin, type I cytoskeletal 19	IPI00479145	46225.37891	5.04	2	82.63000488	99.99994647	47.43000031	99.82273326	3.035711072	2.88735499	2
ACTG1;PSPHL Actin, cytoplasmic 2	IPI00021440	44922.05859	5.31	11	876.7299805	100	183.1100006	100	2.960014502	0.70981878	16
LGALS3 Galectin-3	IPI00465431	27514.25	8.58	2	109.3899994	100	66.76000214	99.99793164	2.954685262	1.4307495	2
TAGLN2 24 kDa protein	IPI00647915	26448.48047	8.41	2	103.4100037	100	52.18999863	99.94075831	2.900969417	0.27883642	2
MYL6 17 kDa protein	IPI00744444	18920.58008	4.54	4	319.519989	100	121.7900009	100	2.900669059	0.42276586	4
- FK506 binding protein12	IPI00759644	10743.65039	7.66	1	57.41999817	99.98223245	57.41999817	99.98223245	2.831240881	0	1
IGKC IGKC protein	IPI00430808	27732.05078	6.15	1	59.65999985	99.98939215	59.65999985	99.98939215	2.817046457	0	1
TF Transferrin variant (Fragment)	IPI00798430	87365.92188	6.68	7	335.3499756	100	63.74000168	99.99585402	2.800448633	0.45973711	7

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VTN Vitronectin precursor	IPI00298971	57939.35156	5.55	5	235.7200012	100	59.11999893	99.98798767	2.748669358	1.68572324	5
CFL2 Cofilin-2	IPI00413344	22273.21094	7.66	1	86.23000336	100	86.23000336	100	2.739273765	0	1
FGG Isoform Gamma-A of Fibrinogen gamma chain precursor	IPI00219713	55011.35938	5.7	1	68.5	99.99861443	68.5	99.99861443	2.712322423	0	1
YWHAZ 14-3-3 protein zeta/delta	IPI00021263	30890.03906	4.73	4	243.2644501	100	89.68000031	100	2.628808383	0.90830703	4
COL6A3 alpha 3 type VI collagen isoform 3 precursor	IPI00072917	345457.3438	6.47	9	391.0899963	100	66.15000153	99.99761973	2.624296983	0.34231047	9
C3 Complement C3 precursor (Fragment)	IPI00783987	204689.0469	6.02	3	150.0100098	100	63.34999847	99.99546448	2.59791271	2.0189775	3
TPM3 Isoform 2 of Tropomyosin alpha-3 chain	IPI00218319	32655.08008	4.75	5	228.7500153	100	52.59000015	99.94597096	2.58023618	1.4557494	5
MIF 12 kDa protein	IPI00790382	12661.19043	9.3	1	54.97999954	99.96883786	54.97999954	99.96883786	2.562223341	0	1
COL6A2 Isoform 2C2A of Collagen alpha-2(VI) chain precursor	IPI00220613	105910.7031	5.38	2	88.63000488	100	53.79000092	99.95901479	2.549904919	0.34120876	2
ALDOA 45 kDa protein	IPI00796333	49776.48828	8.48	2	88.41999817	100	51.41999817	99.92926612	2.548405251	1.10671595	2
HNRPK Isoform 1 of Heterogeneous nuclear ribonucleoprotein K	IPI00216049	54486.71875	5.39	3	124.0444489	100	46.47999954	99.77938891	2.499644615	0.20842101	3
YWHAQ 14-3-3 protein theta	IPI00018146	30857.03906	4.68	4	235.4799957	100	101.9700012	100	2.461015947	1.13243823	4
MYH9 Myosin-9	IPI00019502	257357.9844	5.5	13	642.8356323	100	83.44999695	100	2.443700343	0.63621378	13
CLU clusterin isoform 1	IPI00400826	62857.89844	6.24	1	81.48999786	99.9999304	81.48999786	99.9999304	2.437651022	0	1
NPM1 Isoform 1 of Nucleophosmin	IPI00549248	37589.32031	4.64	2	109.8000031	100	71.08000183	99.99923506	2.28037521	0.58978655	2
RPLP0 60S acidic ribosomal protein P0	IPI00556485	30148.58984	8.36	1	87.63999939	100	87.63999939	100	2.254593957	0	1
YWHAB Isoform Short of 14-3-3 protein beta/alpha	IPI00759832	30949.07031	4.76	4	227.0299988	100	93.51999664	100	2.242713675	0.66149536	4
PRDX2 16 kDa protein	IPI00375400	18010.59961	6.13	4	206.1399994	100	59.18000031	99.98815249	2.218273587	0.85746089	4
LMNA Isoform C of Lamin-A/C	IPI00216952	70902.15625	6.4	10	581.2044678	100	81.94999695	99.99993739	2.10317443	0.46903256	10
ARHGDIA 28 kDa protein	IPI00794402	30709	4.94	2	133.9499969	100	77.98999786	99.99984418	2.075286947	0.21774244	3
TUBB Tubulin beta chain	IPI00011654	52311.16016	4.78	8	527.8399658	100	110.8499985	100	2.053343412	0.38342978	9

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SFN Isoform 2 of 14-3-3 protein sigma	IPI00411765	26671.25	4.77	3	133.5099945	100	58.81000137	99.98709889	2.048069958	0.54740592	3
NME2;NME1 Nucleoside diphosphate kinase B	IPI00026260	19395.17969	8.52	4	209.3000183	100	75.76000214	99.99973961	1.965538636	0.31367589	5
MSN Moesin	IPI00219365	76942.64063	6.08	3	127.3899994	100	53.52999878	99.95648616	1.878474485	0.38922797	3
TUBB2C Tubulin beta-2C chain	IPI00007752	52471.19141	4.79	7	477.6399841	100	110.8499985	100	1.869995021	0.52699208	8
LOC388720 similar to ubiquitin and ribosomal protein S27a precursor	IPI00397808	21877.69922	9.53	2	131.0500031	100	82.11000061	99.99993966	1.865550563	8.02E-02	2
HSPB1 Heat shock protein beta-1	IPI00025512	23966.66992	5.98	1	59.36999893	99.98865963	59.36999893	99.98865963	1.846010606	0	1
TXNDC5;MUTED thioredoxin domain containing 5 isoform 2	IPI00395646	48461.78125	5.77	2	73.72000122	99.99958349	39.97999954	99.01456648	1.840502319	0.15917387	2
ACTN1 Actinin alpha 1 isoform b	IPI00759776	114216.3906	5.25	5	242.2799988	100	67.08000183	99.99807856	1.829901396	0.61640486	5
SERPINB6 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), me	IPI00749398	46902.42188	5.18	1	57.54000092	99.98271668	57.54000092	99.98271668	1.819866301	0	1
COL6A1 Collagen alpha-1(VI) chain precursor	IPI00291136	117302.5391	5.26	2	97.58999634	100	60.84999847	99.99193457	1.748738158	0.3712096	2
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	20345.10938	7.68	5	333.5	100	86.23999786	100	1.744204797	0.24561571	7
TUBA1A Tubulin alpha-1A chain	IPI00180675	53535.80078	4.94	4	298.480011	100	94.84999847	100	1.740585972	0.75456982	4
- Calnexin (Fragment)	IPI00383227	35238.5	4.62	2	105.1200027	100	61.08000183	99.9923506	1.689373411	0.63732366	2
HNRPA2B1 Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	IPI00414696	38478.16016	8.67	3	168.5644531	100	78.44000244	99.99985952	1.67488093	0.37154405	3
ACTN4 Alpha-actinin-4	IPI00013808	113653.2031	5.27	7	397.9899902	100	71.55999756	99.9993151	1.674049454	0.4237082	7
UBE1 Ubiquitin-activating enzyme E1	IPI00645078	126424.8516	5.49	2	94.44999695	100	50.75999832	99.91765685	1.647823861	0.41987788	2
APOE Apolipoprotein E precursor	IPI00021842	38239.98828	5.65	3	240.2999878	100	107.5899963	100	1.619775042	0.820529	3
HNRPA1 Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	IPI00465365	37003.55078	9.27	2	84.23999786	100	46.47999954	99.77938891	1.606419355	0.37644307	2
HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein	IPI00003865	78958.95313	5.37	10	581.6243896	100	119.1800003	100	1.603052718	0.39414573	10
LGALS1 Galectin-1	IPI00219219	16278.33008	5.34	2	105.0299988	100	61.34000015	99.99279511	1.577602815	1.10001871	2
PRDX5 Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial pre	IPI00759663	19174.23047	6.73	1	62.63999939	99.99465894	62.63999939	99.99465894	1.577557478	0	1

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EEF1A1 Elongation factor 1-alpha	IPI00025447	54739.5	9.12	3	202.6699982	100	75.75	99.99973901	1.53799621	0.11003678	3
KRT8 Keratin, type II cytoskeletal 8	IPI00554648	58423.62891	5.52	17	1084.158813	100	102.9000015	100	1.52673046	0.41951301	17
VIL2 Ezrin	IPI00843975	77526.5	5.94	3	123.7044373	100	53.52999878	99.95648616	1.509889126	0.21942795	3
HIST1H2BL Histone H2B type 1-L	IPI00018534	16967.94922	10.31	2	104.4000015	100	60.99000168	99.99219043	1.47182726	6.52E-03	2
KRT79 keratin 6L	IPI00241841	62350.57031	6.75	3	162.3000031	100	63.45999908	99.99557791	1.469764863	0.28791603	3
RPN1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa	IPI00025874	78729.54688	5.87	1	54.65999985	99.96645504	54.65999985	99.96645504	1.461471264	0	1
- CD68 antigen variant (Fragment)	IPI00555602	45637.91016	5.46	2	123.75	100	86.23999786	100	1.458704192	0.38333857	2
TRAP1 57 kDa protein	IPI00646055	62264.05859	7.21	1	78.47000122	99.99986048	78.47000122	99.99986048	1.450983949	0	1
HSPA6 Heat shock 70 kDa protein 6	IPI00339269	77112.71094	5.81	4	267.0200195	100	106.0800018	100	1.430314813	0.57510015	4
HIST1H4E;HIST1H4I;HIST1H4D;HIST1H4L;H	IPI00453473	13088.62012	11.36	3	110.8499985	100	42.18999863	99.40758312	1.428364607	0.16201299	3
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00026602	42374.19922	6.09	2	104.5	100	63.65000153	99.99576721	1.420031869	3.75E-03	2
HSP90AB4P Heat shock protein 90Bd	IPI00555565	66222.17969	4.65	2	111.5200043	100	66.55000305	99.99782916	1.419040562	0.39267435	2
HNRPH1 Heterogeneous nuclear ribonucleoprotein H	IPI00013881	51876.64844	5.89	2	72.22000122	99.99941166	38.95999908	98.75368628	1.416454573	0.88825641	2
SPTBN1 Isoform Short of Spectrin beta chain, brain 1	IPI00328230	275951.75	5.31	2	97.84444427	100	57.93999863	99.98423742	1.400994605	0.28779376	2
S100A9 Protein S100-A9	IPI00027462	15007.73047	5.71	1	55.36999893	99.97151427	55.36999893	99.97151427	1.390751509	0	1
ETFB Isoform 2 of Electron transfer flavoprotein subunit beta	IPI00556451	41287.32813	6.78	3	150.4199982	100	58.50999832	99.9861762	0.697228645	0.39979414	3
FASN Fatty acid synthase	IPI00847250	287598.7813	5.99	8	360.3233032	100	54.15000153	99.96227518	0.687337132	0.47749635	8
GOT2 Aspartate aminotransferase, mitochondrial precursor	IPI00018206	52087.64844	9.14	2	107.4900055	100	59.08000183	99.98787653	0.686418834	0.33327916	2
MDH2 Malate dehydrogenase, mitochondrial precursor	IPI00291006	39765.08984	8.92	6	415.8644409	100	101.9499969	100	0.675011095	0.13145124	6
HSD17B10 Isoform 1 of 3-hydroxyacyl-CoA dehydrogenase type-2	IPI00017726	28818.30078	7.66	3	111.1999969	100	40.88999939	99.20085176	0.668171251	0.26174848	3
PHB2 7 kDa protein	IPI00797822	7920.140137	10.24	1	52.16999817	99.94048486	52.16999817	99.94048486	0.666970392	0	1

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AKR1A1 Alcohol dehydrogenase	IPI00220271	39850.12891	6.32	1	54.59444046	99.96594482	55.77000046	99.97402071	0.66565588	0	1
IDH2 Isocitrate dehydrogenase [NADP], mitochondrial precursor	IPI00011107	56573.30859	8.88	4	189.734436	100	72.62999725	99.99946466	0.655839281	0.14599748	5
ETFA 24 kDa protein	IPI00792673	27117.09961	8.77	1	106.0100021	100	106.0100021	100	0.65360585	0	1
RRBP1 Isoform 1 of Ribosome-binding protein 1	IPI00220967	178629.8125	8.73	4	207.9299927	100	82.16000366	99.99994035	0.650604345	0.32651136	4
IDH1 Isocitrate dehydrogenase [NADP] cytoplasmic	IPI00027223	52332.01172	6.53	7	393.4299927	100	87.31999969	100	0.64561385	0.21956547	9
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	58388.32813	6.3	4	240.5899963	100	75.94999695	99.99975075	0.637108662	0.20139225	4
DLD Dihydrolipoyl dehydrogenase, mitochondrial precursor	IPI00015911	60048.35938	7.59	1	74.77999878	99.99967369	74.77999878	99.99967369	0.63147561	0	1
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	12902.16992	6.28	4	171.4400024	100	50.50999832	99.91277772	0.629212162	0.22606579	4
ATP5B ATP synthase subunit beta, mitochondrial precursor	IPI00303476	59980.98828	5.26	9	558.6644287	100	85.80000305	100	0.625194422	0.21726058	9
ASL 50 kDa protein	IPI00514772	52806.57031	5.99	2	88.28678894	100	53.31000137	99.95422513	0.62373624	0.39021388	2
NNT NAD(P) transhydrogenase, mitochondrial precursor	IPI00337541	123493.2578	8.31	1	67.37000275	99.99820267	67.37000275	99.99820267	0.620804467	0	1
CAT Catalase	IPI00465436	64367.17969	6.9	9	523.9500122	100	93.44999695	100	0.618483152	0.31605441	9
MAOA Amine oxidase [flavin-containing] A	IPI00008483	65674.00781	7.94	2	121.6100006	100	69.40000153	99.99887377	0.614364555	5.47E-02	2
ATP5A1 ATP synthase subunit alpha, mitochondrial precursor	IPI00440493	64270.03906	9.16	5	347.4799805	100	100.2099991	100	0.608422953	0.17922405	5
PNPO 13 kDa protein	IPI00792667	13812.58008	8.93	2	102.4300003	100	55.63999939	99.9732313	0.599260864	7.07E-02	2
TST Thiosulfate sulfurtransferase	IPI00216293	35752.05859	6.77	7	425.1444397	100	112.0299988	100	0.598467154	0.24498046	7
ECH1 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor	IPI00011416	38661.62109	8.16	2	121.8300018	100	76.01999664	99.99975474	0.596524608	0.15325824	2
FMO5 Dimethylaniline monooxygenase [N-oxide-forming] 5	IPI00215760	66454.40625	8.41	1	82.66999817	99.99994696	82.66999817	99.99994696	0.591069761	0	1
ALDH7A1 similar to antiquitin	IPI00786942	63780.78125	8.25	2	85.83999634	100	43.5	99.56184549	0.586066426	0.03649206	2
HADHB Trifunctional enzyme beta subunit, mitochondrial precursor	IPI00022793	56777.03906	9.45	2	107.9500046	100	72.62000275	99.99946343	0.582252881	0.13210817	2
HSD17B4 Peroxisomal multifunctional enzyme type 2	IPI00019912	88068.99219	8.96	1	73.22000122	99.99953267	73.22000122	99.99953267	0.580812275	0	1

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DECR1 2,4-dienoyl-CoA reductase, mitochondrial precursor	IPI00003482	40019.14844	9.35	3	174.25	100	76.26999664	99.99976846	0.562595463	0.36139741	3
NIPSNAP1 Protein NipSnap1	IPI00304435	36019.10938	9.35	3	166.4599915	100	85.98999786	100	0.553891129	9.99E-02	4
CYP2E1 Cytochrome P450 2E1	IPI00007282	61500.80078	8.27	2	66.94000244	99.99801561	33.52000046	95.63858674	0.549995499	0.11496567	2
FAH 33 kDa protein	IPI00793664	34681.60938	7.12	2	72.22999573	99.99941301	38.34999847	98.56574148	0.531857008	0.17621473	2
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	43936.05859	8.75	5	314.8244324	100	106.8799973	100	0.494445138	0.43966706	5
DBI Isoform 2 of Acyl-CoA-binding protein	IPI00218836	13802.13965	5.41	2	95.23000336	100	53.24000168	99.95348135	0.477903985	6.60E-02	2
HADHA Trifunctional enzyme subunit alpha, mitochondrial precursor	IPI00031522	93913.70313	9.16	4	216.5699921	100	74	99.99960949	0.477601944	8.88E-02	4
GALK1 CDNA FLJ26554 fis, clone LNF01773, highly similar to Galactokinase	IPI00442827	44445.10938	6.81	3	137.9000092	100	60.79999924	99.99184118	0.464813636	3.48E-02	3
HMGCL 19 kDa protein	IPI00514407	21853.41016	8.9	1	90.19000244	100	90.19000244	100	0.46208774	0	1
PPIF Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor	IPI00026519	24750.41992	9.48	1	61.11000061	99.99240326	61.11000061	99.99240326	0.461369297	0	1
PEBP1 Phosphatidylethanolamine-binding protein 1	IPI00219446	23439.92969	7.01	6	469.8399963	100	178.5599976	100	0.456541289	0.27485665	6
MAT1A S-adenosylmethionine synthetase isoform type-1	IPI00021772	47392.28906	5.86	3	197.9244385	100	90.23000336	100	0.449442837	0.17599103	3
SELENBP1 53 kDa protein	IPI00745729	57664.26953	6.03	4	205.5900116	100	66.86000061	99.99797872	0.447974117	0.1067351	4
UNQ501 MBC3205	IPI00063130	22277.99023	8.91	1	61.65999985	99.9933069	61.65999985	99.9933069	0.440068717	0	1
ACAT2 Acetyl-CoA acetyltransferase, cytosolic	IPI00291419	44906.64063	6.47	1	75.80999756	99.99974259	75.80999756	99.99974259	0.438262714	0	1
QPRT 17 kDa protein	IPI00853023	17914	7.71	2	109.3199997	100	59.18000031	99.98815249	0.436531711	1.36E-02	2
HAO1 Hydroxyacid oxidase 1	IPI00006934	44682.82031	8.2	3	186.6900024	100	89.73000336	100	0.431740451	0.60183539	3
ALDH4A1 Aldehyde dehydrogenase 4 family, member A1	IPI00647328	65056.12109	7.62	8	435.2200012	100	69.44000244	99.9988841	0.429279272	0.32235099	8
ACADSB Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	IPI00024623	52051.67969	6.53	3	158.3899994	100	61.31999969	99.99276185	0.426572636	0.24722753	3
SARDH Sarcosine dehydrogenase, mitochondrial precursor	IPI00034308	106218.8125	6.8	1	55.95000076	99.97507546	55.95000076	99.97507546	0.425445538	0	1
ALDH1A1 Retinal dehydrogenase 1	IPI00218914	60949.39063	6.3	5	261.1199951	100	87.58999634	100	0.423539563	0.1460814	5

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BDH1 D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	IPI00025341	41766.75	9.11	2	73.09999847	99.99951957	37.18999863	98.12661334	0.421559339	0.92456341	2
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	48966.78125	6.61	10	666.2999878	100	140.7599945	100	0.417691823	0.32497638	10
UGDH UDP-glucose 6-dehydrogenase	IPI00031420	60869.64844	6.73	3	171.8099976	100	74.59999847	99.99965988	0.416727125	0.29226343	3
GOT1 Aspartate aminotransferase, cytoplasmic	IPI00219029	49570.83984	6.52	3	118.25	100	44.95999908	99.68694015	0.412082325	2.92E-02	3
ACAA1 3-ketoacyl-CoA thiolase, peroxisomal precursor	IPI00012828	47604.07031	8.76	5	251.6999817	100	59.43000031	99.98881522	0.410764537	0.47707915	5
PBLD 28 kDa protein	IPI00396138	30189.60938	6.55	2	81.55000305	99.99993135	42.31999969	99.42505366	0.41053028	0.17336574	2
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	35335.42969	8.34	6	381.5900269	100	108.0100021	100	0.409662277	0.32684795	6
ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria	IPI00024990	63211.07813	8.72	7	371.9800415	100	70.38999939	99.99910334	0.40550038	0.17201491	8
ALDH1L1 Formyltetrahydrofolate dehydrogenase isoform a variant	IPI00793673	109020.6328	5.63	3	145.6699982	100	53.16999817	99.95272544	0.405146892	0.37622485	3
LOC645619 similar to Adenylate kinase isoenzyme 4, mitochondrial	IPI00738805	27444.46094	8.47	2	69.98000336	99.99901457	35.90000153	97.47868485	0.4044644	5.89E-02	2
APOC3 13 kDa protein	IPI00657670	13861.62012	7.9	1	85.61000061	100	85.61000061	100	0.385339561	0	1
GLUD1 Glutamate dehydrogenase 1, mitochondrial precursor	IPI00016801	66531.63281	7.66	13	880.25	100	88.37000275	100	0.374184054	0.20381043	15
EPHX1 Epoxide hydrolase 1	IPI00009896	57419.37891	6.77	3	217.8299866	100	118.5999985	100	0.373561952	0.60567448	3
AOX1 Hypothetical protein AOX1	IPI00743616	161854.2031	6.78	2	107.6999969	100	64.90000153	99.99682585	0.372177265	0.22202264	2
FTCD Isoform A of Formimidoyltransferase-cyclodeaminase	IPI00001441	62321.57813	5.58	4	177.4000092	100	51.59999847	99.93213788	0.367568394	0.13668904	4
BHMT2 Betaine--homocysteine S-methyltransferase 2	IPI00014363	43910.42969	5.61	3	123.2244415	100	47.00999832	99.80473363	0.366104567	8.33E-02	3
CBR1 Carbonyl reductase [NADPH] 1	IPI00295386	33322.12891	8.55	2	161.0100098	100	84.68000031	100	0.360663046	1.71E-02	2
ACSL1 Isoform 1 of Long-chain-fatty-acid--CoA ligase 1	IPI00012728	85201.29688	6.81	5	262.4100037	100	79.12999725	99.99988015	0.350712007	0.2083006	6
UGT2B7 similar to UDP-glucuronosyltransferase 2B7 precursor	IPI00787584	65314.41016	8.41	3	179.3999939	100	72.83000183	99.99948876	0.350464401	5.67E-02	3
ALDH2 Mitochondrial aldehyde dehydrogenase 2 variant (Fragment)	IPI00792207	61065.96094	6.63	6	348.1699829	100	73.36000061	99.99954749	0.349704915	0.2526833	6
PHGDH Phosphoglycerate dehydrogenase	IPI00642548	56869.67969	6.47	2	92.38000488	100	53.13999939	99.95239776	0.348773711	0.15128801	2

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UGT2B17 UDP-glucuronosyltransferase 2B17 precursor	IPI00026932	67707.59375	8.76	1	72.83000183	99.99948876	72.83000183	99.99948876	0.344443216	0	1
DAK Dihydroxyacetone kinase	IPI00551024	63392.42188	7.12	2	157.9900055	100	111	100	0.343111969	0.1550338	2
UGP2 Isoform 1 of UTP--glucose-1-phosphate uridylyltransferase	IPI00329331	63091.28906	8.16	6	343.2444458	100	76.88999939	99.99979926	0.330030961	0.04786195	6
ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	IPI00001539	46153.96875	8.32	9	505.5700073	100	83.16999817	100	0.324916873	0.36626289	9
SCP2 sterol carrier protein 2 isoform 2	IPI00433347	61608.94141	6.25	3	146.6900024	100	69.51999664	99.99890446	0.324680292	0.18338335	3
- 105 kDa protein	IPI00794900	115433.2422	7.3	9	364.6000061	100	51.72999954	99.93413915	0.313543115	0.13859138	9
- 14 kDa protein	IPI00788848	15907.24023	5.24	6	355	100	93.44000244	100	0.308022587	0.25488216	8
ACY1 Aminoacylase-1	IPI00009268	48344.23047	5.77	6	283.1600037	100	59.18999863	99.98817973	0.304239303	0.198984	6
DCXR 26 kDa protein	IPI00797249	27252.58984	8.33	5	316.0800171	100	83.98000336	100	0.302553084	6.53E-02	5
CES2 carboxylesterase 2 isoform 1	IPI00332828	72247.0625	6.03	4	227.7000122	100	89.77999878	100	0.300215897	0.17998687	4
PGM1 Phosphoglucomutase 1	IPI00844159	66935.90625	6.2	6	377.908905	100	95.12999725	100	0.295493085	0.14418012	6
AGXT Serine--pyruvate aminotransferase	IPI00009367	46426.73047	8.61	4	230.2799988	100	93.05999756	100	0.293665918	0.13669913	4
GRHPR GRHPR protein (Fragment)	IPI00550682	39375.17188	5.95	2	158.3444366	100	108.4499969	100	0.293602584	8.13E-02	2
PCK2 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial precursor	IPI00294380	74737.8125	7.56	11	640.1799927	100	89.26999664	100	0.277302395	0.29336983	11
BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101	49946.23828	6.58	5	270.7444458	100	80.41000366	99.99991075	0.274906278	9.66E-02	5
SORD Sorbitol dehydrogenase	IPI00216057	42378.10938	8.23	3	181.2599945	100	94.58999634	100	0.270098791	0.3130166	3
PCK2 mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor	IPI00797038	74784.85938	7.57	11	683.4800415	100	89.26999664	100	0.263132145	0.24532861	11
KHK Isoform C of Ketohexokinase	IPI00216136	35220.62891	5.91	3	190.984436	100	93.37999725	100	0.256727697	0.19976701	3
SOD1 Superoxide dismutase	IPI00783680	17838.08984	5.7	3	240.7100067	100	112.2600021	100	0.251869937	3.19E-02	3
HRSP12 Ribonuclease UK114	IPI00005038	15826.7998	8.74	2	124.6999969	100	62.97999954	99.99506113	0.247159478	0.19447979	2
AKR1C3 Aldo-keto reductase family 1 member C3	IPI00291483	41031.17969	8.05	4	177.6499939	100	59.72000122	99.9895377	0.246116768	0.25465726	4

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HMGCS2 Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor	IPI00008934	61333.76953	8.4	6	345.9000244	100	73.31999969	99.9995433	0.237872579	0.32943531	6
MAOB Amine oxidase [flavin-containing] B	IPI00328156	63747.53125	7.2	2	124.8000031	100	69.40000153	99.99887377	0.235839557	0.32826859	2
FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	41289.14844	6.54	3	175.0299988	100	70.54000092	99.99913378	0.229416426	0.23496863	3
ASS1 Argininosuccinate synthase	IPI00640430	24839.67969	6.84	5	223.0700073	100	51.79999924	99.93519219	0.227907106	0.16759224	5
SULT1A1 Sulfotransferase 1A1	IPI00300026	47814.69922	8.61	3	127.7600021	100	44.54999924	99.65594541	0.226966471	0.10918505	3
UGT1A10;UGT1A6 UDP-glucuronosyltransferase 1-10 precursor	IPI00233885	64734.48828	6.88	1	65.73000336	99.99737803	65.73000336	99.99737803	0.219405261	0	1
ARG1 Isoform 1 of Arginase-1	IPI00291560	38451.66016	6.72	2	127.0699997	100	73.52999878	99.99956486	0.217653848	0.13533258	2
ACAT1 Acetyl-CoA acetyltransferase, mitochondrial precursor	IPI00030363	49865.05859	8.98	5	392.9812317	100	124.1800003	100	0.212100424	0.11219495	5
CPS1 Isoform 1 of Carbamoyl-phosphate synthase [ammonia], mitochondrial pre	IPI00011062	180875.9531	6.3	44	2904.68335	100	134.6900024	100	0.206313584	0.24030259	48
CYB5A Isoform 1 of Cytochrome b5	IPI00397860	16616.71094	4.88	5	431.980011	100	172.6000061	100	0.203474699	0.11502888	5
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	61418.91016	8.17	2	109.7700043	100	60.58000183	99.99141724	0.199781537	0.10749474	2
ACSM2A 23 kDa protein	IPI00334599	25689.23047	9.04	2	110.0800018	100	64.44999695	99.99647931	0.183556482	3.79E-02	2
RDH16 Microsomal NAD+-dependent retinol dehydrogenase 4 variant (Fragment)	IPI00555683	23832.68945	7.67	2	94.77999878	100	53.36000061	99.9547491	0.176448788	0.14233921	2
ADH4 Alcohol dehydrogenase 4	IPI00218899	45828.03125	8.25	6	388.0499878	100	82.48999786	99.99994471	0.176143371	0.16239362	7
ADH1A Alcohol dehydrogenase 1A	IPI00218896	45320.80859	8.26	7	474.1499939	100	111.1399994	100	0.154116622	0.21712908	7
CES1 carboxylesterase 1 isoform c precursor	IPI00607693	68199.60938	6.15	11	701.250061	100	98.52999878	100	0.153944084	0.10184486	11
GSTA1 Glutathione S-transferase A1	IPI00657682	29261.05078	8.91	6	325.7600098	100	76.02999878	99.9997553	0.118478966	5.38E-02	6
ADH1B Alcohol dehydrogenase 1B	IPI00473031	45270.91016	8.63	6	435.9699707	100	111.1399994	100	0.116125176	0.11188744	6
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	43462.35156	8	8	572.3044434	100	94.22000122	100	9.27E-02	5.59E-02	9

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio * (117/116)	iTRAQ Standard Deviation * (117/116)	iTRAQ Peptides (117/116)
FN1 Isoform 1 of Fibronectin precursor	IPI00022418	276716.375	5.45	13	709.7888184	100	86.59999847	100	4.69164933	2.22023028	13
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	48966.78125	6.61	10	666.2999878	100	140.7599945	100	3.333623381	0.98232625	10
APOE Apolipoprotein E precursor	IPI00021842	38239.98828	5.65	3	240.2999878	100	107.5899963	100	3.046027758	0.46707844	3
KRT79 keratin 6L	IPI00241841	62350.57031	6.75	3	162.3000031	100	63.45999908	99.99557791	2.880781091	0.16000436	3
POSTN Isoform 2 of Periostin precursor	IPI00218585	96544.46875	7.87	1	72.84999847	99.99949111	72.84999847	99.99949111	2.857461154	0	1
ANXA2 Annexin A2	IPI00455315	43516.26953	7.57	10	572.848938	100	98.91999817	100	2.585622379	1.46772622	10
KRT8 Keratin, type II cytoskeletal 8	IPI00554648	58423.62891	5.52	17	1084.158813	100	102.9000015	100	2.540204083	0.54444182	17
KRT18 Keratin, type I cytoskeletal 18	IPI00784347	51196.89844	5.34	8	415.4400024	100	66.73000336	99.9979173	2.531720197	0.32916576	8
TKT Transketolase variant (Fragment)	IPI00788802	74607.24219	7.9	2	86.19999695	100	52.22000122	99.94116616	2.487795152	1.29598718	2
VTN Vitronectin precursor	IPI00298971	57939.35156	5.55	5	235.7200012	100	59.11999893	99.98798767	2.429800561	0.70269433	5
HSPE1 10 kDa heat shock protein, mitochondrial	IPI00220362	12653.11035	8.89	5	282.7600098	100	79.84999847	99.99989846	2.385210982	0.44461367	6
ETFA 24 kDa protein	IPI00792673	27117.09961	8.77	1	106.0100021	100	106.0100021	100	2.147704605	0	1
QPRT 17 kDa protein	IPI00853023	17914	7.71	2	109.3199997	100	59.18000031	99.98815249	2.135853724	0.35892407	2
VDAC1 20 kDa protein	IPI00790304	22855.44922	6.74	1	56.52000046	99.97814115	56.52000046	99.97814115	2.130542782	0	1
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	68931.10156	5.7	11	582.317749	100	90.54000092	100	2.102235323	0.42340338	11
ECH1 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor	IPI00011416	38661.62109	8.16	2	121.8300018	100	76.01999664	99.99975474	2.101764842	0.38254505	2
HSPA6 Heat shock 70 kDa protein 6	IPI00339269	77112.71094	5.81	4	267.0200195	100	106.0800018	100	2.023154679	0.17015218	4
CTSD Protein	IPI00853455	44335.46875	5.38	2	80.71000671	99.9999167	41.24000168	99.26272906	2.003697141	0.69992828	2
HSPA1A;HSPA1B heat shock 70kDa protein 1A	IPI00845339	77569.67969	5.48	6	344.0700073	100	106.0800018	100	1.943532971	0.22384396	6
- 14 kDa protein	IPI00788848	15907.24023	5.24	6	355	100	93.44000244	100	1.939587243	0.32338065	8
NME2;NME1 Nucleoside diphosphate kinase B	IPI00026260	19395.17969	8.52	4	209.3000183	100	75.76000214	99.99973961	1.892010973	0.50216313	5

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ETFB Isoform 2 of Electron transfer flavoprotein subunit beta	IPI00556451	41287.32813	6.78	3	150.4199982	100	58.50999832	99.9861762	1.828168752	5.98E-02	3
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	20345.10938	7.68	5	333.5	100	86.23999786	100	1.818516558	0.15396059	7
CLU clusterin isoform 1	IPI00400826	62857.89844	6.24	1	81.48999786	99.9999304	81.48999786	99.9999304	1.794800336	0	1
SLC25A3 Isoform B of Phosphate carrier protein, mitochondrial precursor	IPI00215777	44188.96875	9.43	1	47.31000137	99.81776695	47.31000137	99.81776695	1.791957852	0.31032646	2
HSPA9 Stress-70 protein, mitochondrial precursor	IPI00007765	81497.46094	5.87	5	262.230011	100	79.87999725	99.99989916	1.786205156	0.14479074	5
CTSB Cathepsin B precursor	IPI00295741	40882.91016	5.88	2	107.3899994	100	63.43000031	99.99554726	1.736327274	0.33277556	2
TRAP1 57 kDa protein	IPI00646055	62264.05859	7.21	1	78.47000122	99.99986048	78.47000122	99.99986048	1.719844252	0	1
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	43936.05859	8.75	5	314.8244324	100	106.8799973	100	1.693001507	0.16591354	5
HNRPA1 Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	IPI00465365	37003.55078	9.27	2	84.23999786	100	46.47999954	99.77938891	1.688249892	0.71554639	2
CFL2 Cofilin-2	IPI00413344	22273.21094	7.66	1	86.23000336	100	86.23000336	100	1.667398984	0	1
HIST1H2BL Histone H2B type 1-L	IPI00018534	16967.94922	10.31	2	104.4000015	100	60.99000168	99.99219043	1.632490136	0.30528719	2
ALDOA 45 kDa protein	IPI00796333	49776.48828	8.48	2	88.41999817	100	51.41999817	99.92926612	1.631140522	9.87E-02	2
FASN Fatty acid synthase	IPI00847250	287598.7813	5.99	8	360.3233032	100	54.15000153	99.96227518	1.61588821	0.70267146	8
AKR1C3 Aldo-keto reductase family 1 member C3	IPI00291483	41031.17969	8.05	4	177.6499939	100	59.72000122	99.9895377	1.599582689	0.18146628	4
TAGLN2 24 kDa protein	IPI00647915	26448.48047	8.41	2	103.4100037	100	52.18999863	99.94075831	1.593187528	0.12643353	2
GLO1 Lactoylglutathione lyase	IPI00220766	23684.51953	5.12	2	109.3800049	100	58.40999985	99.98585421	1.566522854	1.91E-02	2
LOC645619 similar to Adenylate kinase isoenzyme 4, mitochondrial	IPI00738805	27444.46094	8.47	2	69.98000336	99.99901457	35.90000153	97.47868485	1.559443183	0.32351742	2
TUFM Tu translation elongation factor, mitochondrial	IPI00027107	54583.71875	7.26	4	190.5800171	100	53.54000092	99.95658626	1.550602393	0.33587243	4
TUBB2C Tubulin beta-2C chain	IPI00007752	52471.19141	4.79	7	477.6399841	100	110.8499985	100	1.543717441	0.44777039	8
HSP90AB1 Heat shock protein HSP 90-beta	IPI00414676	94433.0625	4.97	9	578.8600464	100	116.1500015	100	1.535131392	0.46092414	10
NIPSNAP1 Protein NipSnap1	IPI00304435	36019.10938	9.35	3	166.4599915	100	85.98999786	100	1.526254931	0.33494911	4
LGALS3 Galectin-3	IPI00465431	27514.25	8.58	2	109.3899994	100	66.76000214	99.99793164	1.502722393	0.10067532	2
HSD17B10 Isoform 1 of 3-hydroxyacyl-CoA dehydrogenase type-2	IPI00017726	28818.30078	7.66	3	111.1999969	100	40.88999939	99.20085176	1.498503375	0.17842609	3

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TUBA1A Tubulin alpha-1A chain	IPI00180675	53535.80078	4.94	4	298.480011	100	94.84999847	100	1.497069006	0.33278022	4
PRDX5 Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial pre	IPI00759663	19174.23047	6.73	1	62.63999939	99.99465894	62.63999939	99.99465894	1.488526809	0	1
GALK1 CDNA FLJ26554 fis, clone LNF01773, highly similar to Galactokinase	IPI00442827	44445.10938	6.81	3	137.9000092	100	60.79999924	99.99184118	1.48296436	5.00E-02	3
IDH1 Isocitrate dehydrogenase [NADP] cytoplasmic	IPI00027223	52332.01172	6.53	7	393.4299927	100	87.31999969	100	1.479247309	0.24414522	9
TUBB Tubulin beta chain	IPI00011654	52311.16016	4.78	8	527.8399658	100	110.8499985	100	1.464613681	0.45259364	9
NPM1 Isoform 1 of Nucleophosmin	IPI00549248	37589.32031	4.64	2	109.8000031	100	71.08000183	99.99923506	1.454446488	9.87E-02	2
TST Thiosulfate sulfurtransferase	IPI00216293	35752.05859	6.77	7	425.1444397	100	112.0299988	100	1.446275178	0.18044383	7
HNRPA2B1 Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	IPI00414696	38478.16016	8.67	3	168.5644531	100	78.44000244	99.99985952	1.431830561	0.21967077	3
LOC728188;PGAM4 Probable phosphoglycerate mutase 4	IPI00374975	31633.05078	6.19	1	71.55000305	99.99931352	71.55000305	99.99931352	1.428008208	0	1
LOC388720 similar to ubiquitin and ribosomal protein S27a precursor	IPI00397808	21877.69922	9.53	2	131.0500031	100	82.11000061	99.99993966	1.422628587	0.10192314	2
GAPDH Glyceraldehyde 3-phosphate dehydrogenase	IPI00789134	31015.36914	6.45	4	310.7200012	100	121.7099991	100	1.416487881	0.10665591	4
EEF1A1 Elongation factor 1-alpha	IPI00025447	54739.5	9.12	3	202.6699982	100	75.75	99.99973901	1.409278367	8.94E-02	3
YWHAZ 14-3-3 protein zeta/delta	IPI00021263	30890.03906	4.73	4	243.2644501	100	89.68000031	100	1.400213751	0.15106071	4
HIST1H4E;HIST1H4I;HIST1H4D;HIST1H4L;HIST1H4J;HIST1H4A;HIST1H4F;HIST1H4H;HIS	IPI00453473	13088.62012	11.36	3	110.8499985	100	42.18999863	99.40758312	1.394397322	1.11001555	3
HSP90AA1 Isoform 1 of Heat shock protein HSP 90-alpha	IPI00784295	96593.6875	4.94	8	548.6000366	100	121.8899994	100	1.390073383	0.26487711	9
LGALS1 Galectin-1	IPI00219219	16278.33008	5.34	2	105.0299988	100	61.34000015	99.99279511	0.708939818	0.42029336	2
HP HP protein	IPI00478493	43017.64844	6.13	4	237.230011	100	65.5	99.99723543	0.700163902	3.99E-02	4
KHK Isoform C of Ketohexokinase	IPI00216136	35220.62891	5.91	3	190.984436	100	93.37999725	100	0.698774669	4.40E-02	3
FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	41289.14844	6.54	3	175.0299988	100	70.54000092	99.99913378	0.662081159	7.75E-02	3
LDHA Isoform 2 of L-lactate dehydrogenase A chain	IPI00607708	40851.19922	7.94	2	113.9799957	100	60.00999832	99.9902135	0.661987272	0.24257114	2
ARG1 Isoform 1 of Arginase-1	IPI00291560	38451.66016	6.72	2	127.0699997	100	73.52999878	99.99956486	0.659918001	6.69E-02	2
CES1 carboxylesterase 1 isoform c precursor	IPI00607693	68199.60938	6.15	11	701.250061	100	98.52999878	100	0.657871606	8.26E-02	11
SARDH Sarcosine dehydrogenase, mitochondrial precursor	IPI00034308	106218.8125	6.8	1	55.95000076	99.97507546	55.95000076	99.97507546	0.646929345	0	1

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ALDH1L1 Formyltetrahydrofolate dehydrogenase isoform a variant	IPI00793673	109020.6328	5.63	3	145.6699982	100	53.16999817	99.95272544	0.644839622	0.12906938	3
COL6A3 alpha 3 type VI collagen isoform 3 precursor	IPI00072917	345457.3438	6.47	9	391.0899963	100	66.15000153	99.99761973	0.63258632	0.10401701	9
COL6A2 Isoform 2C2A of Collagen alpha-2(VI) chain precursor	IPI00220613	105910.7031	5.38	2	88.63000488	100	53.79000092	99.95901479	0.630573742	0.1086929	2
GRHPR GRHPR protein (Fragment)	IPI00550682	39375.17188	5.95	2	158.3444366	100	108.4499969	100	0.628703184	0.16419832	2
COL6A1 Collagen alpha-1(VI) chain precursor	IPI00291136	117302.5391	5.26	2	97.58999634	100	60.84999847	99.99193457	0.616586669	6.78E-02	2
ACADSB Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	IPI00024623	52051.67969	6.53	3	158.3899994	100	61.31999969	99.99276185	0.611672916	6.76E-02	3
PRDX6 Peroxiredoxin-6	IPI00220301	27847.49023	6	5	201.4100037	100	45.15000153	99.70034113	0.609208833	5.88E-02	5
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	43462.35156	8	8	572.3044434	100	94.22000122	100	0.594610734	6.74E-02	9
ALDH4A1 Aldehyde dehydrogenase 4 family, member A1	IPI00647328	65056.12109	7.62	8	435.2200012	100	69.44000244	99.9988841	0.589857644	0.11958453	8
UNQ501 MBC3205	IPI00063130	22277.99023	8.91	1	61.65999985	99.9933069	61.65999985	99.9933069	0.58968704	0	1
HRSP12 Ribonuclease UK114	IPI00005038	15826.7998	8.74	2	124.6999969	100	62.97999954	99.99506113	0.585925567	0.21657136	2
ASL 50 kDa protein	IPI00514772	52806.57031	5.99	2	88.28678894	100	53.31000137	99.95422513	0.584426323	0.14270184	2
SCP2 sterol carrier protein 2 isoform 2	IPI00433347	61608.94141	6.25	3	146.6900024	100	69.51999664	99.99890446	0.569728249	7.47E-02	3
AKR1A1 Alcohol dehydrogenase	IPI00220271	39850.12891	6.32	1	54.59444046	99.96594482	55.77000046	99.97402071	0.563907492	0	1
ACSL1 Isoform 1 of Long-chain-fatty-acid--CoA ligase 1	IPI00012728	85201.29688	6.81	5	262.4100037	100	79.12999725	99.99988015	0.556263548	8.21E-02	6
ACSM2A 23 kDa protein	IPI00334599	25689.23047	9.04	2	110.0800018	100	64.44999695	99.99647931	0.544518871	0.11531382	2
SULT1A1 Sulfotransferase 1A1	IPI00300026	47814.69922	8.61	3	127.7600021	100	44.54999924	99.65594541	0.541971508	1.73E-02	3
GLUD1 Glutamate dehydrogenase 1, mitochondrial precursor	IPI00016801	66531.63281	7.66	13	880.25	100	88.37000275	100	0.540100997	9.46E-02	15
AOX1 Hypothetical protein AOX1	IPI00743616	161854.2031	6.78	2	107.6999969	100	64.90000153	99.99682585	0.526519389	6.89E-02	2
GSTA1 Glutathione S-transferase A1	IPI00657682	29261.05078	8.91	6	325.7600098	100	76.02999878	99.9997553	0.524475848	7.68E-02	6
SELENBP1 53 kDa protein	IPI00745729	57664.26953	6.03	4	205.5900116	100	66.86000061	99.99797872	0.521206877	7.90E-02	4
ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria	IPI00024990	63211.07813	8.72	7	371.9800415	100	70.38999939	99.99910334	0.520113907	0.1492127	8
BLVRB Flavin reductase	IPI00783862	23637.61914	7.13	2	104.2700043	100	59.13999939	99.98804286	0.50956855	1.61E-02	2

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PCK2 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial precursor	IPI00294380	74737.8125	7.56	11	640.1799927	100	89.26999664	100	0.498647454	0.14971569	11
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	61418.91016	8.17	2	109.7700043	100	60.58000183	99.99141724	0.497844373	2.20E-02	2
CPS1 Isoform 1 of Carbamoyl-phosphate synthase [ammonia], mitochondrial pre	IPI00011062	180875.9531	6.3	44	2904.68335	100	134.6900024	100	0.495179104	9.14E-02	48
PCK2 mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor	IPI00797038	74784.85938	7.57	11	683.4800415	100	89.26999664	100	0.493318438	0.14003596	11
HAO1 Hydroxyacid oxidase 1	IPI00006934	44682.82031	8.2	3	186.6900024	100	89.73000336	100	0.489075782	8.77E-02	3
CAT Catalase	IPI00465436	64367.17969	6.9	9	523.9500122	100	93.44999695	100	0.483585722	0.23064285	9
AGXT Serine--pyruvate aminotransferase	IPI00009367	46426.73047	8.61	4	230.2799988	100	93.05999756	100	0.470013626	3.98E-02	4
SOD1 Superoxide dismutase	IPI00783680	17838.08984	5.7	3	240.7100067	100	112.2600021	100	0.461226296	3.01E-02	3
CYP2E1 Cytochrome P450 2E1	IPI00007282	61500.80078	8.27	2	66.94000244	99.99801561	33.52000046	95.63858674	0.458716174	7.87E-03	2
FTCD Isoform A of Formimidoyltransferase-cyclodeaminase	IPI00001441	62321.57813	5.58	4	177.4000092	100	51.59999847	99.93213788	0.455871169	0.21765755	4
TAGLN Transgelin	IPI00216138	25234.73047	8.87	3	131.3200073	100	52.47000122	99.94445728	0.455016768	0.04230213	3
FTL Ferritin light chain	IPI00852596	21925.33984	5.51	2	98.58000183	100	52.33000183	99.94263763	0.437876205	0.13707333	2
SORD Sorbitol dehydrogenase	IPI00216057	42378.10938	8.23	3	181.2599945	100	94.58999634	100	0.434298367	3.18E-02	3
UGT2B17 UDP-glucuronosyltransferase 2B17 precursor	IPI00026932	67707.59375	8.76	1	72.83000183	99.99948876	72.83000183	99.99948876	0.425171731	0	1
- 105 kDa protein	IPI00794900	115433.2422	7.3	9	364.6000061	100	51.72999954	99.93413915	0.422328867	8.83E-02	9
SPLEN2011805, highly similar to BONE/CARTILAGE	IPI00385748	39528	6.31	3	209.9899902	100	95.19999695	100	0.411923531	0.12898124	3
PBLD 28 kDa protein	IPI00396138	30189.60938	6.55	2	81.55000305	99.99993135	42.31999969	99.42505366	0.41065073	0.13784584	2
ACAT1 Acetyl-CoA acetyltransferase, mitochondrial precursor	IPI00030363	49865.05859	8.98	5	392.9812317	100	124.1800003	100	0.405856689	5.74E-02	5
UGT2B7 similar to UDP-glucuronosyltransferase 2B7 precursor	IPI00787584	65314.41016	8.41	3	179.3999939	100	72.83000183	99.99948876	0.399178773	0.14185989	3
UGP2 Isoform 1 of UTP--glucose-1-phosphate uridylyltransferase	IPI00329331	63091.28906	8.16	6	343.2444458	100	76.88999939	99.99979926	0.395002156	6.19E-02	6
LUM 23 kDa protein	IPI00794403	25919.60938	8.52	2	117.8000031	100	83.20999908	100	0.38313986	0.16077867	2
DCXR 26 kDa protein	IPI00797249	27252.58984	8.33	5	316.0800171	100	83.98000336	100	0.374224565	0.19731429	5
PRELP Prolargin precursor	IPI00020987	46264.33984	9.47	4	194.1799927	100	52.11999893	99.93979572	0.287182882	9.76E-02	4

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RDH16 Microsomal NAD+-dependent retinol dehydrogenase 4 variant (Fragment)	IPI00555683	23832.68945	7.67	2	94.77999878	100	53.36000061	99.9547491	0.273090626	0.11530921	2
ASS1 Argininosuccinate synthase	IPI00640430	24839.67969	6.84	5	223.0700073	100	51.79999924	99.93519219	0.272135418	7.38E-02	5
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1406	5.6	3	199.3300018	100	85.90000153	100	0.239121932	0.1238869	3
ADH4 Alcohol dehydrogenase 4	IPI00218899	45828.03125	8.25	6	388.0499878	100	82.48999786	99.99994471	0.145050483	0.09963193	7
ADH1A Alcohol dehydrogenase 1A	IPI00218896	45320.80859	8.26	7	474.1499939	100	111.1399994	100	0.128981463	7.98E-02	7
COL1A2 Collagen alpha-2(I) chain precursor	IPI00304962	136968.0469	9.08	1	94.27999878	100	94.27999878	100	0.128894413	0	1
ADH1B Alcohol dehydrogenase 1B	IPI00473031	45270.91016	8.63	6	435.9699707	100	111.1399994	100	0.126775249	8.31E-02	6

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio (115/114)	iTRAQ Standard Deviation (115/114)	iTRAQ Peptides (115/114)
FN1 Isoform 1 of Fibronectin precursor	IPI00022418	276716.375	5.45	9	441.6544189	100	82.48999786	99.99994479	3.487115298	1.530472082	11
AKR1D1 CDNA FLJ25413 fis, clone TST03402, highly similar to 3-OXO-5-BETA-STEROID 4-DEHYDROGENASE	IPI00065073	33300.88672	8.11	1	54.40000153	99.96443706	54.40000153	99.96443706	3.280508179	0	1
LOC645619 similar to Adenylate kinase isoenzyme 4, mitochondrial	IPI00738805	27444.46094	8.47	2	70.94000244	99.99921114	37.63999939	98.31345503	2.761734166	0.744524299	2
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	48966.78125	6.61	6	364.9199829	100	89.69000244	100	2.594049314	0.375845991	6
AKR1C3 Aldo-keto reductase family 1 member C3	IPI00291483	41031.17969	8.05	4	198.3399963	100	63.93000031	99.99603724	2.528213075	0.471764218	4
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	68931.10156	5.7	7	437.0189209	100	101.2300034	100	2.404382961	0.771539451	8
HSPA1A;HSPA1B heat shock 70kDa protein 1A	IPI00845339	77569.67969	5.48	7	414.2700195	100	118.5800018	100	2.392320022	0.948908078	7
HSPA6 Heat shock 70 kDa protein 6	IPI00339269	77112.71094	5.81	5	327.7600098	100	118.5800018	100	2.338145577	1.038025901	5
HSPE1 10 kDa heat shock protein, mitochondrial	IPI00220362	12653.11035	8.89	6	309.730011	100	65.75	99.99739386	2.250237954	0.623933664	9
HMGCS2 Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor	IPI00008934	61333.76953	8.4	4	159.3999939	100	50.04999924	99.90317267	2.249225517	0.791181495	5
UGDH UDP-glucose 6-dehydrogenase	IPI00031420	60869.64844	6.73	3	159.980011	100	68.37000275	99.9985744	2.138718845	1.023191528	3
HSPA9 Stress-70 protein, mitochondrial precursor	IPI00007765	81497.46094	5.87	4	237.5700073	100	98.48000336	100	2.001890086	0.986582545	4
HADHB Trifunctional enzyme beta subunit, mitochondrial precursor	IPI00022793	56777.03906	9.45	4	165.1699982	100	49.88999939	99.8995389	1.996888928	0.507476913	5
SOD2 manganese superoxide dismutase isoform B precursor	IPI00607577	22864.7793	8.36	2	99.51000214	100	63.49000168	99.99561472	1.941866614	0.195455917	2
NCL Isoform 1 of Nucleolin	IPI00604620	89719.57031	4.6	1	59.61999893	99.9893095	59.61999893	99.9893095	1.93485054	0	1
LOC388720 similar to ubiquitin and ribosomal protein S27a precursor	IPI00397808	21877.69922	9.53	2	119.4199982	100	67.08000183	99.99808134	1.872844837	0.111362025	2
CES1 carboxylesterase 1 isoform c precursor	IPI00607693	68199.60938	6.15	12	712.789978	100	97.69999695	100	1.855502926	0.30434818	13
GLUD1 Glutamate dehydrogenase 1, mitochondrial precursor	IPI00016801	66531.63281	7.66	9	532	100	87.05000305	100	1.855199834	0.332353267	12
HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein	IPI00003865	78958.95313	5.37	8	423.2900085	100	104.3099976	100	1.832232068	0.340100389	8
MDH2 Malate dehydrogenase, mitochondrial precursor	IPI00291006	39765.08984	8.92	2	108.9799957	100	68.69999695	99.99867871	1.79912193	0.206352254	2
CS citrate synthase precursor, isoform b	IPI00383539	50469.26172	6.74	2	74.97000122	99.99968811	38.63999939	98.66032971	1.709230926	0.666050215	2

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HSP90AB1 Heat shock protein HSP 90-beta	IPI00414676	94433.0625	4.97	6	382.5299988	100	93.37999725	100	1.689681444	0.308332847	6
GANAB Isoform 3 of Neutral alpha-glucosidase AB precursor	IPI00441414	99842.15625	5.43	2	129.8999939	100	69.69999695	99.99895046	1.671290838	5.73E-02	2
PC Pyruvate carboxylase, mitochondrial precursor	IPI00299402	138358.0469	6.37	1	71.01999664	99.99922554	71.01999664	99.99922554	1.654663251	0	1
CALR Protein	IPI00794237	19298.58594	4.47	1	68.75444031	99.99869517	69.93000031	99.9990046	1.616554253	0	1
TRAP1 57 kDa protein	IPI00646055	62264.14453	7.21	1	93.29000092	100	93.29000092	100	1.609612229	0	1
FDX1 Adrenodoxin, mitochondrial precursor	IPI00019326	20618.73047	5.51	2	99.33999634	100	59.38000107	99.9887021	1.597678239	0.393800917	2
EIF4A1 Eukaryotic initiation factor 4A-I	IPI00025491	49332.85938	5.32	1	76.16000366	99.99976286	76.16000366	99.99976286	1.593613043	0	1
GALK1 CDNA FLJ26554 fis, clone LNF01773, highly similar to Galactokinase	IPI00442827	44445.10938	6.81	1	51.36000061	99.92838602	51.36000061	99.92838602	1.588110518	0	1
ALDH1L1 Formyltetrahydrofolate dehydrogenase isoform a variant	IPI00793673	109020.6328	5.63	1	61.16999817	99.99251834	61.16999817	99.99251834	1.556089548	0	1
- Ig kappa chain V-III region SIE	IPI00387115	12435.95996	8.7	1	50.31999969	99.90900911	50.31999969	99.90900911	1.552926352	0	1
ETFA 24 kDa protein	IPI00792673	27117.09961	8.77	1	94.65000153	100	94.65000153	100	1.5364581	0	1
COX5B Cytochrome c oxidase subunit 5B, mitochondrial precursor	IPI00021785	14879.07031	9.07	1	52.40000153	99.94363653	52.40000153	99.94363653	1.518099412	0	1
- FK506 binding protein12	IPI00759644	10743.65039	7.66	1	67.72000122	99.99834424	67.72000122	99.99834424	1.492913987	0	1
IMMT Isoform 3 of Mitochondrial inner membrane protein	IPI00470829	88364.21094	6.31	1	79.62000275	99.9998931	79.62000275	99.9998931	1.490259692	0	1
ETFB Isoform 2 of Electron transfer flavoprotein subunit beta	IPI00556451	41287.32813	6.78	3	121.7099991	100	46.27999878	99.76932635	1.476080466	0.193093175	3
HSPB1 Heat shock protein beta-1	IPI00025512	23966.66992	5.98	2	116.0499954	100	81.83999634	99.99993588	1.455065695	6.71E-02	2
LMNA Isoform C of Lamin-A/C	IPI00216952	70902.15625	6.4	9	479.0600281	100	96.04000092	100	1.436005451	0.266331249	9
HNRPA2B1 Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	IPI00414696	38478.16016	8.67	3	183.4744415	100	68.37999725	99.99857768	1.432510692	5.45E-02	3
ENO1 Isoform MBP-1 of Alpha-enolase	IPI00759806	41357.21094	5.93	2	133.6600037	100	82.93000031	100	1.4168123	2.63E-02	2
HSPA5 HSPA5 protein	IPI00003362	81398.29688	5.07	7	336.980011	100	59.56999969	99.98918571	1.407969116	0.275111092	7
CALR 37 kDa protein	IPI00793605	41138.14063	4.55	4	292.8500061	100	95.69000244	100	1.407363696	0.185347952	4
ACO2 Aconitase 2, mitochondrial	IPI00790739	96473.60938	6.97	2	92.36000061	100	53.18999863	99.95301081	1.401811635	0.311801625	2
KRT19 Keratin, type I cytoskeletal 19	IPI00479145	46225.37891	5.04	2	95.88000488	100	55.40000153	99.97175135	0.705240784	0.182244284	3

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PGM1 Phosphoglucomutase 1	IPI00844159	66935.90625	6.2	1	56.79000092	99.97948848	56.79000092	99.97948848	0.703240934	0	1
MDH1 Malate dehydrogenase, cytoplasmic	IPI00291005	41195.46094	6.91	2	88.06999969	100	47.68999863	99.83327605	0.695662402	0.106523689	2
ANXA4 annexin IV	IPI00793199	39558.51953	5.84	1	66.23999786	99.99767192	66.23999786	99.99767192	0.679906941	0	1
CTSB Cathepsin B precursor	IPI00295741	40882.91016	5.88	1	60.79999924	99.991853	60.79999924	99.991853	0.679439918	0	1
CA1 22 kDa protein	IPI00796435	23598.06055	7.1	2	120.6900024	100	78.69999695	99.99986787	0.677581592	0.323301754	2
BLVRB Flavin reductase	IPI00783862	23637.61914	7.13	2	98.02999878	100	51.36999893	99.9285507	0.656692705	0.10878359	2
CYP2C9 Cytochrome P450 2C9	IPI00007219	61374.14063	8.13	1	58.72999954	99.98687806	58.72999954	99.98687806	0.644867428	0	1
ACY1 Aminoacylase-1	IPI00009268	48344.23047	5.77	2	102.6600037	100	59.47000122	99.98893382	0.636258713	7.19E-02	2
GGTLA1 Isoform 2 of Gamma-glutamyltransferase 5 precursor	IPI00339373	61051.73828	7.67	1	52.38000107	99.94337636	52.38000107	99.94337636	0.61143345	0	1
- Histone 2, H3, pseudogene 2	IPI00455457	17482.80078	11.27	2	64.17999268	99.99625891	32.16999817	94.05710513	0.609401873	1.47E-02	2
BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101	49946.23828	6.58	3	135.5444489	100	60.06000137	99.99033954	0.605661601	0.124221284	3
HBG2;HBE1;HBG1 Hemoglobin subunit gamma-2	IPI00554676	18034.5293	6.64	2	117.3000031	100	59.5	99.98901	0.597563382	5.23E-02	6
HIST3H3 Histone H3.1t	IPI00216402	17606.75	11.13	2	71.22999573	99.9992621	39.06000137	98.78382036	0.593159983	0.030970553	2
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	58388.32813	6.3	4	210.3900146	100	87.55000305	100	0.587386985	0.142071743	4
HBA2;HBA1 Alpha 2 globin variant (Fragment)	IPI00853068	17045.16992	8.72	5	468.5	100	154.5599976	100	0.579116026	0.117389209	20
CAT Catalase	IPI00465436	64367.17969	6.9	6	286.1144409	100	64.13999939	99.9962243	0.564990742	0.107718904	6
HBD;HBB Hemoglobin subunit delta	IPI00473011	17865.5	7.85	9	751.6900024	100	127.4800034	100	0.534643197	0.103774477	24
S100A9 Protein S100-A9	IPI00027462	15007.73047	5.71	1	65.37999725	99.99716209	65.37999725	99.99716209	0.531443647	0	1
HBB Hemoglobin subunit beta	IPI00654755	17808.5	6.75	13	1154.079956	100	127.4800034	100	0.529018809	0.106601313	30
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C 41 kDa protein	IPI00004672	42978.55078	5.91	1	50.18000031	99.90602814	50.18000031	99.90602814	0.518442417	0	1
GPT Alanine aminotransferase 1	IPI00217458	57510.32813	6.77	1	64.27999878	99.99634407	64.27999878	99.99634407	0.508426217	0	1
HBD Hemoglobin Lepore-Baltimore (Fragment)	IPI00829896	12794.0498	6.17	8	654.4799805	100	127.4800034	100	0.503446252	9.16E-02	18
GSTA2 Glutathione S-transferase A2	IPI00745233	29104	8.51	4	192.9399872	100	63.34000015	99.99546061	0.491035057	0.127008813	4

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DCXR 26 kDa protein	IPI00797249	27252.58984	8.33	2	100.3399963	100	53.93999863	99.96046352	0.490472152	7.11E-02	2
KHK Isoform C of Ketohexokinase	IPI00216136	35220.62891	5.91	2	73.91000366	99.9996019	43.31000137	99.5429142	0.477136614	0.165093833	2
CPS1 Isoform 1 of Carbamoyl-phosphate synthase [ammonia], mitochondrial pre	IPI00011062	180875.9531	6.3	30	1745.524536	100	108.4700012	100	0.473984526	0.119502488	31
FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	41289.14844	6.54	2	132.8800049	100	70.26999664	99.99907955	0.431392685	0.115631656	3
UGP2 Isoform 2 of UTP--glucose-1-phosphate uridylyltransferase	IPI00395676	61684.64063	7.69	2	75.56999969	99.99972836	41.09000015	99.23792476	0.427843059	0.13356807	2
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1406	5.6	2	110.9899979	100	59.91999817	99.99002304	0.41446507	9.92E-02	2
ADH1B Alcohol dehydrogenase 1B	IPI00473031	45270.91016	8.63	5	354.6199951	100	88.48999786	100	0.407071247	7.90E-02	5
COL1A2 Collagen alpha-2(I) chain precursor	IPI00304962	136968.0469	9.08	2	165.0800018	100	104.8799973	100	0.364272738	0.214838564	2
HRSP12 Ribonuclease UK114	IPI00005038	15826.7998	8.74	1	58.65999985	99.98666485	58.65999985	99.98666485	0.341732609	0	1
ASS1 Argininosuccinate synthase	IPI00640430	24839.67969	6.84	3	122.1900024	100	53.63999939	99.95763591	0.341630088	0.109785502	3
- 105 kDa protein	IPI00794900	115433.2422	7.3	2	86.55000305	100	51.61999893	99.93254751	0.327526764	9.99E-02	2
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	43462.35156	8	7	426.7044373	100	111.5999985	100	0.28944962	0.127992437	9
DEFA3 Neutrophil defensin 3 precursor	IPI00021827	10946.21973	5.71	2	67.43000031	99.9982299	33.84000015	95.95426112	0.269986635	6.04E-02	2

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio * (117/116)	iTRAQ Standard Deviation * (117/116)	iTRAQ Peptides (117/116)
FDX1 Adrenodoxin, mitochondrial precursor	IPI00019326	20618.73047	5.51	2	99.33999634	100	59.38000107	99.9887021	20.0779693	3.243283157	2
CYP11B1 cytochrome P450, family 11, subfamily B, polypeptide 1 isoform 2 pr	IPI00167781	52252.19922	8.89	2	87.00444031	100	50.79999924	99.91852996	19.5190535	4.545414295	2
AKR1B1 Aldose reductase	IPI00413641	39896.82031	6.51	3	122.8499985	100	59.70999908	99.98952876	15.2378072	5.92131971	3
FDXR Isoform Long of NADPH:adrenodoxin oxidoreductase, mitochondrial precur	IPI00221118	57594.57813	8.67	5	235.1499939	100	69.37999725	99.99887021	5.32286014	2.784525834	5
HBG2;HBE1;HBG1 Hemoglobin subunit gamma-2	IPI00554676	18034.5293	6.64	2	117.3000031	100	59.5	99.98901	4.34617298	0.712485189	6
TPP1 Isoform 3 of Tripeptidyl-peptidase 1 precursor	IPI00554538	62032.14844	5.94	2	146.3399963	100	85.87999725	100	4.1776737	1.604676874	2
HBB Hemoglobin subunit beta	IPI00654755	17808.5	6.75	13	1154.079956	100	127.4800034	100	3.92374306	2.569823908	30
HBA2;HBA1 Alpha 2 globin variant (Fragment)	IPI00853068	17045.16992	8.72	5	468.5	100	154.5599976	100	3.85949225	1.759290529	20
HBD;HBB Hemoglobin subunit delta	IPI00473011	17865.5	7.85	9	751.6900024	100	127.4800034	100	3.55122879	2.779269289	24
HBD Hemoglobin Lepore-Baltimore (Fragment)	IPI00829896	12794.0498	6.17	8	654.4799805	100	127.4800034	100	3.30995209	2.269645048	18
CA1 22 kDa protein	IPI00796435	23598.06055	7.1	2	120.6900024	100	78.69999695	99.99986787	3.05340875	3.638452979	2
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	68931.10156	5.7	7	437.0189209	100	101.2300034	100	2.97814028	1.033906592	8
HSPE1 10 kDa heat shock protein, mitochondrial	IPI00220362	12653.11035	8.89	6	309.730011	100	65.75	99.99739386	2.72746901	0.947192228	9
VIL2 Ezrin	IPI00843975	77526.5	5.94	2	96.58999634	100	51.29999924	99.92738975	2.69835761	0.904637588	2
HSPA9 Stress-70 protein, mitochondrial precursor	IPI00007765	81497.46094	5.87	4	237.5700073	100	98.48000336	100	2.59049674	0.448583396	4
ASAH1 ASAH1 protein	IPI00059685	48400.71094	7.52	2	70.68000031	99.99916	36.27999878	97.69326351	2.57945488	0.785334516	2
SERPINB6 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), me	IPI00749398	46902.42188	5.18	1	73.79000092	99.99959	73.79000092	99.99959074	2.3665219	0	1
DLD Dihydrolipoyl dehydrogenase, mitochondrial precursor	IPI00015911	60048.35938	7.59	1	67.94000244	99.99843	67.94000244	99.99842603	2.36154782	0	1
FGB Fibrinogen beta chain precursor	IPI00298497	61772.66016	8.54	3	126.1300049	100	53.13000107	99.95235715	2.32625421	0.219844022	3
PAPSS2 Isoform B of Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synt	IPI00220873	76578.32813	8.18	1	61.13999939	99.99247	61.13999939	99.99246648	2.31873375	0	1

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FGA Isoform 2 of Fibrinogen alpha chain precursor	IPI00029717	76032.28906	8.23	2	173.0100098	100	91.41000366	100	2.26689511	0.326301945	3
PRDX2 16 kDa protein	IPI00375400	18010.59961	6.13	4	218.9100037	100	79.73999786	99.99989601	2.21949693	0.783754503	4
HSPA6 Heat shock 70 kDa protein 6	IPI00339269	77112.71094	5.81	5	327.7600098	100	118.5800018	100	2.21007407	0.430648475	5
HSPA1A;HSPA1B heat shock 70kDa protein 1A	IPI00845339	77569.67969	5.48	7	414.2700195	100	118.5800018	100	2.12533543	0.395428783	7
RDX Radixin	IPI00017367	78406.29688	6.03	2	104.2144394	100	54.09000015	99.96180576	2.10524166	8.79E-02	2
VIL2 Cytovillin 2 (Fragment)	IPI00384282	18443.30078	9.32	1	51.29999924	99.92739	51.29999924	99.92738975	2.02085574	0	1
PEBP1 Phosphatidylethanolamine-binding protein 1	IPI00219446	23439.92969	7.01	6	290.5799866	100	79.95999908	99.99990115	2.01120544	0.328686366	7
HSPB6 Heat-shock protein beta-6	IPI00022433	19439.91992	7.9	1	51.83000183	99.93573	51.83000183	99.93573157	1.98811072	0	1
HIBADH 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	IPI00013860	38652.03125	8.38	1	72.51999664	99.99945	72.51999664	99.99945173	1.93354793	0	1
DLST Dihydrolipoyllysine-residue succinyltransferase component of 2- oxoglu	IPI00420108	52917.75	9.01	2	95.69999695	100	62.45000076	99.99442817	1.84077688	0.301294237	2
NME2;NME1 Nucleoside diphosphate kinase B	IPI00026260	19395.17969	8.52	3	134.3600006	100	67.33999634	99.99819283	1.80766451	0.27114135	3
PGK1 Phosphoglycerate kinase 1	IPI00169383	51100.66016	8.3	2	79.06999969	99.99988	43.93000031	99.60372394	1.80377091	0.128355825	3
PRDX3 peroxiredoxin 3 isoform b	IPI00374151	27924.48047	7.04	2	66.33999634	99.99772	35.93000031	97.49966711	1.7731312	0.186533349	2
PARK7 Protein DJ-1	IPI00298547	22464.75	6.33	3	190.6999969	100	80.77999878	99.99991815	1.76730078	0.126417256	3
IMMT Isoform 3 of Mitochondrial inner membrane protein	IPI00470829	88364.21094	6.31	1	79.62000275	99.99989	79.62000275	99.9998931	1.71882258	0	1
ANXA5 Annexin A5	IPI00329801	39272.76172	4.94	5	275.3099976	100	89.29000092	100	1.71813522	0.236741215	5
ACADVL Isoform 2 of Very-long-chain specific acyl-CoA dehydrogenase, mitoch	IPI00178744	78527.97656	9.06	2	84.43000031	100	52.02000046	99.93848262	1.70162525	0.183194585	2
HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein	IPI00003865	78958.95313	5.37	8	423.2900085	100	104.3099976	100	1.69971483	0.442463165	8
hCG_2015269 similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase i	IPI00453476	31706.10938	6.67	2	96.81999969	100	51.50999832	99.93081722	1.6992601	6.60E-02	2
CS citrate synthase precursor, isoform b	IPI00383539	50469.26172	6.74	2	74.97000122	99.99969	38.63999939	98.66032971	1.69325536	0.624091275	2
- FK506 binding protein12	IPI00759644	10743.65039	7.66	1	67.72000122	99.99834	67.72000122	99.99834424	1.67101887	0	1
HSP90AB1 Heat shock protein HSP 90-beta	IPI00414676	94433.0625	4.97	6	382.5299988	100	93.37999725	100	1.63770625	0.542045666	6

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MDH2 Malate dehydrogenase, mitochondrial precursor	IPI00291006	39765.08984	8.92	2	108.9799957	100	68.69999695	99.99867871	1.62501412	2.78E-02	2
SPTBN1 Isoform Short of Spectrin beta chain, brain 1	IPI00328230	275951.75	5.31	2	69.13444519	99.9988	35.97999954	97.52828775	1.59769178	0.116097345	2
HNRPA2B1 Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	IPI00414696	38478.16016	8.67	3	183.4744415	100	68.37999725	99.99857768	1.55473451	9.47E-02	3
HSP90AA1 Isoform 1 of Heat shock protein HSP 90-alpha	IPI00784295	96593.6875	4.94	7	401.8800049	100	93.37999725	100	1.5363124	0.27533818	7
YWHAG 14-3-3 protein gamma	IPI00220642	31015.18945	4.8	4	195.6199951	100	65.08999634	99.99696612	1.52296308	0.716977505	5
TPM3 Isoform 2 of Tropomyosin alpha-3 chain	IPI00218319	32655.08008	4.75	2	84	100	47.56000137	99.82821006	1.52071787	0.51817041	3
TPM4 Isoform 1 of Tropomyosin alpha-4 chain	IPI00010779	32340.88086	4.67	3	131.7900085	100	48.59999847	99.86479336	1.4859766	0.426875432	4
MSN Moesin	IPI00219365	76942.64063	6.08	2	98.42443848	100	51.29999924	99.92738975	1.46340782	0.557447884	2
ATP5B ATP synthase subunit beta, mitochondrial precursor	IPI00303476	59980.98828	5.26	6	317.6644592	100	79.31999969	99.99988545	1.45716526	0.534449321	6
S100A9 Protein S100-A9	IPI00027462	15007.73047	5.71	1	65.37999725	99.99716	65.37999725	99.99716209	1.43111454	0	1
YWHAZ 14-3-3 protein zeta/delta	IPI00021263	30890.03906	4.73	4	233.2299805	100	82.76999664	99.99994824	1.40385995	0.474095802	5
TUFM Tu translation elongation factor, mitochondrial	IPI00027107	54583.71875	7.26	4	190.6499939	100	70.38999939	99.99910464	1.400834	0.195583744	5
TRAP1 57 kDa protein	IPI00646055	62264.14453	7.21	1	93.29000092	100	93.29000092	100	1.39096819	0	1
UGT1A10;UGT1A6 UDP-glucuronosyltransferase 1-10 precursor	IPI00233885	64734.48828	6.88	2	92.33000183	100	47.15000153	99.81120186	0.70832374	0.11236795	3
ALDH2 Mitochondrial aldehyde dehydrogenase 2 variant (Fragment)	IPI00792207	61065.96094	6.63	4	178.8300018	100	60.02000046	99.99025015	0.70086969	9.21E-02	4
PGM1 Phosphoglucomutase 1	IPI00844159	66935.90625	6.2	1	56.79000092	99.97949	56.79000092	99.97948848	0.67844088	0	1
DBI Isoform 2 of Acyl-CoA-binding protein	IPI00218836	13802.13965	5.41	2	78.49000549	99.99986	47.95000076	99.84296452	0.67356881	0.468389318	2
COL6A3 alpha 3 type VI collagen isoform 3 precursor	IPI00072917	345457.3438	6.47	15	639.0344849	100	68.26000214	99.99853783	0.67194973	0.158312144	15
ACAA1 17 kDa protein	IPI00790196	18819	9.39	2	95.22000122	100	58.45999908	99.98603638	0.66614352	0.143166834	2
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1406	5.6	2	110.9899979	100	59.91999817	99.99002304	0.66469585	0.118793491	2
ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	IPI00001539	46153.96875	8.32	5	276.7399902	100	85.08000183	100	0.66459384	0.346219958	5
ALDH1A1 Retinal dehydrogenase 1	IPI00218914	60949.39063	6.3	5	216	100	54.45999908	99.96492498	0.64280386	0.280001415	5

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TST Thiosulfate sulfurtransferase	IPI00216293	35752.05859	6.77	6	306.3644409	100	80.23000336	99.9999071	0.62546074	0.319512346	6
SCP2 sterol carrier protein 2 isoform 2	IPI00433347	61608.94141	6.25	1	73.46443939	99.99956	74.63999939	99.99966349	0.62491901	0	1
UGP2 Isoform 2 of UTP--glucose-1-phosphate uridylyltransferase	IPI00395676	61684.64063	7.69	2	75.56999969	99.99973	41.09000015	99.23792476	0.62202285	0.12838789	2
ALDH1L1 Formyltetrahydrofolate dehydrogenase isoform a variant	IPI00793673	109020.6328	5.63	1	61.16999817	99.99252	61.16999817	99.99251834	0.62121347	0	1
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	58388.32813	6.3	4	210.3900146	100	87.55000305	100	0.60627287	0.127901868	4
GSTO1 Glutathione transferase omega-1	IPI00019755	31234.35938	6.23	1	56.38999939	99.97751	56.38999939	99.97750956	0.59766343	0	1
EHHADH Peroxisomal bifunctional enzyme	IPI00216164	86466.10156	9.22	3	142.6100006	100	72	99.99938199	0.59202575	0.148665904	3
PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904	82667.8125	4.96	4	157.3600006	100	55.02000046	99.96916828	0.58048645	0.263627762	4
UGDH UDP-glucose 6-dehydrogenase	IPI00031420	60869.64844	6.73	3	159.980011	100	68.37000275	99.9985744	0.57196598	0.28190222	3
CAT Catalase	IPI00465436	64367.17969	6.9	6	286.1144409	100	64.13999939	99.9962243	0.56456156	0.225109723	6
FASN Fatty acid synthase	IPI00847250	287598.7813	5.99	2	104.1900024	100	60.38999939	99.9910464	0.555684	0.376295845	2
GSTA2 Glutathione S-transferase A2	IPI00745233	29104	8.51	4	192.9399872	100	63.34000015	99.99546061	0.55484335	0.170097667	4
ACADS Short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	IPI00027701	47857.05859	8.13	1	54.95000076	99.96867	54.95000076	99.9686673	0.53320085	0	1
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	35335.42969	8.34	4	247.7799988	100	76.30000305	99.99977039	0.53309522	0.265723652	4
ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria	IPI00024990	63211.07813	8.72	2	75.59999847	99.99973	45.27000046	99.70892975	0.52783435	0.097173422	2
GLUD1 Glutamate dehydrogenase 1, mitochondrial precursor	IPI00016801	66531.63281	7.66	9	532	100	87.05000305	100	0.52717968	0.256583702	12
SULT2A1 Bile salt sulfotransferase	IPI00216133	37496.32813	5.71	1	35.65999985	97.33929	35.65999985	97.33928793	0.49699235	5.49E-02	2
GALK1 CDNA FLJ26554 fis, clone LNF01773, highly similar to Galactokinase	IPI00442827	44445.10938	6.81	1	51.36000061	99.92839	51.36000061	99.92838602	0.49670223	0	1
ANXA4 annexin IV	IPI00793199	39558.51953	5.84	1	66.23999786	99.99767	66.23999786	99.99767192	0.49433877	0	1
RRBP1 Isoform 1 of Ribosome-binding protein 1	IPI00220967	178629.8125	8.73	2	92.01000214	100	51.31000137	99.92755678	0.48021297	0.160008974	2
CYP2C9 Cytochrome P450 2C9	IPI00007219	61374.14063	8.13	1	58.72999954	99.98688	58.72999954	99.98687806	0.47279856	0	1
PC Pyruvate carboxylase, mitochondrial precursor	IPI00299402	138358.0469	6.37	1	71.01999664	99.99923	71.01999664	99.99922554	0.46704795	0	1

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CES2 carboxylesterase 2 isoform 1	IPI00332828	72247.0625	6.03	1	61.04999924	99.99231	61.04999924	99.99230873	0.46436769	0	1
CBR1 Carbonyl reductase [NADPH] 1	IPI00295386	33322.12891	8.55	2	160.5400085	100	86.30000305	100	0.4477089	0.112624062	2
AKR1C3 Aldo-keto reductase family 1 member C3	IPI00291483	41031.17969	8.05	4	198.3399963	100	63.93000031	99.99603724	0.43815841	0.263827719	4
AGXT Serine--pyruvate aminotransferase	IPI00009367	46426.73047	8.61	2	87.47000122	100	56.11999893	99.97606695	0.42967645	0.158243779	2
PCK2 Phosphoenolpyruvate carboxykinase [GTP], mitochondrial precursor	IPI00294380	74737.8125	7.56	8	377.519989	100	59.34000015	99.98859756	0.42267296	0.249940893	9
UGT2B17 UDP-glucuronosyltransferase 2B17 precursor	IPI00026932	67707.59375	8.76	1	62.15999985	99.99404	62.15999985	99.99404341	0.42169992	0	1
GPT Alanine aminotransferase 1	IPI00217458	57510.32813	6.77	1	64.27999878	99.99634	64.27999878	99.99634407	0.41174066	0	1
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	61418.91016	8.17	1	64.84999847	99.99679	64.84999847	99.99679375	0.41136028	0	1
HMGCS2 Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor	IPI00008934	61333.76953	8.4	4	159.3999939	100	50.04999924	99.90317267	0.40378244	0.816362544	5
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	43936.05859	8.75	3	197.2000122	100	109.9100037	100	0.39893402	0.30165356	3
LOC645619 similar to Adenylate kinase isoenzyme 4, mitochondrial	IPI00738805	27444.46094	8.47	2	70.94000244	99.99921	37.63999939	98.31345503	0.39828753	0.126782541	2
ASS1 Argininosuccinate synthase	IPI00640430	24839.67969	6.84	3	122.1900024	100	53.63999939	99.95763591	0.39349609	0.099698287	3
FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	41289.14844	6.54	2	132.8800049	100	70.26999664	99.99907955	0.38934455	0.187888274	3
UGT2B4 UDP-glucuronosyltransferase 2B4 precursor	IPI00301491	66843.75	8.7	2	138.9700012	100	76.80999756	99.99979583	0.38891897	3.28E-02	2
ALDH4A1 Aldehyde dehydrogenase 4 family, member A1	IPI00647328	65056.12109	7.62	5	248.8899994	100	86.48999786	100	0.37204929	0.107857862	5
MAT1A S-adenosylmethionine synthetase isoform type-1	IPI00021772	47392.28906	5.86	2	127.1544418	100	83.33999634	100	0.34340523	0.119832949	2
DCXR 26 kDa protein	IPI00797249	27252.58984	8.33	2	100.3399963	100	53.93999863	99.96046352	0.32498072	0.16360878	2
FTL Ferritin light chain	IPI00852596	21925.33984	5.51	2	105.5099945	100	54.77999878	99.96741648	0.32494578	6.32E-02	2
CYB5A Isoform 1 of Cytochrome b5	IPI00397860	16616.71094	4.88	4	379.5599976	100	183.6000061	100	0.32475639	0.174978719	5
BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101	49946.23828	6.58	3	135.5444489	100	60.06000137	99.99033954	0.3175794	0.239291426	3
ADH1B Alcohol dehydrogenase 1B	IPI00473031	45270.91016	8.63	5	354.6199951	100	88.48999786	100	0.30077176	0.167153887	5
- 14 kDa protein	IPI00788848	15907.24023	5.24	5	308.8699951	100	93.13999939	100	0.29774664	0.314847323	6

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ADH4 Alcohol dehydrogenase 4	IPI00218899	45828.03125	8.25	2	82.66000366	99.99995	43.86999893	99.59821107	0.29671189	3.62E-03	2
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	48966.78125	6.61	6	364.9199829	100	89.69000244	100	0.29328238	0.122597401	6
HRSP12 Ribonuclease UK114	IPI00005038	15826.7998	8.74	1	58.65999985	99.98666	58.65999985	99.98666485	0.27811037	0	1
AKR1D1 CDNA FLJ25413 fis, clone TST03402, highly similar to 3-OXO-5-BETA-	IPI00065073	33300.88672	8.11	1	54.40000153	99.96444	54.40000153	99.96443706	0.26220713	0	1
KRT8 Keratin, type II cytoskeletal 8	IPI00554648	58423.62891	5.52	12	681.9089355	100	86.61000061	100	0.25766139	0.13024774	12
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	43462.35156	8	7	426.7044373	100	111.5999985	100	0.25307092	0.155003019	9
KRT18 Keratin, type I cytoskeletal 18	IPI00784347	51196.89844	5.34	10	420.6199951	100	67.43000031	99.9982299	0.24618872	0.200161765	11
- 105 kDa protein	IPI00794900	115433.2422	7.3	2	86.55000305	100	51.61999893	99.93254751	0.23882092	0.15006211	2
CES1 carboxylesterase 1 isoform c precursor	IPI00607693	68199.60938	6.15	12	712.789978	100	97.69999695	100	0.23456105	0.289282143	13
CPS1 Isoform 1 of Carbamoyl-phosphate synthase [ammonia], mitochondrial pre	IPI00011062	180875.9531	6.3	30	1745.524536	100	108.4700012	100	0.23079239	0.217635843	31
ACY1 Aminoacylase-1	IPI00009268	48344.23047	5.77	2	102.6600037	100	59.47000122	99.98893382	0.19060681	9.14E-02	2
KHK Isoform C of Ketohexokinase	IPI00216136	35220.62891	5.91	2	73.91000366	99.9996	43.31000137	99.5429142	0.18216674	0.173504471	2
KRT19 Keratin, type I cytoskeletal 19	IPI00479145	46225.37891	5.04	2	95.88000488	100	55.40000153	99.97175135	0.15999566	8.66E-02	3
ARG1 Isoform 1 of Arginase-1	IPI00291560	38451.66016	6.72	1	58.56000137	99.98635	58.56000137	99.98635424	0.07846065	0	1

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio * (115/114)	iTRAQ Standard Deviation * (115/114)	iTRAQ Peptides (115/114)
LTBP2 Latent-transforming growth factor beta-binding protein 2 precursor	IPI00292150	207622.5469	5.08	1	62.54000092	99.99492142	62.54000092	99.99492142	104.658011	0	1
MT1X Metallothionein-1X	IPI00008753	8279.200195	8.38	2	128.0400085	100	84.55000305	100	23.9242234	19.45809266	2
MT1H;MT1P2 Metallothionein-1H	IPI00008750	8394.240234	8.49	2	105.9499969	100	62.45999908	99.994827	21.2395437	12.95268355	2
MT1E Metallothionein-1E	IPI00025461	8225.160156	8.38	2	118.9500046	100	84.55000305	100	20.5229264	2.29E+01	2
MT1M Metallothionein-1M	IPI00642651	8033.149902	8.05	2	122.9000015	100	84.55000305	100	19.0680509	2.43E+01	2
- Metallothionein-1F	IPI00746270	15151.62012	8.17	2	105.6300049	100	71.23000336	99.99931334	18.8218372	17.66684305	2
PRELP Prolargin precursor	IPI00020987	46264.33984	9.47	8	448.0200195	100	84.88999939	100	12.7707615	2.670195955	8
FBLN5 Full-length cDNA clone CS0DI085YI08 of Placenta of Homo sapiens	IPI00382428	56833.08984	4.57	3	132.1799927	100	56.20000076	99.97813537	8.65992717	6.679735521	3
OGN Osteoglycin	IPI00515092	34941.69141	8.49	4	177.2900085	100	49.52999878	99.8984354	8.20476636	2.306501125	4
ASPN ASPN protein	IPI00418431	49081.85938	6.03	3	112.2100067	100	42.58000183	99.49679837	7.52104415	2.804192992	3
AKR1B10 Aldo-keto reductase family 1 member B10	IPI00105407	41078.28125	7.12	7	490.6300049	100	97.18000031	100	6.84119627	2.656214326	7
LUM Lumican precursor	IPI00020986	42425.12891	6.16	9	529.9744263	100	85.91999817	100	6.81407128	2.426430431	9
POSTN Isoform 2 of Periostin precursor	IPI00218585	96544.46875	7.87	1	62.83000183	99.99524947	62.83000183	99.99524947	6.70785702	0	1
COL1A2 Collagen alpha-2(I) chain precursor	IPI00304962	136968.0469	9.08	2	131.8500061	100	85.20999908	100	6.52690877	1.448670728	2
BGN Biglycan preproprotein variant (Fragment)	IPI00643384	45356.82031	7.16	7	529.0999756	100	138.6000061	100	6.37695415	2.563716411	7
CFL1 24 kDa protein	IPI00784459	28091.64063	8.13	3	230.4200134	100	90.93000031	100	6.13607265	20.27122084	3
DCN Isoform A of Decorin precursor	IPI00012119	44030.19922	8.75	3	204.0944519	100	89.51000214	100	5.99276418	1.162174019	3
TAGLN Transgelin	IPI00216138	25234.73047	8.87	7	393.2200317	100	96.01000214	100	5.44227728	7.678081372	8
CSRP1 Cysteine and glycine-rich protein 1	IPI00442073	24699.9707	8.9	3	297.3399963	100	168.1399994	100	5.43849809	3.155947561	3
CLU clusterin isoform 1	IPI00400826	62857.89844	6.24	3	200.7744446	100	92.27999878	100	5.28852796	3.599673089	3
LSP1 50 kDa protein	IPI00554652	54843.82031	5.42	1	92.48000336	100	92.48000336	100	5.23139084	0	1
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1406	5.6	4	287.7600098	100	98.44000244	100	4.89498933	1.891593154	4

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NID1 Isoform 2 of Nidogen-1 precursor	IPI00384542	127664.8828	5.29	2	121.8199997	100	77.61000061	99.99984197	4.78397404	2.612946878	2
IGFBP7 Insulin-like growth factor-binding protein 7 precursor	IPI00016915	32243.50977	8.25	1	61.40000153	99.99339699	61.40000153	99.99339699	4.45164234	0	1
FLNA Filamin-A	IPI00333541	305957.375	5.7	29	2074.378174	100	134.0500031	100	4.22114196	2.073562741	29
HIST2H2AB Histone H2A type 2-B	IPI00216730	16003.11035	10.88	2	73.97000122	99.99963462	41.65000153	99.3766355	3.94987782	0.530556835	2
VIM Vimentin	IPI00418471	56977.44141	5.06	25	1802.358765	100	136.3699951	100	3.91551457	1.264033399	25
CALD1 Isoform 2 of Caldesmon	IPI00218694	76226.46875	6.37	4	288.1199951	100	107.3099976	100	3.87340549	1.637916455	4
COL14A1 Isoform 3 of Collagen alpha-1(XIV) chain precursor	IPI00402215	195721.9844	5.16	5	381.1444397	100	135.8600006	100	3.83547973	2.46855347	5
HSPB6 Heat-shock protein beta-6	IPI00022433	19439.91992	7.9	2	77.02999878	99.99981939	45.70000076	99.75467481	3.63087591	0.153739909	2
ANXA2 Annexin A2	IPI00455315	43516.26953	7.57	13	894.2489624	100	142.4600067	100	3.5744064	1.896433874	14
HSPG2 Basement membrane-specific heparan sulfate proteoglycan core protein	IPI00024284	487110.1563	6.06	3	105.0067749	100	37.59999847	98.4160467	3.50153407	0.157090052	3
ARHGDIB 13 kDa protein	IPI00791712	14875.75977	4.69	1	116.0599976	100	116.0599976	100	3.49527137	0	1
MARCKS Myristoylated alanine-rich C-kinase substrate	IPI00219301	35850.28125	4.47	1	90.79000092	100	90.79000092	100	3.45338156	0	1
GSTP1 19 kDa protein	IPI00793319	20948.17969	5.67	2	137.4700012	100	90.75	100	3.44526495	4.76E-02	2
ALB Isoform 1 of Serum albumin precursor	IPI00745872	79715.90625	5.92	40	2784.528809	100	195.3800049	100	3.36749049	1.169666579	54
CRIP2 Cysteine-rich protein 2	IPI00006034	26434.21094	9.01	1	53.93000031	99.96312414	53.93000031	99.96312414	3.36661396	0	1
TAGLN2 24 kDa protein	IPI00647915	26448.48047	8.41	7	509.8900146	100	106.1100006	100	3.33269828	1.839249697	7
SERPINA1 Alpha-1-antitrypsin precursor	IPI00553177	51885.51172	5.37	14	954.3599243	100	115.3000031	100	3.25645762	1.270569399	14
TPM1 Isoform 3 of Tropomyosin alpha-1 chain	IPI00216135	38040.28906	4.72	7	411.734436	100	95.33000183	100	3.20212438	1.126004174	7
ANXA1 Annexin A1	IPI00549413	25333.10938	5.39	4	285.1400146	100	112.1699982	100	3.1737076	0.866148037	4
TPM4 Isoform 1 of Tropomyosin alpha-4 chain	IPI00010779	32340.88086	4.67	8	505.9144287	100	95.33000183	100	3.08817283	0.64967053	8
GSN Isoform 2 of Gelsolin precursor	IPI00646773	87445.10938	5.58	3	122.9599991	100	43.18000031	99.56172955	3.07178112	0.921114052	3
CNN3 Calponin-3	IPI00216682	40129.14844	5.69	1	55.27000046	99.97291417	55.27000046	99.97291417	3.06800245	0	1
VTN Vitronectin precursor	IPI00298971	57939.35156	5.55	6	280.3200073	100	73.66000366	99.99960759	3.06759651	1.177036838	6

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SERPINH1 CDNA FLJ16712 fis, clone UTERU2032279, highly similar to 47 kDa HE	IPI00442080	30003.93945	9.62	1	62.81000137	99.99522754	62.81000137	99.99522754	3.03424554	0	1
MYH11 smooth muscle myosin heavy chain 11 isoform SM2B	IPI00744256	254257.9219	5.44	8	545.8088989	100	144.9100037	100	2.99247621	1.827895861	8
LMNA Isoform C of Lamin-A/C	IPI00216952	70902.15625	6.4	20	1336.18457	100	129.7400055	100	2.9795141	0.562513271	20
LOC646913 similar to cell division cycle 10 isoform 1	IPI00737735	61445.96875	7.55	1	94.05999756	100	94.05999756	100	2.9734518	0	1
ACTG2 Actin, gamma-enteric smooth muscle	IPI00025416	45052.03906	5.31	16	1215.809937	100	171.8300018	100	2.9447524	2.362217172	22
LMNB1 Lamin-B1	IPI00217975	72358.14844	5.11	2	114.4199982	100	79.47000122	99.99989702	2.90208586	0.85401967	2
YWHAZ 14-3-3 protein zeta/delta	IPI00021263	30890.03906	4.73	10	767.694458	100	147.3800049	100	2.87645589	0.6446227	11
SET Isoform 2 of Protein SET	IPI00301311	35108.05859	4.12	1	66.54000092	99.99797818	66.54000092	99.99797818	2.87522486	0	1
MIF 12 kDa protein	IPI00790382	12661.19043	9.3	2	110.0899963	100	58.97999954	99.98847231	2.81211438	0.230462546	3
PKM2 Isoform M2 of Pyruvate kinase isozymes M1/M2	IPI00479186	63832.46094	7.96	5	329.75	100	109.0699997	100	2.79179249	1.791310373	5
FUS Fus-like protein (Fragment)	IPI00260715	55689.03125	9.46	2	144.7799988	100	72.94999695	99.99953789	2.79090173	1.061129248	2
IGKC IGKC protein	IPI00430808	27732.05078	6.15	4	405.3300171	100	169.0700073	100	2.78447743	0.383220055	4
TPM2 Isoform 2 of Tropomyosin beta chain	IPI00220709	38056.12109	4.63	7	450.6799927	100	95.33000183	100	2.76924719	1.409365656	7
ACTC1 Actin, alpha cardiac muscle 1	IPI00023006	45148.14063	5.23	16	1231.529907	100	171.8300018	100	2.75318541	1.942606295	23
- Hypothetical protein	IPI00807428	26545.32031	5.66	4	380.25	100	124.9400024	100	2.73325627	0.699173395	4
MYL6 17 kDa protein	IPI00744444	18920.58008	4.54	6	504	100	135.4100037	100	2.71287517	0.70382937	8
HNRPL heterogeneous nuclear ribonucleoprotein L isoform b	IPI00465225	54634.78125	7.22	1	91.26999664	100	91.26999664	100	2.71155933	0	1
IGLV3-25 IGLV3-25 protein	IPI00550162	27143.41992	5.23	4	379.6399841	100	124.9400024	100	2.67936233	0.745953638	4
ITGB1 integrin beta 1 isoform 1A precursor	IPI00645194	99377.10938	5.27	1	104.6800003	100	104.6800003	100	2.67136079	0	1
HNRPA1 Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	IPI00465365	37003.55078	9.27	5	350.9200134	100	115.3700027	100	2.64361214	0.86223201	5
ANXA5 Annexin A5	IPI00329801	39272.76172	4.94	10	643.960022	100	112.4300003	100	2.62216781	1.267939925	10
COL6A3 alpha 3 type VI collagen isoform 3 precursor	IPI00072917	345457.3438	6.47	35	1893.973511	100	127.8799973	100	2.61710408	0.884991847	36
HIST1H2BI;HIST1H2BG;HIST1H2BF;HIST1H2	IPI00020101	16921.91016	10.31	5	357.2099915	100	107.5100021	100	2.61105341	0.435735167	8

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COL6A2 Isoform 2C2 of Collagen alpha-2(VI) chain precursor	IPI00304840	117254.4375	5.85	4	192.9400024	100	75.01999664	99.99971309	2.55851357	0.694370684	4
COL6A3 alpha 3 type VI collagen isoform 4 precursor	IPI00072918	345401.0313	6.48	35	1887.693481	100	127.8799973	100	2.54926238	0.8218367	36
GGTLA1 Isoform 2 of Gamma-glutamyltransferase 5 precursor	IPI00339373	61051.73828	7.67	2	126.8100052	100	85.98000336	100	2.53733169	2.09E-01	2
SFPQ Isoform Long of Splicing factor, proline-and glutamine-rich	IPI00010740	81090.10938	9.45	3	224.2399902	100	111.5100021	100	2.53502581	0.429913032	3
HPX Hemopexin precursor	IPI00022488	55409.48047	6.55	2	119.8600006	100	75.11000061	99.99971898	2.52604094	6.33E-01	2
SERPINF1 25 kDa protein	IPI00796279	26706.00977	5.84	1	63.97000122	99.99634622	63.97000122	99.99634622	2.52410869	0	1
- Hypothetical protein	IPI00784807	56014.51953	6.56	6	367.8200073	100	84.55000305	100	2.50599106	1.295226003	6
CTSS Cathepsin S precursor	IPI00299150	42009.60938	8.61	2	102.1800003	100	68.06999969	99.99857852	2.46678877	0.894047237	2
- Ig kappa chain V-III region SIE	IPI00387115	12435.95996	8.7	1	79.19999695	99.99989042	79.19999695	99.99989042	2.43874871	0	1
- Ig kappa chain V-III region B6	IPI00387113	12295.89063	9.34	1	77.33677673	99.99983171	79.19999695	99.99989042	2.43874871	0	1
MYH10 Isoform 2 of Myosin-10	IPI00479307	260063.1719	5.46	11	768.4022217	100	144.9100037	100	2.43613307	0.452570188	11
LCP1 Plastin-2	IPI00010471	77185.35938	5.2	7	353.4099731	100	76.11000061	99.99977678	2.42810102	0.908979286	7
VCL Isoform 2 of Vinculin	IPI00307162	135558.7656	5.5	5	314.5144348	100	106.8600006	100	2.42535015	0.843440365	5
TPM3 tropomyosin 3 isoform 1	IPI00183968	38592.33984	4.68	5	321.2999878	100	95.33000183	100	2.42269262	1.191990153	5
ARL6IP5 PRA1 family protein 3	IPI00007426	23184.64063	9.77	1	52.77000046	99.95183382	52.77000046	99.95183382	2.40448552	0	1
IGHM IGHM protein	IPI00761159	57955.55078	7.53	10	806.7399292	100	132.1900024	100	2.40113246	0.913000549	10
HLA-DPB1 HLA class II histocompatibility antigen, DP(W4) beta chain precurs	IPI00103082	30666.89063	8.83	1	62.77999878	99.99519446	62.77999878	99.99519446	2.39997254	0	1
AHNAK AHNAK nucleoprotein isoform 1	IPI00021812	748355.625	5.8	4	224.1851196	100	89.66999817	100	2.39476711	1.2683173	4
NPM1 Isoform 1 of Nucleophosmin	IPI00549248	37589.32031	4.64	6	362.230011	100	104.3899994	100	2.37286745	0.490212817	6
- Hypothetical protein DKFZp686M24218	IPI00784998	57403.42969	7.89	4	245.0899963	100	84.55000305	100	2.37068051	0.763240113	4
- MHC-F3 REPEAT, fibronectin type III REPEAT=CLONE 3.9KF3-2	IPI00743608	191267.9063	4.89	3	132.1712341	100	56.95999908	99.98164551	2.34470743	0.487972031	3
IGHG1 Hypothetical protein DKFZp686P15220	IPI00645363	56996.17188	8.13	10	825.8999634	100	132.1900024	100	2.34429502	0.874852037	10
IGHA1 IGHA1 protein	IPI00166866	57142.32031	6.26	6	370.0299988	100	105.3799973	100	2.34145908	2.18E-01	7

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ACTG1;PSPHL Actin, cytoplasmic 2	IPI00021440	44922.05859	5.31	16	1344.609985	100	214.6799927	100	2.33200543	0.680408253	22
DKFZp686D0972 hypothetical protein LOC345651	IPI00003269	44988.21875	5.39	6	360.3200073	100	85.76000214	100	2.31383247	0.366666094	8
XRCC5 ATP-dependent DNA helicase 2 subunit 2	IPI00220834	92329.03906	5.55	2	71.95999908	99.99941958	40.38000107	99.16489302	2.3136101	6.09E-01	2
G3BP2 Isoform B of Ras GTPase-activating protein-binding protein 2	IPI00179890	53856.42969	5.27	1	55.70000076	99.97546748	55.70000076	99.97546748	2.30879692	0	1
ACTN2 Alpha-actinin-2	IPI00019884	112024.9219	5.31	6	276.4533386	100	66.94999695	99.99816032	2.25631397	0.258964121	7
TF Transferrin variant (Fragment)	IPI00798430	87365.92188	6.68	25	1678.903442	100	111.4899979	100	2.24823666	0.504521273	25
HNRPA3 Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	IPI00419373	42922.89844	9.1	4	364.6300049	100	172.4499969	100	2.24647791	0.274565562	4
COL4A2 Collagen type IV alpha 2	IPI00477950	179684.2344	8.86	2	91.20999908	100	58.72999954	99.98778925	2.24080758	1.64E-02	2
APOA1 Apolipoprotein A-I precursor	IPI00021841	34071.30859	5.56	6	287.7000122	100	65.45999908	99.99740736	2.23609317	0.36530168	6
FN1 Isoform 1 of Fibronectin precursor	IPI00022418	276716.375	5.45	11	526.9788818	100	64.12999725	99.99647838	2.19600038	1.034150409	11
C20orf77 Uncharacterized protein C20orf77	IPI00009659	41289.62109	5.73	1	58.81000137	99.98801213	58.81000137	99.98801213	2.17422432	0	1
- FK506 binding protein12	IPI00759644	10743.65039	7.66	1	54.33000183	99.96636883	54.33000183	99.96636883	2.14425899	0	1
COL6A1 Collagen alpha-1(VI) chain precursor	IPI00291136	117302.5391	5.26	4	258.6099854	100	100.1800003	100	2.14081077	1.219080756	5
COL18A1 Isoform 3 of Collagen alpha-1(XVIII) chain precursor	IPI00414694	141995.6406	6.04	3	141.230011	100	66.54000092	99.99797818	2.13652519	0.832744318	3
MYH9 Myosin-9	IPI00019502	257357.9844	5.5	42	3132.524414	100	144.9100037	100	2.12479204	0.656929606	43
IGHM Hypothetical protein DKFZp686I15212	IPI00418153	62655.28125	8.39	7	379.1400146	100	84.55000305	100	2.122753	0.627275333	7
XRCC6 70 kDa protein	IPI00465430	78696.84375	6.23	3	193.5500031	100	94.98000336	100	2.11794227	1.102584544	3
APCS Serum amyloid P-component precursor	IPI00022391	27335.35938	6.1	2	148.230011	100	79.61000061	99.99990029	2.10981998	0.376387643	2
YWHAQ 14-3-3 protein theta	IPI00018146	30857.03906	4.68	6	311.9400024	100	88.83000183	100	2.10728475	0.535643449	6
CAP1 Adenylyl cyclase-associated protein	IPI00639931	58646.21094	8.24	2	136.5599976	100	73.62000275	99.99960396	2.09801547	0.240358481	2
HIST3H2A Histone H2A type 3	IPI00031562	16129.2002	11.05	4	242.1699829	100	135.9299927	100	2.08742194	1.343221694	5
HDGF Hepatoma-derived growth factor	IPI00020956	30896.2793	4.7	2	118.7844391	100	72.22000122	99.99945331	2.08417928	0.414675489	2
SFN Isoform 2 of 14-3-3 protein sigma	IPI00411765	26671.25	4.77	4	189.7100067	100	54.90000153	99.97050543	2.07517412	0.362938173	4

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SRP9 Hypothetical protein DKFZp564M2223	IPI00419797	8474.950195	6.81	1	52.93999863	99.95368279	52.93999863	99.95368279	2.0519497	0	1
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C Isoform 1 of HLA class I histoco	IPI00472448	42869.39063	5.77	5	242.5700073	100	61.74000168	99.99389421	2.0391788	0.138453578	5
HNRPH2 Heterogeneous nuclear ribonucleoprotein H'	IPI00026230	51910.53125	5.89	5	268.5	100	99.12999725	100	2.03819639	0.51560158	5
KRT19 Keratin, type I cytoskeletal 19	IPI00479145	46225.37891	5.04	6	295.4400024	100	65.37999725	99.99735916	2.03661785	2.618510416	6
TTR 13 kDa protein	IPI00646384	14770.61035	5.34	3	221.7900085	100	95.23999786	100	2.02328728	0.223763829	3
EWSR1 CDNA FLJ32119 fis, clone PEBLM1000034, highly similar to RNA-	IPI00065554	65261.13281	9.43	1	53.86000061	99.96252496	53.86000061	99.96252496	2.0220847	0	1
ACTN1 Actinin alpha 1 isoform b	IPI00759776	114216.3906	5.25	20	1306.753296	100	139.1100006	100	2.01879239	0.42815741	21
HNRPH1 HNRPH1 protein	IPI00479191	53875.41016	6.33	5	288.3544312	100	99.12999725	100	2.01536292	0.559324779	5

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio * (117/116)	iTRAQ Standard Deviation * (117/116)	iTRAQ Peptides (117/116)
AKR1B10 Aldo-keto reductase family 1 member B10	IPI00105407	41078.28125	7.12	7	490.6300049	100	97.18000031	100	7.123890909	1.692446185	7
PGM2 Phosphoglucomutase-2	IPI00550364	75710.97656	6.28	2	153.0200043	100	102.2600021	100	4.448052748	2.146895462	3
LOC728320 similar to lactotransferrin	IPI00788271	62413.83984	6.43	2	136.8300018	100	76.44000244	99.99979311	3.779153087	1.074014684	2
HBD Hemoglobin Lepore-Baltimore (Fragment)	IPI00829896	12794.0498	6.17	9	727.8300171	100	137.0299988	100	3.625005948	1.39880615	11
HBB Hemoglobin subunit beta	IPI00654755	17808.5	6.75	13	1234.580078	100	139.4900055	100	3.31471078	1.418526684	18
OS9 amplified in osteosarcoma isoform 4 precursor	IPI00604451	80767.53125	4.81	1	65.12999725	99.99720268	65.12999725	99.99720268	3.314359622	0	1
SLC4A1 Erythroid anion exchange protein	IPI00788779	68660.35938	4.78	2	90.36000061	100	47.61999893	99.84233245	3.279293312	1.209274147	2
DEFA3 Neutrophil defensin 3 precursor	IPI00021827	10946.21973	5.71	2	66.11000061	99.99776775	33.18999863	95.62737376	3.254040647	0.342414917	2
HBD;HBB Hemoglobin subunit delta	IPI00473011	17865.5	7.85	13	1094.660034	100	137.0299988	100	3.246160908	0.679019173	15
S100A8 Protein S100-A8	IPI00007047	12745.88965	6.51	6	342.2744751	100	77.48000336	99.99983717	3.219759622	0.766994811	6
NUCB2 Nucleobindin-2 precursor	IPI00009123	57484.05078	5.03	2	126.3499985	100	71.94999695	99.99941824	2.899157565	1.007252253	2
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472282	42025.16016	5.89	4	205.4544373	100	61.74000168	99.99389421	2.843580489	0.817836584	4
HBG2;HBE1;HBG1 Hemoglobin subunit gamma-2	IPI00554676	18034.5293	6.64	2	84.96000671	100	51.81000137	99.93991832	2.815035465	0.172274998	2
S100A9 Protein S100-A9	IPI00027462	15007.73047	5.71	5	422.9100037	100	134.5599976	100	2.762495753	0.71043372	5
RPN2 Ribophorin II	IPI00383680	72001.89063	5.7	1	69.76999664	99.99903896	69.76999664	99.99903896	2.607302498	0	1
HBA2;HBA1 Alpha 2 globin variant (Fragment)	IPI00853068	17045.16992	8.72	6	582.5	100	229.7299957	100	2.591589199	0.761376222	19
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00026602	42374.19922	6.09	4	204.0400085	100	61.74000168	99.99389421	2.579925886	1.05386237	4
PKM2 Isoform M2 of Pyruvate kinase isozymes M1/M2	IPI00479186	63832.46094	7.96	5	329.75	100	109.0699997	100	2.54574153	0.639404747	5
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472138	41982.19141	5.9	5	276.2000122	100	63.97000122	99.99634622	2.537511395	0.853799057	5
SEL1L Isoform 2 of Sel-1 homolog precursor	IPI00555723	36763.62891	4.77	1	91.08999634	100	91.08999634	100	2.519071293	0	1
LSP1 50 kDa protein	IPI00554652	54843.82031	5.42	1	92.48000336	100	92.48000336	100	2.509160472	0	1
PYGB Glycogen phosphorylase, brain form	IPI00004358	105395.1719	6.4	2	87.47000122	100	54.81999969	99.96995707	2.385929941	0.212140518	2

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LYZ Lysozyme C precursor	IPI00019038	17902.35938	9.38	2	120.5200043	100	89.75	100	2.376883312	0.293678474	2
UBE1L2 Isoform 2 of Ubiquitin-activating enzyme E1-like protein 2	IPI00827491	73283.60156	7.29	2	94.93000031	100	48.06999969	99.85785151	2.367610106	0.363398914	2
WARS tryptophanyl-tRNA synthetase isoform b	IPI00412737	53848.82813	6.03	3	121.7200012	100	50.18999863	99.91275464	2.316721901	0.453871478	3
PKLR Pyruvate kinase L	IPI00743713	67899.96875	7.6	4	254.7200012	100	81.97000122	99.99994209	2.30529557	0.481581329	4
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C Isoform 1 of HLA class I histoco	IPI00472448	42869.39063	5.77	5	242.5700073	100	61.74000168	99.99389421	2.305110095	0.281869015	5
CA1 Carbonic anhydrase 1	IPI00215983	31634.69922	6.59	3	257.0899963	100	101.2900009	100	2.290426165	0.829497613	3
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472903	42843.35156	6.52	5	250.7000122	100	61.74000168	99.99389421	2.284441765	0.500516039	5
SERPINB1 Leukocyte elastase inhibitor	IPI00027444	47127.14063	5.9	2	170.8600006	100	118.9499969	100	2.270544388	0.715635753	2
GBP1 Interferon-induced guanylate-binding protein 1	IPI00028564	76194.35156	5.97	5	276.7299805	100	81.90000153	99.99994115	2.238426637	0.234848304	5
EIF5 Eukaryotic translation initiation factor 5	IPI00022648	56760.42188	5.41	1	66.48000336	99.99795006	66.48000336	99.99795006	2.186656479	0	1
CCT6A chaperonin containing TCP1, subunit 6A isoform b	IPI00552590	59959.64844	6.85	1	61.59999847	99.99369417	61.59999847	99.99369417	2.167958591	0	1
CANX Calnexin precursor	IPI00020984	75958.53906	4.47	7	465.5144348	100	83.55000305	100	2.145721468	0.30738692	7
PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904	82667.8125	4.96	17	1002.425659	100	142.8500061	100	2.138753623	0.433052752	17
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00644631	43142.39063	6.5	3	129.2600098	100	63.97000122	99.99634622	2.100769075	6.65E-02	3
MIF 12 kDa protein	IPI00790382	12661.19043	9.3	2	110.0899963	100	58.97999954	99.98847231	2.100398253	0.126610338	3
PDIA4 Protein	IPI00852792	21271.91992	8.33	5	274.0899963	100	86.45999908	100	2.087016322	0.250960018	5
VARS similar to Valyl-tRNA synthetase (Valine--tRNA ligase) (ValRS) (Protei	IPI00646425	42804.14844	9.44	1	57.88000107	99.98514946	57.88000107	99.98514946	2.078790881	0	1
EEF1G;LOC729998 similar to Elongation factor 1-gamma	IPI00738381	55298.73828	7.09	6	307.8099976	100	82.68000031	100	2.078047461	0.5442416	6
NME1;NME2 Nucleoside diphosphate kinase	IPI00604590	36163.17969	8.7	8	503.9377747	100	113.2799988	100	2.052168598	0.354718509	8
ARPC2 Actin-related protein 2/3 complex subunit 2	IPI00005161	38147.87109	6.84	1	65.26999664	99.99729141	65.26999664	99.99729141	2.048490828	0	1
ARL6IP5 PRA1 family protein 3	IPI00007426	23184.64063	9.77	1	52.77000046	99.95183382	52.77000046	99.95183382	2.048039321	0	1
HSPA5 HSPA5 protein	IPI00003362	81398.29688	5.07	22	1967.191406	100	151.8399963	100	2.036456694	0.232681477	23
- CDNA FLJ41483 fis, clone BRTHA2002808, highly similar to GAMMA- INTERFERO	IPI00446576	17847.26953	4.57	1	55.33000183	99.97328581	55.33000183	99.97328581	2.034800619	0	1

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MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472222	42679.30078	6.02	5	281.7744446	100	94.26999664	100	2.024358367	0.294927	5
PDIA3 55 kDa protein	IPI00657680	62595.51953	6.42	19	1612.418823	100	192.4400024	100	2.011223819	0.341646378	20
RAN 26 kDa protein	IPI00792352	29358.91016	8.51	3	139.8299866	100	67	99.99818138	2.000303418	0.324738723	3
FGB Fibrinogen beta chain precursor	IPI00298497	61772.66016	8.54	11	732.4000244	100	115.3000031	100	1.993790379	0.310594438	11
STAT1 Isoform Beta of Signal transducer and activator of transcription 1-al	IPI00218188	91515.17188	6.02	6	361.9700317	100	79.08000183	99.99988735	1.983432364	0.492587584	6
PSMA4 Proteasome subunit beta type	IPI00789638	30677.13086	6.91	1	63.59999847	99.99602129	63.59999847	99.99602129	1.966454743	0	1
SRP9 Hypothetical protein DKFZp564M2223	IPI00419797	8474.950195	6.81	1	52.93999863	99.95368279	52.93999863	99.95368279	1.95624833	0	1
LCP1 Plastin-2	IPI00010471	77185.35938	5.2	7	353.4099731	100	76.11000061	99.99977678	1.948382673	0.46354034	7
FDPS Farnesyl diphosphate synthase	IPI00101405	51970.89063	5.83	4	331.4300232	100	117.8700027	100	1.923686938	0.647013125	4
- Farnesyl pyrophosphate synthetase like-4 protein (Fragment)	IPI00382869	42840.89844	4.87	4	252.730011	100	102.9800034	100	1.923686938	0.647013125	4
C3 Complement C3 precursor (Fragment)	IPI00783987	204689.0469	6.02	8	397.230011	100	75.95999908	99.99976893	1.917471773	0.354338109	9
HNRPAB Isoform 1 of Heterogeneous nuclear ribonucleoprotein A/B	IPI00329355	41002.28906	9.04	2	94.48999786	100	54.22999954	99.96558544	1.914916618	0.360357999	2
CCT5 T-complex protein 1 subunit epsilon	IPI00010720	66337.35156	5.45	3	162.7399902	100	82.09999847	99.9999438	1.909663205	0.17252162	3
GBP2 GBP2 protein	IPI00848358	76021.07813	5.54	2	132.6799927	100	75.37999725	99.99973592	1.900440109	0.033929903	2
PDIA6 Isoform 1 of Protein disulfide-isomerase A6 precursor	IPI00644989	52733.64063	4.95	9	570.8900146	100	108.1800003	100	1.893954218	0.617604415	11
HSP90B1 Endoplasmin precursor	IPI00027230	104018.3516	4.76	23	1668.059937	100	138.4100037	100	1.887056529	0.388206162	24
NAPB Beta-soluble NSF attachment protein	IPI00748037	37843.85938	5.32	2	79.61000061	99.99990029	43.75	99.61563643	1.886482472	0.2151396	2
ARHGDIB 13 kDa protein	IPI00791712	14875.75977	4.69	1	116.0599976	100	116.0599976	100	1.872277198	0	1
CCT2 T-complex protein 1 subunit beta	IPI00297779	63200.62109	6.01	2	158.8399963	100	89.55999756	100	1.865851694	1.87E-02	2
CTSS Cathepsin S precursor	IPI00299150	42009.60938	8.61	2	102.1800003	100	68.06999969	99.99857852	1.859019847	0.214055188	2
EPHX1 Epoxide hydrolase 1	IPI00009896	57419.37891	6.77	13	796.0800781	100	102.8399963	100	1.854227328	0.456533738	14
EWSR1 CDNA FLJ32119 fis, clone PEBLM1000034, highly similar to RNA-	IPI00065554	65261.13281	9.43	1	53.86000061	99.96252496	53.86000061	99.96252496	1.852724885	0	1
ARPC3 12 kDa protein	IPI00796102	13215.08008	8.52	2	77	99.99981814	40.08000183	99.10516691	1.837952912	5.15E-02	2

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MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00646225	42792.37891	6.02	5	265.6544189	100	94.26999664	100	1.837015265	0.24886544	5
XRCC5 ATP-dependent DNA helicase 2 subunit 2	IPI00220834	92329.03906	5.55	2	71.95999908	99.99941958	40.38000107	99.16489302	1.830851987	0.18427055	2
PPIB peptidylprolyl isomerase B precursor	IPI00646304	27661.94922	9.42	10	713.3944702	100	105.7900009	100	1.815333042	0.168546768	11
SAMHD1 SAM domain and HD domain-containing protein 1	IPI00294739	79521.28906	6.69	3	119.7599945	100	43.88000107	99.62697142	1.805975726	0.614678945	3
RAB1B Ras-related protein Rab-1B	IPI00008964	24743.49023	5.55	1	81.81999969	99.99994006	81.81999969	99.99994006	1.80286808	0	1
CCT8 T-complex protein 1 subunit theta	IPI00784090	66090.99219	5.42	1	70.30999756	99.99915132	70.30999756	99.99915132	1.802445244	0	1
HYOU1 Hypoxia up-regulated protein 1 precursor	IPI00000877	122683.2188	5.16	7	475.25	100	139.1399994	100	1.793325289	0.402444295	7
SERPINB6 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), me	IPI00749398	46902.42188	5.18	1	69.33000183	99.99893649	69.33000183	99.99893649	1.792798806	0	1
DDOST dolichyl-diphosphooligosaccharide-protein glycosyltransferase precurs	IPI00297084	54075.30078	6.09	2	96.75	100	50.77999878	99.9238373	1.788077331	0.436364235	2
HNRPU heterogeneous nuclear ribonucleoprotein U isoform a	IPI00644079	101350.8203	5.76	3	183.8200073	100	84.73000336	100	1.779424994	0.699230604	3
LMAN2 Vesicular integral-membrane protein VIP36 precursor	IPI00009950	43071.33984	6.46	2	115.7400055	100	57.97000122	99.98545405	1.769161746	0.130659921	2
MARCKS Myristoylated alanine-rich C-kinase substrate	IPI00219301	35850.28125	4.47	1	90.79000092	100	90.79000092	100	1.761123681	0	1
TMEM4 Isoform 1 of MIR-interacting saposin-like protein precursor	IPI00443909	22355.31055	4.81	1	63.38000107	99.99581455	63.38000107	99.99581455	1.752790913	0	1
CFL1 24 kDa protein	IPI00784459	28091.64063	8.13	3	230.4200134	100	90.93000031	100	1.747577969	0.241923967	3
HSD17B4 Peroxisomal multifunctional enzyme type 2	IPI00019912	88068.99219	8.96	10	579.4000244	100	122.5	100	1.741526205	0.217869352	10
FUS Fus-like protein (Fragment)	IPI00260715	55689.03125	9.46	2	144.7799988	100	72.94999695	99.99953789	1.727308752	0.125416197	2
PRDX2 16 kDa protein	IPI00375400	18010.59961	6.13	7	430.25	100	116.0800018	100	1.722672783	0.280553283	7
CCT3 chaperonin containing TCP1, subunit 3 isoform c	IPI00552715	61849.64844	6.1	3	153.3900146	100	62.06000137	99.99432792	1.717416452	0.358002051	3
APOE Apolipoprotein E precursor	IPI00021842	38239.98828	5.65	7	451.1099854	100	114.8099976	100	1.696669467	0.260778943	7
CKAP4 CKAP4 protein (Fragment)	IPI00433214	72955.86719	9.34	4	349.0400085	100	132.6600037	100	1.693948501	0.490005217	4
UBE2L3 ubiquitin-conjugating enzyme E2L 3 isoform 2	IPI00386512	15678.38965	8.56	1	68.70999908	99.99877329	68.70999908	99.99877329	1.684709928	0	1
ECGF1 50 kDa protein	IPI00852987	52423.58984	5.36	2	115.1900024	100	59.70999908	99.99025589	1.678616426	0.241869527	2
GUSB Isoform Short of Beta-glucuronidase precursor	IPI00219516	72974.11719	6.48	2	81.22999573	99.99993133	48.04999924	99.85719537	1.676991052	4.82E-02	2

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ACTR3 Actin-like protein 3	IPI00028091	51165.26953	5.61	2	134.019989	100	67.20999908	99.99826722	1.676107829	0.110372498	2
METTL7A Methyltransferase-like protein 7A precursor	IPI00022300	30730.71094	8.7	2	153.6300049	100	113.4000015	100	1.668445027	8.81E-02	2
FKBP1A Peptidyl-prolyl cis-trans isomerase	IPI00647507	12759.03027	9.17	1	87.26999664	100	87.26999664	100	1.667848134	0	1
TUBB2A Tubulin beta-2A chain	IPI00013475	52501.16016	4.78	15	1204.310059	100	162.5500031	100	1.66702441	0.324620613	19
ENO1 Isoform alpha-enolase of Alpha-enolase	IPI00465248	53031.82031	7.01	9	704.8300171	100	114.75	100	1.663599099	0.556065902	9
RPN1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa	IPI00025874	78729.54688	5.87	3	145.2399902	100	60.29999924	99.99149367	1.660330083	9.80E-02	3
HLA-DPB1 HLA class II histocompatibility antigen, DP(W4) beta chain precurs	IPI00103082	30666.89063	8.83	1	62.77999878	99.99519446	62.77999878	99.99519446	1.659716825	0	1
- Elongation factor 1-alpha	IPI00472724	57485.78125	9.15	8	534.1099854	100	159.0899963	100	1.657829732	0.223293158	8
SET Isoform 2 of Protein SET	IPI00301311	35108.05859	4.12	1	66.54000092	99.99797818	66.54000092	99.99797818	1.654555515	0	1
HNRPA1 Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	IPI00465365	37003.55078	9.27	5	350.9200134	100	115.3700027	100	1.647061187	0.258954283	5
HNRPA3 Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	IPI00419373	42922.89844	9.1	4	364.6300049	100	172.4499969	100	1.637812338	0.261979499	4
YWHAZ 14-3-3 protein zeta/delta	IPI00021263	30890.03906	4.73	10	767.694458	100	147.3800049	100	1.635589819	0.333753224	11
CAPZB Capping protein (Actin filament) muscle Z-line, beta	IPI00642256	32963.14844	6.45	4	238.2600098	100	67.91000366	99.99852517	1.633026798	0.259294356	4
LMNB1 Lamin-B1	IPI00217975	72358.14844	5.11	2	114.4199982	100	79.47000122	99.99989702	1.626918706	0.395887233	2
TUBB Tubulin beta chain	IPI00011654	52311.16016	4.78	18	1517.410034	100	162.5500031	100	1.600245678	0.212054029	22
RPL3 RPL3 protein	IPI00642267	33597.94141	10.17	1	55.58000183	99.97478018	55.58000183	99.97478018	1.593345198	0	1
TUBA1B Similar to Tubulin alpha-ubiquitous chain	IPI00792677	49578.05859	4.96	8	602.0299683	100	105.6200027	100	1.591544625	0.272330093	8
SSR4 Protein	IPI00646864	13775.66992	6.69	2	95.76000214	100	57.68000031	99.98444958	1.586927813	0.104710569	2
CAPRIN1 membrane component chromosome 11 surface marker 1 isoform 1	IPI00150961	82632.4375	5.14	1	93.27999878	100	93.27999878	100	1.57978274	0	1
RHOA Transforming protein RhoA precursor	IPI00027500	24622.31055	5.83	3	148.7000122	100	74.91000366	99.99970573	1.575018385	0.132446577	3
GANAB Isoform 3 of Neutral alpha-glucosidase AB precursor	IPI00441414	99842.15625	5.43	8	467.0700073	100	120.5899963	100	1.57360297	0.213494531	8
TXNDC4 Thioredoxin domain-containing protein 4 precursor	IPI00401264	50287.66016	5.09	4	190.2900085	100	65.73999786	99.99756924	1.573438936	0.23722306	4
EEF1D eukaryotic translation elongation factor 1 delta isoform 1	IPI00642971	77348.54688	6.02	3	256.4200134	100	112.2600021	100	1.57157341	0.18012651	3

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SND1 Staphylococcal nuclease domain-containing protein 1	IPI00140420	110982.1797	6.74	3	198.8800049	100	98.45999908	100	1.571370555	5.32E-02	3
YWHAG 14-3-3 protein gamma	IPI00220642	31015.18945	4.8	6	305.3500061	100	81.72000122	99.99993866	1.569419143	0.175399453	6
ANXA5 Annexin A5	IPI00329801	39272.76172	4.94	10	643.960022	100	112.4300003	100	1.565566175	0.420239581	10
GSN Isoform 2 of Gelsolin precursor	IPI00646773	87445.10938	5.58	3	122.9599991	100	43.18000031	99.56172955	1.555542318	0.162631652	3
TMED10 Transmembrane emp24 domain-containing protein 10 precursor	IPI00028055	27690.30078	6.97	3	119.1699982	100	43.88999939	99.62782921	1.554334324	9.40E-02	3
P4HB Protein disulfide-isomerase precursor	IPI00010796	64315.26953	4.76	23	1598.709961	100	126.6200027	100	1.548710343	0.238274646	25
- 31 kDa protein	IPI00165486	34730.76172	9.96	1	57.5	99.98379152	57.5	99.98379152	1.534565075	0	1
TPP1 Isoform 3 of Tripeptidyl-peptidase 1 precursor	IPI00554538	62032.14844	5.94	2	108.3499985	100	61.45999908	99.99348758	1.525824822	0.14558524	2
SSBP1 Single-stranded DNA-binding protein, mitochondrial precursor	IPI00029744	18545.23047	9.59	1	60.54000092	99.991951	60.54000092	99.991951	1.524386572	0	1
- 30 kDa protein	IPI00472119	35896.37109	9.78	1	57.56000137	99.98401392	57.56000137	99.98401392	1.522094277	0	1
AADAC Arylacetamide deacetylase	IPI00383879	49123.19141	8.75	2	188.3144531	100	117.9400024	100	1.519739058	6.85E-02	2
IDH1 Isocitrate dehydrogenase [NADP] cytoplasmic	IPI00027223	52332.01172	6.53	15	1231.119873	100	119.1299973	100	1.517181492	0.186849873	16
PSME1 29 kDa protein	IPI00479722	32701.33008	5.27	5	252.9244385	100	74	99.99963714	1.51517464	0.162943307	5
SFN Isoform 2 of 14-3-3 protein sigma	IPI00411765	26671.25	4.77	4	189.7100067	100	54.90000153	99.97050543	1.510126619	0.113427678	4
UBA52 ubiquitin and ribosomal protein L40 precursor	IPI00456429	17541.21094	9.87	3	238.2799988	100	125.8199997	100	1.506173048	0.213686634	3
ATIC Bifunctional purine biosynthesis protein PURH	IPI00289499	70461.78906	6.27	2	89.55999756	100	49.04999924	99.88656625	1.505165246	0.276951631	2
CSTB Cystatin-B	IPI00021828	12618.79004	6.96	3	206.7600098	100	90.56999969	100	1.499930481	0.189615146	3
CALR Protein	IPI00794237	19298.58008	4.47	3	291.7744446	100	149.8500061	100	1.499731813	0.124424466	4
TUBB3 Tubulin beta-3 chain	IPI00013683	53216.46094	4.83	11	954.8900146	100	162.5500031	100	1.498445038	0.266654383	12
EEF2 Elongation factor 2	IPI00186290	105563.6484	6.41	5	335.8600159	100	114.25	100	1.494151093	0.391063665	5
UGDH UDP-glucose 6-dehydrogenase	IPI00031420	60869.64844	6.73	7	445.5599976	100	123.0299988	100	1.487731171	0.338008222	7
PSME2 proteasome activator subunit 2	IPI00746205	30834.65039	5.54	5	328.8600159	100	108.9800034	100	1.487402722	0.286986874	6
PSMB1 Proteasome subunit beta type 1 precursor	IPI00025019	28672.58008	8.27	1	64.75	99.99694689	64.75	99.99694689	1.486049343	0	1

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PFN1 Profilin-1	IPI00216691	16766.75	8.44	6	549.4399414	100	135.8699951	100	1.485521972	0.269390985	6
ILF3 Isoform 1 of Interleukin enhancer-binding factor 3	IPI00298788	105105.8906	8.86	1	60.36999893	99.99162967	60.36999893	99.99162967	1.484554131	0	1
PSMA1 Isoform Long of Proteasome subunit alpha type 1	IPI00472442	32610.50977	6.51	2	69.42999268	99.9989607	36.50999832	97.96416589	1.483274333	0.289929946	2
CALR 37 kDa protein	IPI00793605	41138.14063	4.55	8	696.8199463	100	149.8500061	100	1.483042681	0.320696253	9
TUBB2C Tubulin beta-2C chain	IPI00007752	52471.19141	4.79	17	1414.25	100	162.5500031	100	1.478723236	0.394178225	21
HNRPM Isoform 2 of Heterogeneous nuclear ribonucleoprotein M	IPI00383296	79706.89844	8.94	3	153.4100037	100	65.18000031	99.9972347	1.478241028	0.15196225	3
FN1 Isoform 1 of Fibronectin precursor	IPI00022418	276716.375	5.45	11	526.9788818	100	64.12999725	99.99647838	1.471742451	0.496467701	11
HNRPL heterogeneous nuclear ribonucleoprotein L isoform b	IPI00465225	54634.78125	7.22	1	91.26999664	100	91.26999664	100	1.469265951	0	1
CLTC Isoform 2 of Clathrin heavy chain 1	IPI00455383	203165.7031	5.48	5	260.1999817	100	89.83999634	100	1.463700961	0.25263785	5
LOC641827;LOC649440 Similar to eukaryotic translation elongation factor 1 b	IPI00397392	28469.74023	4.66	2	166.6399994	100	120.8700027	100	1.456239998	0.167810707	2
RAB10 Ras-related protein Rab-10	IPI00016513	25878.90039	8.59	1	54.18000031	99.96518694	54.18000031	99.96518694	1.44043929	0	1
FGG Isoform Gamma-A of Fibrinogen gamma chain precursor	IPI00219713	55011.35938	5.7	5	500.0499878	100	134.6600037	100	1.439582455	0.362254194	5
HSP90AB4P Heat shock protein 90Bd	IPI00555565	66222.17969	4.65	3	160.8899994	100	74.90000153	99.99970505	1.439329108	8.30E-02	3
- CD68 antigen variant (Fragment)	IPI00555602	45637.91016	5.46	2	162.3099976	100	92.26000214	100	1.439298407	0.160670772	2
LOC652826 similar to 26S protease regulatory subunit 6B	IPI00738042	51256.71875	5.17	1	62.45999908	99.994827	62.45999908	99.994827	1.437973319	0	1
CAP1 Adenylyl cyclase-associated protein	IPI00639931	58646.21094	8.24	2	136.5599976	100	73.62000275	99.99960396	1.432156379	0.226279047	2
GPI Glucose-6-phosphate isomerase	IPI00027497	68475.72656	8.43	6	396.6500244	100	88.26000214	100	1.430878738	0.134030316	6
RPS29 ribosomal protein S29 isoform 2	IPI00639942	9222.080078	10.08	1	60.09999847	99.99109278	60.09999847	99.99109278	1.428291613	0	1
PYGL 97 kDa protein	IPI00783313	107098.9297	6.71	10	617.7299805	100	107.4899979	100	1.425746226	0.407381088	10
HSP90AB1 Heat shock protein HSP 90-beta	IPI00414676	94433.0625	4.97	16	961.0300293	100	114.0599976	100	1.423396462	0.353215844	17
PAICS phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazol	IPI00815732	53853.98828	7.86	1	59.75	99.99034522	59.75	99.99034522	1.420894208	0	1
YWHAQ 14-3-3 protein theta	IPI00018146	30857.03906	4.68	6	311.9400024	100	88.83000183	100	1.419688879	0.210138503	6
HLA-DRA major histocompatibility complex, class II, DR alpha precursor	IPI00464948	30468.91016	4.91	2	121.6200027	100	85.83000183	100	1.418710128	0.37020355	2

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HNRPH1 HNRPH1 protein	IPI00479191	53875.41016	6.33	5	288.3544312	100	99.12999725	100	1.417129537	0.18195718	5
TUBA1C Tubulin alpha-1C chain	IPI00218343	53295.64844	4.96	8	576.9599609	100	96.26999664	100	1.4134727	0.455975793	8
NCL Isoform 1 of Nucleolin	IPI00604620	89719.57031	4.6	6	308.8599854	100	76.70999908	99.99980558	1.411614405	0.367224258	6
TGM2 Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2	IPI00294578	82951.92188	5.11	9	564.0100098	100	96.11000061	100	1.410509044	0.278126164	10
NDUFS2 NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	IPI00025239	56146.01172	7.21	1	65.11000061	99.99718977	65.11000061	99.99718977	1.404833937	0	1
VIL2 Cytovillin 2 (Fragment)	IPI00384282	18443.30078	9.32	4	202.1444244	100	59.50999832	99.98979666	1.403527879	0.105225389	5
MSN Moesin	IPI00219365	76942.64063	6.08	15	970.904541	100	128.3999939	100	1.402689312	0.138648159	17
GBE1 1,4-alpha-glucan-branching enzyme	IPI00296635	85817.03906	5.87	4	227.6300049	100	101.1299973	100	1.397669327	0.266686131	4
LMAN1 ERGIC-53 protein precursor	IPI00026530	62207.39063	6.3	5	304.928894	100	140.9199982	100	1.396233488	0.118257977	5
EFHD2 EF-hand domain family, member D2	IPI00552365	32619.2207	5.26	2	78.59443665	99.99987402	43.91999817	99.63039111	1.391297994	0.371903582	2
FMO5 Dimethylaniline monooxygenase [N-oxide-forming] 5	IPI00215760	66454.40625	8.41	3	184.4499969	100	71.70999908	99.99938519	0.709903875	9.56E-02	3
AK3 GTP:AMP phosphotransferase	IPI00478236	20052.85938	8.73	4	274.3399963	100	101.1800003	100	0.709408981	8.70E-02	4
MYH10 Isoform 2 of Myosin-10	IPI00479307	260063.1719	5.46	11	768.4022217	100	144.9100037	100	0.708849958	0.543628596	11
SERPINF1 25 kDa protein	IPI00796279	26706.00977	5.84	1	63.97000122	99.99634622	63.97000122	99.99634622	0.707564514	0	1
CYP2C8 45 kDa protein	IPI00843846	49430.42188	8.91	2	66.67999268	99.99804231	33.66999817	96.08490412	0.707068352	0.121367153	2
DPYS Dihydropyrimidinase	IPI00028910	62048.10938	6.81	4	200.9299927	100	63.56000137	99.99598448	0.705557091	0.172436273	4
ECH1 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor	IPI00011416	38661.62109	8.16	3	155.1600037	100	72.68000031	99.99950825	0.705521696	0.134118312	3
- 105 kDa protein	IPI00794900	115433.2422	7.3	11	662.0700073	100	105.5100021	100	0.704733875	0.185420773	12
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	26915.57031	5.15	3	192.7400055	100	83.06999969	100	0.703304949	0.174481279	3
HADHA Trifunctional enzyme subunit alpha, mitochondrial precursor	IPI00031522	93913.70313	9.16	14	1023.834351	100	106.2200012	100	0.696449442	0.16805208	14
ADH5 Alcohol dehydrogenase class 3	IPI00746777	45140.69141	7.45	3	149.6299896	100	60.16999817	99.99123519	0.696433267	9.83E-03	3
TUFM Tu translation elongation factor, mitochondrial	IPI00027107	54583.71875	7.26	5	355.9200134	100	121.3099976	100	0.68858296	0.127606501	5
POR Hypothetical protein DKFZp686G04235	IPI00792395	82665.85938	5.38	4	224.5899963	100	74.80000305	99.99969818	0.683497704	0.082151649	4

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HP Haptoglobin precursor	IPI00641737	52573.75	6.28	9	601.0400391	100	89.75	100	0.682809915	0.118559096	9
ACY1 Aminoacylase-1	IPI00009268	48344.23047	5.77	8	442.0400391	100	92.38999939	100	0.680613529	0.135348474	8
PDLIM5 PDZ and LIM domain 5 isoform e	IPI00103146	26878.82031	9.93	1	62.52999878	99.99490971	62.52999878	99.99490971	0.680148321	0	1
ASPN ASPN protein	IPI00418431	49081.85938	6.03	3	112.2100067	100	42.58000183	99.49679837	0.679656027	5.15E-02	3
NDUFAB1 Acyl carrier protein, mitochondrial precursor	IPI00022442	18696.14063	4.82	2	109.3999939	100	72.27999878	99.99946081	0.679066493	0.061676869	2
ATP5O ATP synthase O subunit, mitochondrial precursor	IPI00007611	26090.96094	9.97	2	76.22000122	99.99978236	44.70999908	99.69186409	0.678946988	0.114995202	2
MDH2 Malate dehydrogenase, mitochondrial precursor	IPI00291006	39765.08984	8.92	13	938.9788208	100	132.3899994	100	0.673156752	8.05E-02	13
HSPE1 10 kDa heat shock protein, mitochondrial	IPI00220362	12653.11035	8.89	7	409.1000366	100	79.08000183	99.99988735	0.671865854	0.071045973	8
MT1X Metallothionein-1X	IPI00008753	8279.200195	8.38	2	128.0400085	100	84.55000305	100	0.669831346	0.290858872	2
SERPINC1 SERPINC1 protein	IPI00844156	32447.10938	9.03	1	93.75	100	93.75	100	0.668372987	0	1
AIFM1 Isoform 3 of Apoptosis-inducing factor 1, mitochondrial precursor	IPI00157908	72532.10938	9.03	4	302.9499817	100	95.19999695	100	0.668207494	0.118614694	4
CYP2D7P1 Cytochrome P450	IPI00418408	60228.42188	8.59	1	59.20000076	99.98904173	59.20000076	99.98904173	0.660998292	0	1
PPIF Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor	IPI00026519	24750.41992	9.48	2	96.66000366	100	58.97999954	99.98847231	0.660376281	7.86E-03	2
AK2 Isoform 2 of Adenylate kinase isoenzyme 2, mitochondrial	IPI00218988	28472.61914	7.71	3	217.8199921	100	79.13999939	99.99988889	0.660273141	0.036265494	3
MT1E Metallothionein-1E	IPI00025461	8225.160156	8.38	2	118.9500046	100	84.55000305	100	0.659852271	0.272426604	2
ACO1 Iron-responsive element-binding protein 1	IPI00008485	105951.1797	6.23	7	397.25	100	93.86000061	100	0.655598098	0.168110263	7
PHB Prohibitin variant (Fragment)	IPI00791634	31847.21094	6.02	4	198.4200134	100	60.79000092	99.99240125	0.654964161	8.44E-02	4
COX4I1 Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor	IPI00006579	22634.39063	9.52	3	184.4199982	100	76.25	99.99978386	0.654863622	0.226997347	3
SOD1 Superoxide dismutase	IPI00783680	17838.08984	5.7	4	223.6600037	100	105.1299973	100	0.653589343	2.63E-02	5
BCKDHA CDNA FLJ45695 fis, clone FEBRA2013570, highly similar to 2- oxoisova	IPI00444329	57253.05859	6.09	1	60.38000107	99.99164893	60.38000107	99.99164893	0.652488042	0	1
ACAA1 3-ketoacyl-CoA thiolase, peroxisomal precursor	IPI00012828	47604.07031	8.76	5	341.3900146	100	106.0999985	100	0.652013255	0.326294671	5
ACADVL Isoform 2 of Very-long-chain specific acyl-CoA dehydrogenase, mitoch	IPI00178744	78527.97656	9.06	2	98.63999939	100	51.63999939	99.93751982	0.650976908	2.00E-02	2
GLUL Glutamine synthetase	IPI00010130	45423.51172	6.43	1	57.79999924	99.98487337	57.79999924	99.98487337	0.650677891	0	1

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MAT1A S-adenosylmethionine synthetase isoform type-1	IPI00021772	47392.28906	5.86	5	278.5844421	100	85.16999817	100	0.649028921	0.120258391	5
ACADM Hypothetical protein DKFZp686M24262	IPI00513827	55018.78906	7.94	3	145.5699921	100	78.76999664	99.99987901	0.643608556	5.43E-02	3
COX6C Cytochrome c oxidase polypeptide VIc precursor	IPI00015972	9927.879883	10.38	2	116.1100006	100	58.75999832	99.98787331	0.636859867	0.199775587	2
QPRT 17 kDa protein	IPI00853023	17914	7.71	1	55.06999969	99.97163765	55.06999969	99.97163765	0.636228468	0	1
OGDH oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform 1	IPI00098902	124171.8594	6.4	2	129.1199951	100	86.63999939	100	0.636106362	0.171345692	2
ASL 50 kDa protein	IPI00514772	52806.57031	5.99	7	422.3667908	100	81	99.9999276	0.634559644	8.01E-02	7
NIT2 Nitrilase family member 2	IPI00549467	33646.80078	6.82	3	176.2399902	100	74.56999969	99.99968177	0.633058787	0.168699829	3
ALDH3A2 Isoform 2 of Fatty aldehyde dehydrogenase	IPI00394758	63761.19141	9.06	1	78.23999786	99.99986331	78.23999786	99.99986331	0.63012025	0	1
SUCLG1 succinate-CoA ligase, GDP-forming, alpha subunit	IPI00759493	39717.12109	9.01	3	220.9200134	100	119.0500031	100	0.628229097	2.19E-02	3
KRT10 57 kDa protein	IPI00383111	60122.17188	5.09	2	70.30999756	99.99915132	36	97.71049171	0.628064365	0.336423222	2
PHB2 Prohibitin-2	IPI00027252	36156.25	9.83	3	147.1699982	100	52.86000061	99.95282171	0.626564015	0.175493665	3
CYP1A2 Isoform 1 of Cytochrome P450 1A2	IPI00719591	62467.67188	9.18	1	82.29000092	99.9999462	82.29000092	99.9999462	0.622057257	0	1
SUCLG2 Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precurso	IPI00096066	51941.89844	6.15	8	465.4588928	100	83.80000305	100	0.621125826	0.430143742	8
ACO2 Aconitase 2, mitochondrial	IPI00790739	96473.60938	6.97	2	125.0844421	100	85.44999695	100	0.616294678	5.11E-02	2
CALD1 Isoform 2 of Caldesmon	IPI00218694	76226.46875	6.37	4	288.1199951	100	107.3099976	100	0.615760202	9.79E-02	4
EPHX2 Epoxide hydrolase 2	IPI00104341	68213.03906	5.91	1	62.13999939	99.99443145	62.13999939	99.99443145	0.612473552	0	1
LTB4DH Leukotriene B4 12-hydroxydehydrogenase	IPI00643630	9274.419922	9.4	3	268.9200134	100	103.9800034	100	0.60449042	4.38E-02	3
AOX1 Hypothetical protein AOX1	IPI00743616	161854.2031	6.78	11	534.8544922	100	108.5800018	100	0.600030347	0.285428294	11
COL6A2 Isoform 2C2 of Collagen alpha-2(VI) chain precursor	IPI00304840	117254.4375	5.85	4	192.9400024	100	75.01999664	99.99971309	0.595130883	0.134443954	4
ALDH8A1 aldehyde dehydrogenase 8A1 isoform 2	IPI00172476	51159.08984	5.97	2	93.44000244	100	51.66999817	99.93794991	0.590137413	3.72E-02	2
ETFA Electron transfer flavoprotein subunit alpha, mitochondrial precursor	IPI00010810	39221.92969	8.62	6	639.1044312	100	153.6499939	100	0.588809851	9.74E-02	7
GCSH;LOC730107 Glycine cleavage system H protein, mitochondrial precursor	IPI00011604	20522.83984	4.91	1	51.47000122	99.93502563	51.47000122	99.93502563	0.581687169	0	1
ETFB Isoform 2 of Electron transfer flavoprotein subunit beta	IPI00556451	41287.32813	6.78	5	248.4299927	100	55.77999878	99.97591524	0.574464202	0.147273966	5

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CRYL1 Lambda-crystallin	IPI00645031	36297.23828	5.68	2	66.19999695	99.99781354	34.09000015	96.4457972	0.572842951	1.67E-03	2
- HDCMB21P	IPI00384863	14111.21973	5.17	1	92.70999908	100	92.70999908	100	0.571261218	0	1
COL6A3 alpha 3 type VI collagen isoform 4 precursor	IPI00072918	345401.0313	6.48	35	1887.693481	100	127.8799973	100	0.563478974	0.23673822	36
HADHB Trifunctional enzyme beta subunit, mitochondrial precursor	IPI00022793	56777.03906	9.45	8	515.9699707	100	94.51999664	100	0.562244657	0.110463435	8
SLC27A5 Bile acyl-CoA synthetase	IPI00016827	78658.29688	7.81	2	71.59888458	99.99936926	40.20999908	99.13155502	0.561489058	1.41E-02	2
COL6A3 alpha 3 type VI collagen isoform 3 precursor	IPI00072917	345457.3438	6.47	35	1893.973511	100	127.8799973	100	0.560801078	0.235707359	36
HSPB6 Heat-shock protein beta-6	IPI00022433	19439.91992	7.9	2	77.02999878	99.99981939	45.70000076	99.75467481	0.560728068	0.12795191	2
KRT79 keratin 6L	IPI00241841	62350.57031	6.75	4	202.9299927	100	61.38000107	99.99336651	0.560202029	0.149295629	4
AKR7A3 Aflatoxin B1 aldehyde reductase member 3	IPI00293721	39376.69141	6.67	5	244.0900116	100	60.40999985	99.99170642	0.560046812	0.278333522	5
ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria	IPI00024990	63211.07813	8.72	15	1078.744385	100	132.8600006	100	0.558758958	0.139314367	16
COL1A2 Collagen alpha-2(I) chain precursor	IPI00304962	136968.0469	9.08	2	131.8500061	100	85.20999908	100	0.558443576	2.22E-02	2
ALDH5A1 aldehyde dehydrogenase 5A1 precursor, isoform 1	IPI00336008	63482.35938	8.41	1	52.31000137	99.94645214	52.31000137	99.94645214	0.553893937	0	1
PC Pyruvate carboxylase, mitochondrial precursor	IPI00299402	138358.0469	6.37	11	651.5643921	100	112.0999985	100	0.552496157	0.127067577	11
FTL Ferritin light chain	IPI00852596	21925.33984	5.51	7	496.5900269	100	94.73999786	100	0.547436401	7.69E-02	7
OGN Osteoglycin	IPI00515092	34941.69141	8.49	4	177.2900085	100	49.52999878	99.8984354	0.546735988	0.238702858	4
PPA1 CDNA FLJ45159 fis, clone BRAWH3043295, highly similar to Inorganic pyr	IPI00444797	17858.00977	8.71	1	86.70999908	100	86.70999908	100	0.54653992	0	1
HAGH Hydroxyacylglutathione hydrolase	IPI00745553	32141.91016	6.86	2	136.4299927	100	87.30999756	100	0.546189968	0.342022528	2
SORD Sorbitol dehydrogenase	IPI00216057	42378.10938	8.23	5	276.1699829	100	81.12000275	99.99992957	0.545841347	0.1071126	5
MT-CO2 Cytochrome c oxidase subunit 2	IPI00017510	26406.33008	4.67	1	106.5599976	100	106.5599976	100	0.545428153	0	1
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	12902.16992	6.28	4	209.3899994	100	65.72000122	99.99755802	0.532763254	0.162697763	4
MUT Methylmalonyl-CoA mutase, mitochondrial precursor	IPI00024934	90636.34375	6.48	2	128.0700073	100	96.76000214	100	0.52869817	7.01E-02	2
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	43462.35156	8	15	1184.474365	100	141.0700073	100	0.518644944	8.18E-02	17
GSTA1 Glutathione S-transferase A1	IPI00657682	29261.05078	8.91	11	671.8044434	100	130.4600067	100	0.516008977	0.116624691	12

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GSTA2 Glutathione S-transferase A2	IPI00745233	29104	8.51	11	686.0444336	100	130.4600067	100	0.515643674	0.116368807	12
UQCRH Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondria	IPI00296022	11826.04004	4.39	1	67.86000061	99.99850809	67.86000061	99.99850809	0.513484015	0	1
CES2 carboxylesterase 2 isoform 1	IPI00332828	72247.0625	6.03	8	456.0800171	100	103.1900024	100	0.513480209	8.19E-02	8
ALDH2 Mitochondrial aldehyde dehydrogenase 2 variant (Fragment)	IPI00792207	61065.96094	6.63	7	435.7000122	100	96.18000031	100	0.511926767	0.118996751	8
HGD Homogentisate 1,2-dioxygenase	IPI00303174	54236.85938	6.54	5	318.4799805	100	74.81999969	99.99969957	0.510809195	7.60E-02	5
ALDH1L1 Formyltetrahydrofolate dehydrogenase isoform a variant	IPI00793673	109020.6328	5.63	11	744.1188965	100	110.1600037	100	0.508596793	0.29913287	11
SHMT1 Isoform 2 of Serine hydroxymethyltransferase, cytosolic	IPI00220668	53489.17969	7.59	1	88.37999725	100	88.37999725	100	0.507727081	0	1
FBLN5 Full-length cDNA clone CS0DI085YI08 of Placenta of Homo sapiens	IPI00382428	56833.08984	4.57	3	132.1799927	100	56.20000076	99.97813537	0.505664441	9.02E-02	3
RDH16 Retinol dehydrogenase 16	IPI00289551	38852.73828	8.83	3	163.0044403	100	67.73000336	99.99846276	0.502669767	0.406188699	3
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	35335.42969	8.34	11	870.3544312	100	134.75	100	0.499812613	6.65E-02	11
NDUFA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	IPI00011770	10562.08984	9.42	3	160.7200012	100	75.68000031	99.99975354	0.494365543	8.02E-02	3
COL6A1 Collagen alpha-1(VI) chain precursor	IPI00291136	117302.5391	5.26	4	258.6099854	100	100.1800003	100	0.490695131	0.134964348	5
SDHA Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondri	IPI00305166	77793.53125	7.06	5	349.6200256	100	100.5699997	100	0.490293863	0.200222067	5
BPHL Isoform 1 of Valacyclovir hydrolase precursor	IPI00384428	35828.30078	9.2	1	51.68000031	99.93809265	51.68000031	99.93809265	0.486897	0	1
KRT18 Keratin, type I cytoskeletal 18	IPI00784347	51196.89844	5.34	16	850.7600098	100	94.44000244	100	0.485844446	0.106923598	18
BAAT Bile acid CoA:amino acid N-acyltransferase	IPI00017819	48856.32031	6.49	5	356.1700134	100	113.3000031	100	0.482728015	0.103011503	5
- MHC-F3 REPEAT, fibronectin type III REPEAT=CLONE 3.9KF3-2	IPI00743608	191267.9063	4.89	3	132.1712341	100	56.95999908	99.98164551	0.481714567	0.220730978	3
KRT8 Keratin, type II cytoskeletal 8	IPI00554648	58423.62891	5.52	26	1823.793457	100	156.5399933	100	0.480256368	0.15353718	26
SFXN1 Sideroflexin-1	IPI00009368	37842.55078	9.22	1	53.63000107	99.96048681	53.63000107	99.96048681	0.479781645	0	1
SFXN3 sideroflexin 3	IPI00793874	38103.92188	9.25	1	53.43000031	99.9586246	53.43000031	99.9586246	0.479781645	0	1
ALDH1B1 Aldehyde dehydrogenase X, mitochondrial precursor	IPI00103467	62178.58984	6.36	5	338.539978	100	118.3899994	100	0.476440031	9.83E-02	5
COL14A1 Isoform 3 of Collagen alpha-1(XIV) chain precursor	IPI00402215	195721.9844	5.16	5	381.1444397	100	135.8600006	100	0.470622489	0.257324199	5
PHGDH Phosphoglycerate dehydrogenase	IPI00642548	56869.67969	6.47	2	112.0400009	100	71.95999908	99.99941958	0.469667239	0.195750831	2

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CYP2E1 Cytochrome P450 2E1	IPI00007282	61500.80078	8.27	6	336.0299988	100	72.08000183	99.9994354	0.459706211	0.336680882	6
KRT19 Keratin, type I cytoskeletal 19	IPI00479145	46225.37891	5.04	6	295.4400024	100	65.37999725	99.99735916	0.456963995	0.195414024	6
ALDH4A1 Aldehyde dehydrogenase 4 family, member A1	IPI00647328	65056.12109	7.62	11	746.3499756	100	102.4700012	100	0.455714328	5.83E-02	11
HEBP1 Heme-binding protein 1	IPI00148063	23623.80078	5.71	1	52.02000046	99.94275439	52.02000046	99.94275439	0.452278296	0	1
C21orf33 Isoform Long of ES1 protein homolog, mitochondrial precursor	IPI00024913	31020.9707	8.5	3	303.1544495	100	137.2200012	100	0.44612891	2.17E-02	3
HMGCL 19 kDa protein	IPI00514407	21853.41016	8.9	1	88.65000153	100	88.65000153	100	0.445642072	0	1
ASS1 Argininosuccinate synthase	IPI00020632	56147.66016	8.6	10	658.1799927	100	139.2599945	100	0.438203818	0.203211714	10
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1406	5.6	4	287.7600098	100	98.44000244	100	0.43527248	0.223062965	4
SDHB Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondria	IPI00294911	35997.07813	9.03	2	116.4100037	100	84.76000214	100	0.429081515	7.26E-02	2
DCI Isoform 2 of 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor	IPI00398758	32932.46875	9.07	2	136.6000061	100	100.1100006	100	0.428459758	0.011239714	2
FTCD Isoform C of Formimidoyltransferase-cyclodeaminase	IPI00218976	64571.53125	5.24	6	364.9444275	100	104.5899963	100	0.426107298	0.291685228	6
ACOT1 Acyl-coenzyme A thioesterase 1	IPI00333838	49306.28906	6.9	1	79.73000336	99.99990301	79.73000336	99.99990301	0.419423437	0	1
ADI1 Isoform 1 of 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	IPI00651738	23402.88086	5.43	1	69.87000275	99.99906083	69.87000275	99.99906083	0.417946208	0	1
DBT Lipoamide acyltransferase component of branched-chain alpha-keto acid d	IPI00003944	59823.44141	8.71	3	253.0500031	100	114.3300018	100	0.41653184	3.88E-02	3
BGN Biglycan preproprotein variant (Fragment)	IPI00643384	45356.82031	7.16	7	529.0999756	100	138.6000061	100	0.414329618	0.292252371	7
GLYAT Isoform 1 of Glycine N-acyltransferase	IPI00402759	37221.21094	8.38	3	123.1199951	100	51.84000015	99.9403319	0.414070373	2.33E-02	3
GLUD1 Glutamate dehydrogenase 1, mitochondrial precursor	IPI00016801	66531.63281	7.66	20	1495.669922	100	102.6399994	100	0.413532409	0.134364046	20
FAHD2A Fumarylacetoacetate hydrolase domain-containing protein 2A	IPI00329742	37730.39063	8.48	1	90.91999817	100	90.91999817	100	0.41232654	0	1
CYP2C9 Cytochrome P450 2C9	IPI00007219	61374.14063	8.13	4	184.980011	100	79.22000122	99.99989092	0.406128629	0.187510942	4
PCK2 mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor	IPI00797038	74784.85938	7.57	21	1416.350098	100	147.8399963	100	0.402712008	0.118873868	22
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	61418.91016	8.17	8	609.6400146	100	135.1499939	100	0.402705094	0.120273234	8
GRHPR Glyoxylate reductase/hydroxypyruvate reductase	IPI00037448	38271.94141	7.01	8	678.5844727	100	146.9900055	100	0.402661675	0.141361989	8
BDH1 D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	IPI00025341	41766.75	9.11	6	276.8944397	100	73.88999939	99.99962783	0.399764781	9.77E-02	6

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ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	IPI00001539	46153.96875	8.32	13	1005.26001	100	155.6999969	100	0.398372899	0.165019982	14
HRSP12 Ribonuclease UK114	IPI00005038	15826.7998	8.74	4	284.8699951	100	84.55000305	100	0.395929352	8.53E-02	4
CYP3A5 Cytochrome P450 3A5	IPI00025831	63206.72266	8.86	1	70.5	99.99918765	70.5	99.99918765	0.393749205	0	1
COX5A Cytochrome c oxidase subunit 5A, mitochondrial precursor	IPI00025086	18053.88086	6.3	3	204.5699921	100	112.3799973	100	0.377587665	4.11E-02	3
TAGLN Transgelin	IPI00216138	25234.73047	8.87	7	393.2200317	100	96.01000214	100	0.375624993	0.110354396	8
GOT2 Aspartate aminotransferase, mitochondrial precursor	IPI00018206	52087.64844	9.14	6	484.5700073	100	167.9900055	100	0.366842272	0.071128545	6
FABP1 FABP1 protein (Fragment)	IPI00010290	18729.4707	9.52	7	470.559967	100	121.6399994	100	0.363843824	0.140424786	11
ALDH1L2 Aldehyde dehydrogenase family 1 member L2	IPI00298308	112632.0703	6.13	2	157.6699982	100	110.1600037	100	0.360466816	5.07E-02	2
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	43936.05859	8.75	9	531.4944458	100	106.7699966	100	0.35217937	0.140004678	9
DAK Dihydroxyacetone kinase	IPI00551024	63392.42188	7.12	5	456.0200195	100	180.9900055	100	0.350158309	0.42096784	5
SULT2A1 Bile salt sulfotransferase	IPI00216133	37496.32813	5.71	10	744.4200439	100	124.8899994	100	0.343372164	9.33E-02	11
DCN Isoform A of Decorin precursor	IPI00012119	44030.19922	8.75	3	204.0944519	100	89.51000214	100	0.343058336	0.158672975	3
ARG1 Isoform 2 of Arginase-1	IPI00398768	39380.19922	6.72	6	397.0599976	100	111.8499985	100	0.342711174	0.241772841	6
DCXR 26 kDa protein	IPI00797249	27252.58984	8.33	4	262.4100037	100	110.0100021	100	0.340316501	0.116913804	4
FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	41289.14844	6.54	6	549.8900146	100	118.0100021	100	0.338723414	0.103589414	6
BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101	49946.23828	6.58	14	775.5488892	100	126.4800034	100	0.337667181	0.111413602	14
HADH Isoform 2 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precu	IPI00298406	47125.23047	9.34	5	377.3800049	100	114.0500031	100	0.327374691	9.15E-02	5
ECHDC2 Enoyl coenzyme A hydratase domain-containing protein 2	IPI00384676	32534.50977	9.03	2	89.79000092	100	56.33000183	99.97878016	0.324639167	4.52E-02	2
PRELP Prolargin precursor	IPI00020987	46264.33984	9.47	8	448.0200195	100	84.88999939	100	0.324486836	0.323152772	8
GNMT Glycine N-methyltransferase	IPI00215925	35681.57031	6.55	2	69.83000183	99.99905214	36.93000031	98.15182884	0.324368536	3.66E-02	2
ACADSB Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	IPI00024623	52051.67969	6.53	3	223.0599976	100	91.02999878	100	0.323251694	0.13380618	3
CYB5A Isoform 1 of Cytochrome b5	IPI00397860	16616.71094	4.88	6	572.4099731	100	227.0399933	100	0.318273955	3.96E-02	6
LUM Lumican precursor	IPI00020986	42425.12891	6.16	9	529.9744263	100	85.91999817	100	0.317284738	0.239601669	9

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LTBP2 Latent-transforming growth factor beta-binding protein 2 precursor	IPI00292150	207622.5469	5.08	1	62.54000092	99.99492142	62.54000092	99.99492142	0.316430123	0	1
CPS1 Isoform 1 of Carbamoyl-phosphate synthase [ammonia], mitochondrial pre	IPI00011062	180875.9531	6.3	63	4790.559082	100	157.8999939	100	0.296128713	8.97E-02	70
PAH Phenylalanine-4-hydroxylase	IPI00017579	56707.82031	6.15	1	69.76000214	99.99903674	69.76000214	99.99903674	0.282829783	0	1
PBLD MAWD binding protein isoform b	IPI00651719	33923.37891	6.5	3	224.3500061	100	118.0999985	100	0.281783128	0.093163638	3
CYP3A4 Cytochrome P450 3A4	IPI00465138	63244.41016	8.27	2	107.8800049	100	70.5	99.99918765	0.278803614	0.114945566	2
SULT1A1 Sulfotransferase 1A1	IPI00300026	47814.69922	8.61	7	510.0544128	100	127.8099976	100	0.275130539	2.78E-02	7
ADH1C Alcohol dehydrogenase 1C	IPI00465343	45428	8.63	11	791.6699829	100	120.9300003	100	0.273645349	0.195502242	12
NNMT Nicotinamide N-methyltransferase	IPI00027681	33091.32031	5.56	2	90.05000305	100	49.61999893	99.9005185	0.272222291	0.018431746	2
GPT Alanine aminotransferase 1	IPI00217458	57510.32813	6.77	3	193.9199982	100	84.44999695	100	0.268620924	6.38E-02	3
ACSL1 Isoform 1 of Long-chain-fatty-acid--CoA ligase 1	IPI00012728	85201.29688	6.81	9	539.8499756	100	103.1100006	100	0.268495774	8.19E-02	9
ADH1B Alcohol dehydrogenase 1B	IPI00473031	45270.91016	8.63	11	887.3900146	100	120.9300003	100	0.261623901	0.105814352	13
ADH1A Alcohol dehydrogenase 1A	IPI00218896	45320.80859	8.26	13	1029.309937	100	120.9300003	100	0.260818255	0.175423462	15
HPD 40 kDa protein	IPI00795913	44884.14063	5.93	4	245.9500122	100	80.48000336	99.99991839	0.25954813	0.144771824	4
CTH Isoform 2 of Cystathionine gamma-lyase	IPI00221301	42918.19141	6.43	1	58.97000122	99.98844574	58.97000122	99.98844574	0.252362398	0	1
COQ9 Isoform 1 of Ubiquinone biosynthesis protein COQ9, mitochondrial precu	IPI00470631	37064.78125	5.61	1	134.4299927	100	134.4299927	100	0.237080354	0	1
REEP6 Receptor expression-enhancing protein 6	IPI00647161	22153.98047	8.74	1	110.3899994	100	110.3899994	100	0.228044335	0	1
ADH4 Alcohol dehydrogenase 4	IPI00218899	45828.03125	8.25	10	680.0299683	100	96.80000305	100	0.224337989	0.162764303	11
GGTLA1 Isoform 2 of Gamma-glutamyltransferase 5 precursor	IPI00339373	61051.73828	7.67	2	126.8100052	100	85.98000336	100	0.218421715	0.160263842	2

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg Itraq ratio * (115/114)	iTRAQ Standard Deviation * (115/114)	iTRAQ Peptides (115/114)
DEFA3 Neutrophil defensin 3 precursor	IPI00021827	10946.21973	5.71	2	75.76000214	99.99976171	42.81000137	99.52999851	7.856763064	0.11414292	2
AKR1B10 Aldo-keto reductase family 1 member B10	IPI00105407	41078.28125	7.12	7	509.4899902	100	91.45999908	100	7.773800844	10.0275884	7
COL14A1 Isoform 3 of Collagen alpha-1(XIV) chain precursor	IPI00402215	195721.9844	5.16	1	101.0599976	100	101.0599976	100	6.505353851	0	1
BGN CDNA FLJ35635 fis, clone SPLEN2011805, highly similar to	IPI00385748	39528	6.31	5	245.0299988	100	68.23000336	99.99865073	6.364955502	3.16732957	5
COL1A2 Collagen alpha-2(I) chain precursor	IPI00304962	136968.0469	9.08	2	130.4900055	100	87.87000275	100	6.073615549	1.03064137	2
PRELP Prolargin precursor	IPI00020987	46264.33984	9.47	3	139.0700073	100	50.68999863	99.9234228	5.986039846	4.6455314	3
LYZ Lysozyme C precursor	IPI00019038	17902.35938	9.38	1	95.75	100	95.75	100	5.557095071	0	1
TAGLN Transgelin	IPI00216138	25234.73047	8.87	3	206.8999939	100	92	100	5.359155604	2.44506301	3
LUM Lumican precursor	IPI00020986	42425.12891	6.16	7	367.3844604	100	67.23999786	99.99830527	4.829051829	3.96004274	7
DCN Isoform A of Decorin precursor	IPI00012119	44030.19922	8.75	2	118.9944382	100	68.26999664	99.9986631	4.636626341	3.62943916	2
LSP1 50 kDa protein	IPI00554652	54843.82031	5.42	1	85.93000031	100	85.93000031	100	4.445154074	0	1
ORM1 Alpha-1-acid glycoprotein 1 precursor	IPI00022429	25840.99023	4.93	3	179.0500031	100	68.11000061	99.99861293	4.019642008	0.7518576	4
UBA52 ubiquitin and ribosomal protein L40 precursor	IPI00456429	17541.21094	9.87	6	366.0700073	100	139.6600037	100	3.999801025	0.86418169	6
LTF 73 kDa protein	IPI00789477	80974.52344	8.2	3	156.7799988	100	77.13999939	99.99982658	3.909418845	1.64333493	3
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1406	5.6	3	209.4100037	100	73.65000153	99.99961265	3.827926465	2.41995572	3
CLU clusterin isoform 1	IPI00400826	62857.89844	6.24	2	92.61444092	100	58.84999847	99.98830233	3.659645102	0.64027381	2
FGB Fibrinogen beta chain precursor	IPI00298497	61772.66016	8.54	12	830.1599731	100	110.4000015	100	3.463031404	1.48047343	12
ACSL4 Isoform Short of Long-chain-fatty-acid--CoA ligase 4	IPI00219897	83902.50781	8.33	3	134.4499969	100	46.13999939	99.78167703	3.410263795	2.37826278	3
LAMA4 Isoform 2 of Laminin subunit alpha-4 precursor	IPI00735310	218700.1875	5.93	1	70.91999817	99.99927373	70.91999817	99.99927373	3.379817119	0	1
ALB Isoform 1 of Serum albumin precursor	IPI00745872	79715.90625	5.92	41	2774.008789	100	179.8800049	100	3.353519341	1.11709249	49
FLNA Filamin-A	IPI00333541	305957.375	5.7	11	666.2888184	100	115.1999969	100	3.302385298	1.47261963	11
ANXA2 Annexin A2	IPI00455315	43516.26953	7.57	10	580.9888916	100	124.4499969	100	3.075363312	1.18083811	10

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FN1 fibronectin 1 isoform 2 preproprotein	IPI00845263	280315.25	5.36	18	1097.723389	100	111.7300034	100	3.054956222	1.61314633	18
SERPINA1 Alpha-1-antitrypsin precursor	IPI00553177	51885.51172	5.37	13	969.6444702	100	130.0099945	100	3.036878306	1.17773054	16
S100A9 Protein S100-A9	IPI00027462	15007.73047	5.71	6	487.2399902	100	139.8899994	100	2.951139672	0.46197809	6
SOD2 manganese superoxide dismutase isoform A precursor	IPI00847322	27176.83984	8.35	6	414.6799927	100	122.3499985	100	2.855297856	0.46280991	6
IGHM IGHM protein	IPI00761159	57955.55078	7.53	10	906.2800903	100	136.2599945	100	2.838502697	0.7595165	11

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio * (117/116)	iTRAQ Standard Deviation * (117/116)	iTRAQ Peptides (117/116)
COL14A1 Isoform 3 of Collagen alpha-1(XIV) chain precursor	IPI00402215	195721.9844	5.16	1	101.0599976	100	101.0599976	100	2.072425955	0	1
RPS14 40S ribosomal protein S14	IPI00026271	18272.75	10.07	1	69.23999786	99.9989307	69.23999786	99.9989307	1.679352185	0	1
ECGF1 50 kDa protein	IPI00852987	52423.58984	5.36	1	58.63000107	99.9876945	58.63000107	99.9876945	1.582487717	0	1
LSP1 50 kDa protein	IPI00554652	54843.82031	5.42	1	85.93000031	100	85.93000031	100	1.567364877	0	1
AGL Isoform 6 of Glycogen debranching enzyme	IPI00219066	185998.375	6.26	1	69.20999908	99.99892329	69.20999908	99.99892329	1.521345765	0	1
COL1A2 Collagen alpha-2(I) chain precursor	IPI00304962	136968.0469	9.08	2	130.4900055	100	87.87000275	100	1.510999423	0.03921568	2
CSTB Cystatin-B	IPI00021828	12618.79004	6.96	2	83.93000031	100	50.38999939	99.91794606	1.496362852	5.67E-02	3
PRSS1 Trypsin-1 precursor	IPI00011694	29161.24023	6.08	1	81.45999908	99.99993586	81.45999908	99.99993586	1.470828836	0	1
TGFBI Transforming growth factor-beta-induced protein ig-h3 precursor	IPI00018219	80036.35156	7.62	2	111.3500061	100	77.58000183	99.99984329	1.449882512	0.37291565	2
SEC31A Isoform 4 of Protein transport protein Sec31A	IPI00515103	138953.7344	7.03	3	141.0188904	100	51.18000031	99.93159319	1.428385418	0.18288652	3
GSTP1 Glutathione S-transferase P	IPI00219757	25397.2207	5.43	1	104.0800018	100	104.0800018	100	1.403326044	0	1
RPL28 Ribosomal protein L28 variant (Fragment)	IPI00816097	11793.78027	10.42	1	78.51000214	99.9998735	78.51000214	99.9998735	0.693904468	0	1
RAP1A Ras-related protein Rap-1A precursor	IPI00019345	23841.94922	6.38	2	136.5200043	100	78.5	99.99987321	0.693302948	0.10799761	2
RPL14 RPL14 protein	IPI00555744	29336.74023	10.94	2	91.94000244	100	49.11000061	99.88982088	0.68544742	0.21269961	2
RPS29 ribosomal protein S29 isoform 2	IPI00639942	9222.080078	10.08	1	56.15999985	99.97826802	56.15999985	99.97826802	0.66280005	0	1
CLU clusterin isoform 1	IPI00400826	62857.89844	6.24	2	92.61444092	100	58.84999847	99.98830233	0.662329599	6.43E-02	2
APOC3 13 kDa protein	IPI00657670	13861.62012	7.9	1	64.51000214	99.9968224	64.51000214	99.9968224	0.656835827	0	1
UQCRH Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondria	IPI00296022	11826.04004	4.39	1	73.61000061	99.99960907	73.61000061	99.99960907	0.639803629	0	1
HIST1H1B Histone H1.5	IPI00217468	32071.38086	10.91	1	92.31999969	100	92.31999969	100	0.628362736	0	1
SNTB1 Isoform 2 of Beta-1-syntrophin	IPI00216858	44616.67188	9.13	1	56.08000183	99.977864	56.08000183	99.977864	0.61594014	0	1
DDX21 Isoform 2 of Nucleolar RNA helicase 2	IPI00477179	91110.35156	9.42	2	132.9199982	100	93.43000031	100	0.607575762	0.11629702	2
PLG Plasminogen precursor	IPI00019580	99918.28125	7.04	3	127.2900085	100	59.29999924	99.98945372	0.60073279	0.1163334	3

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- Ig kappa chain V-III region SIE	IPI00387115	12435.95996	8.7	1	58.79000092	99.9881396	58.79000092	99.9881396	0.585375145	0	1
- Ig kappa chain V-III region B6	IPI00387113	12295.89063	9.34	1	56.92678452	99.98178535	58.79000092	99.9881396	0.585375145	0	1
FGG Isoform Gamma-A of Fibrinogen gamma chain precursor	IPI00219713	55011.35938	5.7	9	500.9499817	100	84.5	100	0.567892953	0.20829345	9
FGA Isoform 2 of Fibrinogen alpha chain precursor	IPI00029717	76032.28906	8.23	11	840.444458	100	133.3000031	100	0.521675923	0.19703553	12
FGB Fibrinogen beta chain precursor	IPI00298497	61772.66016	8.54	12	830.1599731	100	110.4000015	100	0.461917825	9.78E-02	12

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio * (115/114)	iTRAQ Standard Deviation * (115/114)	iTRAQ Peptides (115/114)
FGB Fibrinogen beta chain precursor	IPI00298497	61772.66016	8.54	21	1354.390137	100	113.9700012	100	12.41724255	5.9032913	26
- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	IPI00783024	15665.44043	9.65	1	91.43000031	100	91.43000031	100	10.10147016	0	1
POSTN Isoform 2 of Periostin precursor	IPI00218585	96544.46875	7.87	1	70.58000183	99.99924036	70.58000183	99.99924036	9.961197502	0	1
FGG Isoform Gamma-A of Fibrinogen gamma chain precursor	IPI00219713	55011.35938	5.7	14	825.9499512	100	124.9800034	100	9.310750424	3.5919684	14
DEFA3 Neutrophil defensin 3 precursor	IPI00021827	10946.21973	5.71	4	150.5100098	100	42.83000183	99.5475116	9.054118193	6.7386449	4
FGA Isoform 2 of Fibrinogen alpha chain precursor	IPI00029717	76032.28906	8.23	25	1683.264526	100	121.5500031	100	8.873750269	4.8371029	27
S100P Protein S100-P	IPI00017526	12023.44043	4.75	1	102.4000015	100	102.4000015	100	7.21369809	0	1
IGHG2 Hypothetical protein DKFZp686I04196 (Fragment)	IPI00399007	50615.94141	7.63	7	463.8200378	100	116.6100006	100	6.729833394	6.0572009	8
FN1 Isoform 1 of Fibronectin precursor	IPI00022418	276716.375	5.45	20	1147.833252	100	89.23999786	100	6.705884937	4.4933018	21
SERPINA3 Isoform 1 of Alpha-1-antichymotrypsin precursor	IPI00847635	51646.92188	5.33	7	438.1344604	100	125.1999969	100	6.455902983	1.9635636	7
IGHA1 CDNA FLJ25298 fis, clone STM07683, highly similar to Protein Tro alph	IPI00386524	56728.32813	6.21	11	724.1699829	100	131.3699951	100	6.436333584	1.6584694	13
IGL@ IGL@ protein	IPI00658130	27441.46094	8.14	5	431.1600037	100	123.9300003	100	6.409485481	1.869191	5
IGHA2 Hypothetical protein DKFZp686C02218 (Fragment)	IPI00642017	57449.87891	6.67	9	571.6900024	100	134.4400024	100	6.376704938	1.7254594	11
- Hypothetical protein	IPI00807428	26545.32031	5.66	4	396.3999939	100	123.9300003	100	6.335395908	2.5007228	4
IGHM Hypothetical protein DKFZp686I15212	IPI00418153	62655.28125	8.39	8	585.1699829	100	121.8600006	100	6.186590908	2.5441143	9
SERPINA1 Alpha-1-antitrypsin precursor	IPI00553177	51885.51172	5.37	10	685.5	100	125.5599976	100	6.157651046	1.2727903	10
MPO Isoform H14 of Myeloperoxidase precursor	IPI00236554	77088.74219	9.3	5	247.3599854	100	66.40000153	99.99801113	6.095339518	2.4020806	5
IGHM IGHM protein	IPI00761159	57955.55078	7.53	10	917.5299683	100	145.4600067	100	6.023900665	3.9470889	12
FKBP5 51 kDa protein	IPI00743671	59312.21094	5.79	1	71.45999908	99.99937969	71.45999908	99.99937969	5.753093099	0	1
IGKV1-5 IGKV1-5 protein	IPI00419424	28320.14063	6.3	7	651.9500122	100	142.8000031	100	5.642667893	1.9932317	8
GC Vitamin D-binding protein precursor	IPI00555812	60697.32813	5.4	4	192.0644379	100	72.72000122	99.9995359	5.527661656	1.8702396	4

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CLU clusterin isoform 1	IPI00400826	62857.89844	6.24	2	108.4644394	100	77.80999756	99.99985625	5.494775625	1.2567174	2
IGHG4 Ig gamma-4 chain C region	IPI00829814	39932.16016	7.18	7	371.6900024	100	93.20999908	100	5.453336664	4.5451462	7
PLG Plasminogen precursor	IPI00019580	99918.28125	7.04	6	383.6099854	100	92.73000336	100	5.403589844	1.203747	6
IGL@ IGL@ protein	IPI00745660	27232.34961	7.59	4	343.9200134	100	123.9300003	100	5.397535835	0.9828402	4
IGHM IGHM protein	IPI00479708	73773.75	6.86	6	337.1399841	100	130.2899933	100	5.33276366	3.1217384	6
LTF 73 kDa protein	IPI00789477	80974.52344	8.2	3	104.1800003	100	36.65000153	98.12238095	5.324688968	2.8622551	4
IGHG1 Hypothetical protein DKFZp686P15220	IPI00645363	56996.17188	8.13	10	916.4799805	100	145.4600067	100	5.294315363	3.1276834	12
CP Ceruloplasmin precursor	IPI00017601	132466.3281	5.44	5	324.809967	100	118.5	100	5.06778401	4.0739102	5
ANXA1 Annexin A1	IPI00218918	43626.42969	6.57	4	350.3200073	100	118.4100037	100	4.807958823	1.8914651	4
ALB Isoform 1 of Serum albumin precursor	IPI00745872	79715.90625	5.92	43	2745.158447	100	115.1600037	100	4.784888043	1.9857847	59
- Ig kappa chain V-III region SIE	IPI00387115	12435.95996	8.7	1	77.12000275	99.9998315	77.12000275	99.9998315	4.747285583	0	1
- Ig kappa chain V-III region B6	IPI00387113	12295.89063	9.34	1	75.25678253	99.99974122	77.12000275	99.9998315	4.747285583	0	1
APOA4 apolipoprotein A-IV precursor	IPI00847179	49520.91016	5.28	7	295.5844421	100	56.18000031	99.97907779	4.619751947	2.0154697	7
LBP Lipopolysaccharide-binding protein precursor	IPI00032311	56800.25	6.23	2	143.1199951	100	75.59999847	99.99976088	4.600992044	1.433581	2
C9 Complement component C9 precursor	IPI00022395	69800.9375	5.43	2	92.00999451	100	59.50999832	99.99028131	4.499831492	0.7558639	2
AZGP1 alpha-2-glycoprotein 1, zinc	IPI00166729	37445.41016	5.71	2	101.1967773	100	59.52999878	99.99032596	4.496562314	1.6212749	2
APOA4 Apolipoprotein A-IV precursor	IPI00304273	49547.92188	5.28	7	292.2544556	100	56.18000031	99.97907779	4.412591559	1.3277459	7
A2M Alpha-2-macroglobulin precursor	IPI00478003	177285.7656	6	9	436.3699951	100	63.31000137	99.99594858	4.381167572	2.0328209	9
VTN Vitronectin precursor	IPI00298971	57939.35156	5.55	8	471.8200073	100	107.4599991	100	4.34201784	2.0699817	8
LYZ Lysozyme C precursor	IPI00019038	17902.35938	9.38	2	128.1699982	100	92.77999878	100	4.208624448	0.4487407	2
APOA1 Apolipoprotein A-I precursor	IPI00021841	34071.30859	5.56	8	417.7588806	100	67.41000366	99.99842381	3.978969929	2.7917361	8
C3 Complement C3 precursor (Fragment)	IPI00783987	204689.0469	6.02	12	661.1099854	100	88.48000336	100	3.880763376	2.0592109	12
- 10 kDa protein	IPI00259410	11159.19043	6.23	1	58.93000031	99.98889272	58.93000031	99.98889272	3.880414106	0	1

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- Ig kappa chain V-I region DEE	IPI00387025	12753.91992	9.43	1	57.75444031	99.98543993	58.93000031	99.98889272	3.880414106	0	1
- Ig kappa chain V-I region OU	IPI00387098	12437.78027	9.94	1	57.75444031	99.98543993	58.93000031	99.98889272	3.880414106	0	1
CFH Complement factor H	IPI00515041	146209.4219	6.35	3	136.8000031	100	53.09000015	99.95738057	3.875536229	0.3569699	3
GSN Isoform 2 of Gelsolin precursor	IPI00646773	87445.10938	5.58	8	365.710022	100	67.58000183	99.99848432	3.804021154	1.3196541	8
SERPINC1 SERPINC1 protein	IPI00844156	32447.10938	9.03	4	201.3600006	100	94.70999908	100	3.733905731	1.7263869	4
TTR 13 kDa protein	IPI00646384	14770.61035	5.34	2	140.5200043	100	91.56999969	100	3.663669704	0.1973862	2
LSM8 U6 snRNA-associated Sm-like protein LSm8	IPI00219871	10684.41016	4.34	1	68.25	99.998701	68.25	99.998701	3.619554939	0	1
HRG Histidine-rich glycoprotein precursor	IPI00022371	63635.03125	7.09	1	59.49000168	99.99023646	59.49000168	99.99023646	3.584225627	0	1
CFB Isoform 2 of Complement factor B precursor (Fragment)	IPI00218508	74644.8125	6.11	2	87.40000153	100	46.90999985	99.82314895	3.580169145	0.4672555	2
SERPINC1 Antithrombin III variant	IPI00032179	58498.30859	6.11	3	115.7700043	100	42.33000183	99.49229966	3.438398746	1.282044	3
IFITM1 Interferon-induced transmembrane protein 1	IPI00300620	14931.44043	7.78	2	192.5400085	100	112.5299988	100	3.398483901	2.3756874	3
SERPINH1 Serpin H1 precursor	IPI00032140	51543.67969	8.75	5	412.0200195	100	145.7799988	100	3.362311968	1.6429696	5
C4B;C4A complement component 4B preproprotein	IPI00418163	205105.2656	6.89	4	163.0944366	100	49.29999924	99.89799823	3.354061032	0.5958582	5
HPX Hemopexin precursor	IPI00022488	55409.48047	6.55	3	166.0299988	100	91.66999817	100	3.332318829	1.7609427	4
SERPINB1 Leukocyte elastase inhibitor	IPI00027444	47127.14063	5.9	2	93.13999939	100	57.5	99.98456141	3.313973483	0.6418931	2
APOB Apolipoprotein B-100 precursor	IPI00022229	567947.0625	6.61	5	253.0844421	100	92.09999847	100	3.155435562	1.1254397	5
S100A9 Protein S100-A9	IPI00027462	15007.73047	5.71	5	473.7599792	100	143.7299957	100	3.106782863	0.6319131	8
F2 70 kDa protein	IPI00784409	75432.22656	5.64	2	93.02999878	100	59.70000076	99.99069733	3.101762834	0.5591597	2
S100A8 Protein S100-A8	IPI00007047	12745.88965	6.51	5	246.9644623	100	57.88999939	99.98588738	3.026061989	0.4060154	5
HP Haptoglobin precursor	IPI00641737	52573.75	6.28	12	821.3200073	100	109.9599991	100	2.998685157	0.4106641	14
RTN4 Isoform 2 of Reticulon-4	IPI00298289	42931.25	4.71	1	82.09999847	99.99994647	82.09999847	99.99994647	2.914596692	0	1
HNRPH1 HNRPH1 protein	IPI00479191	53875.41016	6.33	6	476.8544312	100	147.8399963	100	2.905955321	1.3974767	7
TF Transferrin variant (Fragment)	IPI00798430	87365.92188	6.68	22	1126.348877	100	98.70999908	100	2.875403865	1.0882451	22

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LGALS1 Galectin-1	IPI00219219	16278.33008	5.34	2	152.7799988	100	90.55000305	100	2.863065894	0.1346352	2
RCN3 Reticulocalbin-3 precursor	IPI00101037	38766.19922	4.74	2	105.1900024	100	56.11000061	99.97873783	2.842719805	2.9776675	2
ORM1 Alpha-1-acid glycoprotein 1 precursor	IPI00022429	25840.99023	4.93	3	261.8900146	100	106.5100021	100	2.804392111	0.2972795	3
- 2,3-bisphosphoglycerate mutase variant (Fragment)	IPI00556284	18558.81055	6.59	1	74.06999969	99.9996599	74.06999969	99.9996599	2.795621774	0	1
AHSG 29 kDa protein	IPI00795830	31274.16992	4.77	2	60.70999908	99.99262762	30.79999924	92.77882762	2.66793087	2.6643007	2
LSP1 50 kDa protein	IPI00554652	54843.82031	5.42	1	87.08000183	100	87.08000183	100	2.667818628	0	1
APOE Apolipoprotein E precursor	IPI00021842	38239.98828	5.65	5	346.5999756	100	121.8099976	100	2.624189174	0.6842099	5
LUM 23 kDa protein	IPI00794403	25919.60938	8.52	3	212.9199982	100	92.41000366	100	2.604090243	0.1795785	3
PRKDC Isoform 2 of DNA-dependent protein kinase catalytic subunit	IPI00376215	508806.4375	6.81	1	84.68000031	100	84.68000031	100	2.600128958	0	1
HNRPH2 Heterogeneous nuclear ribonucleoprotein H'	IPI00026230	51910.53125	5.89	6	436.9400024	100	147.8399963	100	2.570387801	1.9086134	7
ARPC2 Actin-related protein 2/3 complex subunit 2	IPI00005161	38147.87109	6.84	5	198.3944397	100	52.09000015	99.94634532	2.489408673	0.7672243	5
NAP1L1 43 kDa protein	IPI00789029	47959.44141	4.45	2	114.3499985	100	72.48999786	99.99951066	2.488313587	1.5962477	2
TRIM28 Isoform 2 of Transcription intermediary factor 1-beta	IPI00438230	85861.78906	5.67	2	159.1699982	100	106.3499985	100	2.486671601	0.329186	2
PSMC3 26S protease regulatory subunit 6A	IPI00018398	54730.94141	5.13	3	120.4000015	100	56.70999908	99.98148142	2.464893055	0.887885	3
A1BG 41 kDa protein	IPI00644018	42068.62109	5.5	2	68.49000549	99.99877084	38.83000183	98.86340052	2.431373771	0.1697634	2
YWHAZ 14-3-3 protein zeta/delta	IPI00021263	30890.03906	4.73	9	615.1844482	100	142.6799927	100	2.430456858	0.964619	9
COL1A2 Collagen alpha-2(I) chain precursor	IPI00304962	136968.0469	9.08	2	150.8000031	100	86.65000153	100	2.412886112	0.5153256	2
FSCN1 FSCN1 protein	IPI00747810	59288.51172	7.93	2	83.77999878	100	51.22000122	99.93444474	2.351865211	3.83E-02	2
ANXA7 Isoform 2 of Annexin A7	IPI00021771	52673.87891	6.25	1	77.56999969	99.99984808	77.56999969	99.99984808	2.301853704	0	1
CKAP4 CKAP4 protein (Fragment)	IPI00433214	72955.86719	9.34	10	674.2144775	100	99.13999939	100	2.287005397	1.4223606	10
- Rheumatoid factor D5 light chain (Fragment)	IPI00816799	13282.5498	9.15	1	61.18000031	99.99338382	61.18000031	99.99338382	2.280691044	0	1
BGN CDNA FLJ35635 fis, clone SPLEN2011805, highly similar to	IPI00385748	39528	6.31	4	198.6600037	100	68.30999756	99.99871883	2.279520057	0.9537916	4
DDX3Y ATP-dependent RNA helicase DDX3Y	IPI00293616	78372.53125	7.24	2	128.5800018	100	76.30999756	99.99979695	2.236079067	0.4423616	2

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STX7 Isoform 2 of Syntaxin-7	IPI00552913	29491.90039	5.02	1	67.40000153	99.99842018	67.40000153	99.99842018	2.233677757	0	1
COL6A3 alpha 3 type VI collagen isoform 4 precursor	IPI00072918	345401.0313	6.48	31	1747.334717	100	110.0500031	100	2.230964967	1.0447581	33
GSTP1 Glutathione S-transferase P	IPI00219757	25397.2207	5.43	3	164.3399963	100	66.19999695	99.99791739	2.174025472	0.3151039	3
ARPC3 12 kDa protein	IPI00796102	13215.08008	8.52	2	81.86999512	99.99994356	48.81999969	99.88607798	2.170654826	0.6971714	2
HNRPM Isoform 2 of Heterogeneous nuclear ribonucleoprotein M	IPI00383296	79706.89844	8.94	3	279.6699829	100	137.0299988	100	2.165247577	0.5364623	3
ARHGDIB 13 kDa protein	IPI00791712	14875.75977	4.69	2	168.4499969	100	128.8600006	100	2.16009022	0.2719841	2
NID2 NID2 protein	IPI00293033	111838.1875	5.38	2	93.08999634	100	54.43000031	99.96869544	2.145019197	0.616331	2
B2M B2M protein	IPI00796379	15076.12988	6.06	2	156.0100098	100	83.06999969	100	2.144708521	0.111012	2
ACTR3 Actin-like protein 3	IPI00028091	51165.26953	5.61	3	120.8099976	100	47.50999832	99.84596912	2.108060764	0.3238271	3
CYBB Cytochrome b-245 heavy chain	IPI00218646	71069.92188	8.9	1	91.33000183	100	91.33000183	100	2.105822832	0	1
VIM Vimentin	IPI00418471	56977.44141	5.06	23	1567.598633	100	114.6600037	100	2.104318013	0.7306668	26
GART Isoform Long of Trifunctional purine biosynthetic protein adenosine-3	IPI00025273	118791.6875	6.26	2	73.77000427	99.99963558	40.43000031	99.213665	2.091232779	0.3315155	2
HNRPF Heterogeneous nuclear ribonucleoprotein F	IPI00003881	48367.07813	5.38	4	221.8399963	100	109.75	100	2.072902227	0.5381524	4
C1S 75 kDa protein	IPI00743907	81580.29688	5.2	1	73.19000244	99.99958351	73.19000244	99.99958351	2.063512627	0	1
EIF4A1 Eukaryotic initiation factor 4A-I	IPI00025491	49332.85938	5.32	6	392.460022	100	118.6399994	100	2.059831144	1.0682674	7
RAC1 Isoform B of Ras-related C3 botulinum toxin substrate 1 precursor	IPI00219675	26798.57031	8.87	3	112.2099991	100	44.45999908	99.6891093	2.05560662	0.7959509	3
ERH Enhancer of rudimentary homolog	IPI00029631	13541.16016	5.63	2	135.75	100	96.52999878	100	2.052781748	0.5445948	2
RBM8A Isoform 2 of RNA-binding protein 8A	IPI00216659	21665.92969	5.64	1	111.5599976	100	111.5599976	100	2.043273795	0	1
MYH14 Isoform 5 of Myosin-14	IPI00029818	180709.0469	6.27	4	274.0744324	100	91.20999908	100	2.038690192	0.3858594	4
PKM2 58 kDa protein	IPI00784179	63980.44141	7.95	7	317.2000122	100	69.29000092	99.99897763	2.033596032	1.8681983	7
CCT7 chaperonin containing TCP1, subunit 7 isoform b	IPI00552072	40821.19141	6.04	1	72.73999786	99.99953804	72.73999786	99.99953804	2.029156189	0	1
HNRPA1 Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	IPI00465365	37003.55078	9.27	8	431.0100098	100	96.29000092	100	2.024902077	1.6538914	8
HNRPU heterogeneous nuclear ribonucleoprotein U isoform a	IPI00644079	101350.8203	5.76	5	259.6799927	100	70.44000244	99.99921547	2.008647525	0.82917	5

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TAGLN Transgelin	IPI00216138	25234.73047	8.87	5	302.4500122	100	89.48000336	100	2.005715396	0.1842202	5
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1406	5.6	4	270.4700012	100	104.8799973	100	1.99853832	0.5335837	4
MARCKS Myristoylated alanine-rich C-kinase substrate	IPI00219301	35850.28125	4.47	1	96.12000275	100	96.12000275	100	1.994727871	0	1
PCNA Proliferating cell nuclear antigen	IPI00021700	31474.51953	4.57	2	83.98999786	100	42.63999939	99.52727595	1.981602596	2.1532418	2
HNRPH3 Isoform 2 of Heterogeneous nuclear ribonucleoprotein H3	IPI00216492	36558.57031	6.36	3	217.6100006	100	79.33000183	99.9998987	1.978276332	0.6832766	3
IGF2BP2 Insulin-like growth factor 2 mRNA-binding protein 2	IPI00180983	67944.92969	8.22	1	68.97000122	99.99889946	68.97000122	99.99889946	1.968549684	0	1
IGF2BP3 64 kDa protein	IPI00746216	71308.52344	9.12	1	68.97000122	99.99889946	68.97000122	99.99889946	1.968549684	0	1
FLNA Filamin-A	IPI00333541	305957.375	5.7	17	991.5889282	100	112.0699997	100	1.927150925	0.7789952	17
DKFZp686D0972 hypothetical protein LOC345651	IPI00003269	44988.21875	5.39	6	366.0299683	100	86.11000061	100	1.919147952	0.5525134	8
GBP5 CTCL tumor antigen GBP-5ta (Fragment)	IPI00645391	61674.92188	5.52	2	89.22999573	100	58.25999832	99.98703992	1.908707005	0.1065657	2
YWHAH 14-3-3 protein eta	IPI00216319	31363.33008	4.76	6	292.8800049	100	64.13999939	99.99665337	1.906021069	0.4418584	6
CPNE1 53 kDa protein	IPI00852917	56975.76172	5.52	2	119.5	100	86.37000275	100	1.903531477	0.6271852	2
HNRPA3 Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	IPI00419373	42922.89844	9.1	4	374.2299805	100	178.1799927	100	1.898002176	1.1872072	5
YWHAG 14-3-3 protein gamma	IPI00220642	31015.18945	4.8	7	386.2000122	100	73.48999786	99.99961131	1.896552192	0.5344562	7
ACTG1;PSPHL Actin, cytoplasmic 2	IPI00021440	44922.05859	5.31	17	1177.290039	100	135.5800018	100	1.880646106	0.5297015	27
PSMD3 26S proteasome non-ATPase regulatory subunit 3	IPI00011603	66216	8.47	2	98.75	100	66.81999969	99.99819446	1.871599504	0.0403988	2
HMOX1 33 kDa protein	IPI00747450	35080.30078	8.72	1	58.81000137	99.98858154	58.81000137	99.98858154	1.856586533	0	1
NONO Non-POU domain-containing octamer-binding protein	IPI00304596	58321.69141	9.01	5	213.7644501	100	52.49000168	99.95106637	1.847189697	0.578229	5
PTGES3 19 kDa protein	IPI00789101	21682.35938	4.76	2	124.1699982	100	78.91999817	99.99988867	1.837413842	6.60E-02	2
SFPQ Isoform Long of Splicing factor, proline- and glutamine-rich	IPI00010740	81090.10938	9.45	5	249.9644318	100	65.47000122	99.99753619	1.834075517	0.6930046	5
ANXA11 Annexin A11	IPI00552303	19910.25	7.63	2	112.3600006	100	63.65999985	99.99626227	1.826493533	0.3563469	2
MYH10 Isoform 2 of Myosin-10	IPI00479307	260063.1719	5.46	9	456.8056335	100	104.7799988	100	1.819013661	0.9204365	9
MYH9 Myosin-9	IPI00019502	257357.9844	5.5	45	2882.604248	100	127.2200012	100	1.818237774	0.5821137	46

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YWHAQ 14-3-3 protein theta	IPI00018146	30857.03906	4.68	8	405.230011	100	91.94000244	100	1.80847221	0.5204737	8
HIST1H2BI;HIST1H2BG;HIST1H2BF;HIST1H2	IPI00020101	16921.91016	10.31	4	270.0700073	100	102.5400009	100	1.80170744	0.4890485	11
PA2G4 41 kDa protein	IPI00794875	47417.53125	6.82	4	233.8500061	100	79.51999664	99.99990304	1.799023917	0.3213148	4
ACTG2 Actin, gamma-enteric smooth muscle	IPI00025416	45052.03906	5.31	12	786.8900146	100	115.3899994	100	1.798472192	0.5372273	19
EIF4A3 Eukaryotic initiation factor 4A-III	IPI00009328	50527.51172	6.3	2	124.3899994	100	71.06999969	99.99932141	1.798107646	0.4579668	3
MYL6 17 kDa protein	IPI00744444	18920.58008	4.54	5	482.3500061	100	131.6999969	100	1.77027477	0.2367583	6
OTUB1 Hypothetical protein DKFZp564E242	IPI00000581	34180.75	4.9	1	95.68000031	100	95.68000031	100	1.763256892	0	1
ACTC1 Actin, alpha cardiac muscle 1	IPI00023006	45148.14063	5.23	12	800.7900391	100	115.3899994	100	1.760549247	0.4735275	21
YWHAB Isoform Short of 14-3-3 protein beta/alpha	IPI00759832	30949.07031	4.76	8	409.40448	100	96.88999939	100	1.759109233	0.6086951	8
DHX9 ATP-dependent RNA helicase A	IPI00844578	151431.7344	6.41	5	250.1688995	100	62.77000046	99.99541217	1.755607852	0.4352823	6
SFN Isoform 2 of 14-3-3 protein sigma	IPI00411765	26671.25	4.77	4	213.9900055	100	64.13999939	99.99665337	1.754667943	0.3838283	4
ARPC4 actin related protein 2/3 complex subunit 4 isoform b	IPI00607772	10554.03027	6.84	2	87.73999786	100	56.97999954	99.98259766	1.74827399	7.23E-03	2
COL6A1 Collagen alpha-1(VI) chain precursor	IPI00291136	117302.5391	5.26	7	492.5200195	100	110.4700012	100	1.746920651	0.1496196	7
NDUFS2 NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	IPI00025239	56146.01172	7.21	1	62.25	99.99482861	62.25	99.99482861	1.743114543	0	1
HCLS1 Hematopoietic lineage cell-specific protein	IPI00026156	59241.48828	4.74	5	207.5399933	100	54.18999863	99.96691678	1.732525816	1.0277794	5
HSP90AB1 Heat shock protein HSP 90-beta	IPI00414676	94433.0625	4.97	30	1951.044434	100	115.0299988	100	1.73181602	0.9471513	33
PKLR Pyruvate kinase L	IPI00743713	67899.96875	7.6	3	140.9700012	100	69.29000092	99.99897763	1.723734413	0.6054856	3
MATR3 100 kDa protein	IPI00789551	110688.2734	5.71	2	94.50999451	100	54.47999954	99.96905377	1.723535818	7.26E-02	2
NCL Isoform 1 of Nucleolin	IPI00604620	89719.57031	4.6	10	590.4199829	100	103.3899994	100	1.722700593	0.8444746	11
- Transforming growth factor, beta-induced, 68kDa variant (Fragment)	IPI00556324	27690.46094	5.33	1	77.80000305	99.99985592	77.80000305	99.99985592	1.721331012	0	1
PFN1 Profilin-1	IPI00216691	16766.75	8.44	8	600.2699585	100	142.2599945	100	1.714901522	0.734022	8
KRT19 Keratin, type I cytoskeletal 19	IPI00479145	46225.37891	5.04	7	341.1699829	100	83.98000336	100	1.710563791	0.8207215	7
PFKM CDNA FLJ44241 fis, clone THYMU3008436, highly similar to 6-	IPI00465179	101419.0313	8.2	1	56.61999893	99.98109365	56.61999893	99.98109365	1.706116229	0	1

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LMNB1 LMNB1 protein	IPI00790831	48786.14063	4.99	6	246.4799805	100	68.48999786	99.99877084	1.700971254	0.4200787	6
ALDOA Fructose-bisphosphate aldolase A	IPI00465439	43651.62891	8.3	10	774.1444092	100	120.5299988	100	1.693642539	0.7375481	10
ILK Integrin-linked protein kinase	IPI00013219	55688.23828	8.3	1	72.62000275	99.99952509	72.62000275	99.99952509	1.683716652	0	1
CLTC Isoform 2 of Clathrin heavy chain 1	IPI00455383	203165.7031	5.48	8	418.0299988	100	73.05999756	99.99957085	1.674421285	0.9930723	9
ANXA2 Annexin A2	IPI00455315	43516.26953	7.57	14	874.848877	100	104.6299973	100	1.673743489	0.4657385	14
HIST3H3 Histone H3.1t	IPI00216402	17606.75	11.13	4	167.8199921	100	54.75999832	99.97098599	1.66937617	0.3689901	4
EIF4A2 Isoform 2 of Eukaryotic initiation factor 4A-II	IPI00409717	49956.14063	5.33	4	318.9299927	100	118.6399994	100	1.666609992	1.2554873	5
COL6A2 Isoform 2C2A of Collagen alpha-2(VI) chain precursor	IPI00220613	105910.7031	5.38	3	195.9599915	100	74.73999786	99.99970852	1.664949191	0.4251385	3
TUBB Tubulin beta chain	IPI00011654	52311.16016	4.78	18	1291.790039	100	144.4199982	100	1.659437419	0.6396325	21
LCP1 Plastin-2	IPI00010471	77185.35938	5.2	8	366.1999817	100	72.69999695	99.99953376	1.655249558	0.5203204	8
NUMA1 Isoform 1 of Nuclear mitotic apparatus protein 1	IPI00292771	260878.9688	5.63	2	121.7400055	100	63.68000031	99.99627945	1.651112674	0.1357461	2
STAT1 Isoform Beta of Signal transducer and activator of transcription 1-al	IPI00218188	91515.17188	6.02	6	272.4599915	100	69.06999969	99.99892451	1.650141086	0.9811945	6
SAA1;SAA2 Serum amyloid A protein precursor	IPI00552578	14433.66992	6.28	3	307.8399963	100	156.3099976	100	1.649195549	0.4554382	3
TUBA1B Similar to Tubulin alpha-ubiquitous chain	IPI00792677	49578.05859	4.96	11	934.1499634	100	165.2400055	100	1.645599936	0.5736838	13
DYNLL1 Dynein light chain 1, cytoplasmic	IPI00019329	12081.2998	6.89	2	84.43000031	100	45.15000153	99.73477926	1.643114846	6.73E-02	2
EMILIN1 EMILIN-1 precursor	IPI00013079	109415.4531	5.1	2	136.2799988	100	92.22000122	100	1.639988624	0.5416282	2
APOC3 13 kDa protein	IPI00657670	13861.62012	7.9	1	109.9199982	100	109.9199982	100	1.628990486	0	1
DYNC1I2 Isoform 2B of Cytoplasmic dynein 1 intermediate chain 2	IPI00302712	77936.72656	5.1	1	66.86000061	99.99821101	66.86000061	99.99821101	1.621869371	0	1
ARF5 17 kDa protein	IPI00853337	18726.14063	6.74	1	73.23999786	99.99958827	73.23999786	99.99958827	1.596322024	0	1
SAA1;SAA2 serum amyloid A2	IPI00006146	14428.79004	9.2	3	245.9299927	100	94.40000153	100	1.593610038	0.5222085	3
ARF3 ADP-ribosylation factor 3	IPI00215917	22649.98047	6.84	2	81.80000305	99.99994264	44.75	99.70919114	1.589681557	0.250007	2
RAN 26 kDa protein	IPI00792352	29358.91016	8.51	3	182.4000092	100	85.73999786	100	1.587407123	0.6179264	3
ANXA5 Annexin A5	IPI00329801	39272.76172	4.94	12	753.3899536	100	105.2900009	100	1.582858736	0.4432637	12

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CTSS Cathepsin S precursor	IPI00299150	42009.60938	8.61	1	63.11000061	99.99575764	63.11000061	99.99575764	1.582598874	0	1
LGALS3BP Galectin-3-binding protein precursor	IPI00023673	68905.42969	5.13	4	212.230011	100	94.05000305	100	1.579800053	0.3402115	4
BCAP31 21 kDa protein	IPI00639976	22905.44922	8.94	3	135.6300049	100	58.34999847	99.98730573	1.57895904	0.6957274	3
PLEC1 plectin 1 isoform 6	IPI00186711	568646.6875	5.74	9	372.9801331	100	65.80000305	99.99771647	1.578606393	0.7132134	9
DSTN 15 kDa protein	IPI00643237	18687.19922	8.84	1	55.95999908	99.97799062	55.95999908	99.97799062	1.573136108	0	1
RPS7 40S ribosomal protein S7	IPI00013415	25713.66016	10.09	2	97.09999847	100	48.88999939	99.88789946	1.562806921	0.1929502	2
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00743359	42850.23828	6.08	3	115.8099976	100	42.18000031	99.47445779	1.560256705	0.4772893	3
YWHAE 14-3-3 protein epsilon	IPI00000816	32029.69922	4.63	8	505.2099609	100	132.5399933	100	1.556450597	0.5594842	8
FUBP1 Isoform 2 of Far upstream element-binding protein 1	IPI00644386	73175.53125	7.74	3	119.7200012	100	45.81999969	99.77269569	1.55643709	0.5860938	3
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00742968	42765.21875	5.91	4	152.1199951	100	45.75	99.76900231	1.555103368	0.3854709	4
HIST1H1D Histone H1.3	IPI00217466	31265.17969	11.02	2	105.9199982	100	71.88999939	99.99943817	1.552994885	0.233981	2
TUBB2A Tubulin beta-2A chain	IPI00013475	52501.16016	4.78	14	1052.599976	100	144.4199982	100	1.540607386	0.5591041	17
PDHB Isoform 2 of Pyruvate dehydrogenase E1 component subunit beta, mitocho	IPI00549885	40188.14063	5.64	1	87.01000214	100	87.01000214	100	1.540355886	0	1
HLA-DRB1;HLA-DRB5;LOC730415;hCG_1998957;HLA-	IPI00815988	14149.65039	5.91	3	153.1999969	100	76.62999725	99.99981137	1.538129854	0.7516925	3
HMGB1 High mobility group protein B1	IPI00419258	31352.75977	5.62	2	186.3544464	100	96.87000275	100	1.535736102	1.0810478	2
TNS3 tensin 3	IPI00658152	166503.375	6.34	1	74.55000305	99.99969549	74.55000305	99.99969549	1.533971904	0	1
CCT2 T-complex protein 1 subunit beta	IPI00297779	63200.62109	6.01	3	197.9300079	100	69.55000305	99.99903704	1.526447327	0.3281597	3
TUBB2C Tubulin beta-2C chain	IPI00007752	52471.19141	4.79	17	1309.77002	100	144.4199982	100	1.524432112	0.5128577	20
TMPO Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma	IPI00181409	43512.75	9.18	1	57.25	99.98364662	57.25	99.98364662	1.51749335	0	1
TUBB3 Tubulin beta-3 chain	IPI00013683	53216.46094	4.83	11	828.3200073	100	144.4199982	100	1.517015114	0.4999962	12
APCS Serum amyloid P-component precursor	IPI00022391	27335.35938	6.1	1	71.68000031	99.99941033	71.68000031	99.99941033	1.5152239	0	1
NHP2L1 NHP2-like protein 1	IPI00026167	15932.73047	8.72	2	77.66000366	99.9998512	40.93000031	99.2991782	1.514569261	0.1277811	2
SNRP70 Isoform 3 of U1 small nuclear ribonucleoprotein 70 kDa	IPI00219484	21454.14063	7.82	1	58.11444092	99.98659819	59.29000092	99.98977631	1.510611353	0	1

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SAMHD1 SAM domain and HD domain-containing protein 1	IPI00294739	79521.28906	6.69	6	352.8399963	100	97.97000122	100	1.508418286	0.3213406	6
TUBB6 43 kDa protein	IPI00643158	44746.64063	4.71	7	327.5299988	100	83.66000366	100	1.50533307	0.5064512	7
PTBP1 polypyrimidine tract-binding protein 1 isoform a	IPI00183626	64630.35156	9.21	2	118.6999969	100	69.20999908	99.99895862	1.501639526	7.44E-02	2
- Tryptophanyl-tRNA synthetase (Fragment)	IPI00383754	12867.94043	4.57	1	62.81444168	99.99545887	63.99000168	99.99653576	1.499615305	0	1
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472284	42123.23047	5.77	6	278.3599854	100	76.51999664	99.99980653	1.495260368	0.3147671	6
HNRPD Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	IPI00220684	37704.55859	8.23	3	179.5599976	100	79.04000092	99.99989171	1.494500722	0.3398456	4
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472676	42024.01172	5.55	6	292.5099792	100	76.51999664	99.99980653	1.489127242	0.3215919	6
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472943	42316.07031	5.84	3	134.269989	100	50.02000046	99.91358133	1.485178178	0.5127508	3
ALDH16A1 Aldehyde dehydrogenase family 16 member A1	IPI00217920	87917.74219	6.35	1	74	99.99965437	74	99.99965437	1.482258431	0	1
TUBB6 TUBB6 protein	IPI00646779	52874.32813	4.8	9	606.7999878	100	144.4199982	100	1.474440062	0.5173359	10
MCCC2 Isoform 2 of Methylcrotonoyl-CoA carboxylase beta chain, mitochondria	IPI00789428	61882.76172	7.59	3	144.8500061	100	63.04000092	99.99568871	1.466712228	2.0151389	3
RPS3 40S ribosomal protein S3	IPI00011253	29833.74023	9.68	2	98.37999725	100	63.09999847	99.99574786	1.465484638	0.1581078	2
PFKL Liver phosphofructokinase isoform a	IPI00784216	96819.92188	8.17	2	106.9300003	100	59.36000061	99.98993978	1.462342175	0.2437741	2
HLA-DRA major histocompatibility complex, class II, DR alpha precursor	IPI00464948	30468.91016	4.91	2	123.0800018	100	78.25	99.9998701	1.459834572	0.5707349	2
UBE1 Ubiquitin-activating enzyme E1	IPI00645078	126424.8516	5.49	2	105.7799988	100	65.90000153	99.99776845	1.449224297	4.68E-02	2
XRCC6 ATP-dependent DNA helicase 2 subunit 1	IPI00644712	78669.82813	6.23	4	244.4944305	100	98.86000061	100	1.448476068	0.716455	4
DYNC1H1 532 kDa protein	IPI00477531	576722	6.03	4	157.3933105	100	55.36000061	99.97472986	1.447052939	0.3254075	4
LOC653888 similar to Actin-related protein 2/3 complex subunit 1B	IPI00737530	45280.69141	9.11	1	87.95999908	100	87.95999908	100	1.44286733	0	1
HSPG2 Basement membrane-specific heparan sulfate proteoglycan core protein	IPI00024284	487110.1563	6.06	7	277.0344238	100	54.72999954	99.97078488	1.442045774	1.2560232	7
COL14A1 Isoform 3 of Collagen alpha-1(XIV) chain precursor	IPI00402215	195721.9844	5.16	2	73.08999634	99.99957381	37.04000092	98.28364332	1.441838496	0.2369642	2
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00718924	42211.23828	5.96	6	281.6699829	100	76.51999664	99.99980653	1.440332069	0.2296209	6
SCAMP3 Isoform 2 of Secretory carrier-associated membrane protein 3	IPI00306383	37073.82813	7.53	2	113.1800079	100	68.44000244	99.99875661	1.438629459	9.34E-02	2
RHOA Transforming protein RhoA precursor	IPI00027500	24622.31055	5.83	2	99.72000122	100	55.41999817	99.97507657	1.432768417	0.8001399	2

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- Elongation factor 1-alpha	IPI00472724	57485.78125	9.15	11	706.2999878	100	110.4199982	100	1.430951474	0.5253133	12
- 140 kDa protein	IPI00829641	149651.875	7.92	3	206.5200043	100	80.63999939	99.99992508	1.429835322	0.2047226	3
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472282	42025.16016	5.89	6	267.5244446	100	76.51999664	99.99980653	1.426254021	0.4222042	6
TPM4 Isoform 1 of Tropomyosin alpha-4 chain	IPI00010779	32340.88086	4.67	8	475.269989	100	102.9800034	100	1.423207559	0.3668562	8
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472903	42843.35156	6.52	5	220.2600098	100	50.02000046	99.91358133	1.420413722	0.4989142	5
HSP90AB4P Heat shock protein 90Bd	IPI00555565	66222.17969	4.65	7	425.6400146	100	103.3799973	100	1.417303742	0.8307596	7
OSTF1 Osteoclast-stimulating factor 1	IPI00414836	26502.21094	5.46	1	79.80999756	99.9999093	79.80999756	99.9999093	1.416332798	0	1
RCN1 Reticulocalbin-1 precursor	IPI00015842	42898.60156	4.86	3	134.0799866	100	53.45999908	99.96086118	1.410986976	0.8203622	3
COTL1 Coactosin-like protein	IPI00017704	18043.26953	5.54	2	102.9499969	100	53.81000137	99.96389166	1.405608029	0.4405755	2
HNRPL heterogeneous nuclear ribonucleoprotein L isoform b	IPI00465225	54634.78125	7.22	5	330.8099976	100	90.86000061	100	1.395462	0.7600105	5
ECGF1 46 kDa protein	IPI00853163	47964.32813	5.35	2	117.0200043	100	58.99000168	99.98904512	0.709960587	0.2917728	2
- 17 kDa protein	IPI00794543	18448.19922	4.06	4	180.6399994	100	53.84000015	99.96414022	0.709538955	0.2530146	5
DDAH1 NG,NG-dimethylarginine dimethylaminohydrolase 1	IPI00220342	34258.19922	5.53	2	109.4100037	100	57.08000183	99.98299379	0.708909642	9.18E-02	2
RPL10 Ribosomal protein L10	IPI00646899	30498.25	10.2	3	116.25	100	47.00999832	99.82717451	0.705977674	0.1780875	3
PSME1 29 kDa protein	IPI00479722	32701.33008	5.27	5	246.464447	100	71	99.99931038	0.703753652	0.2267562	5
SLC25A13 Mitochondrial aspartate-glutamate carrier protein	IPI00007084	80339.20313	8.79	2	67.47999573	99.99844901	35.45999908	97.53050741	0.701523198	3.42E-02	2
ACAT2 Acetyl-CoA acetyltransferase, cytosolic	IPI00291419	44906.64063	6.47	2	119.5299988	100	77.04000092	99.99982836	0.700233296	8.50E-02	2
COX4I1 COX4I1 protein	IPI00645361	10672.90039	8.64	3	152.1500092	100	79.16000366	99.99989466	0.700031485	0.3279608	3
LTB4DH NADP-dependent leukotriene B4 12-hydroxydehydrogenase	IPI00292657	40639.17188	8.45	3	169.0899963	100	81.90000153	99.99994395	0.697922439	0.2437829	3
PPIB peptidylprolyl isomerase B precursor	IPI00646304	27661.94922	9.42	8	450.2444458	100	85.15000153	100	0.689899124	0.1151863	10
PSMB2 Proteasome subunit beta type 2	IPI00028006	24687.88086	6.51	2	76.77000427	99.99981736	44.40999985	99.68550941	0.680048896	0.1599511	2
ATP5A1 ATP synthase subunit alpha, mitochondrial precursor	IPI00440493	64270.03906	9.16	14	811.444458	100	127.6500015	100	0.678550992	0.2904419	15
RPS13 40S ribosomal protein S13	IPI00221089	19947.99023	10.53	4	197.3200073	100	71.76999664	99.99942243	0.675449132	0.2256954	4

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RPS2 40S ribosomal protein S2	IPI00013485	35134.92969	10.25	4	180.7644348	100	74.16999817	99.99966764	0.674202045	0.6080656	4
MAT2B Isoform 1 of Methionine adenosyltransferase 2 subunit beta	IPI00002324	40396.42188	6.9	2	109.7099991	100	56.90999985	99.98231489	0.672663819	0.2057659	2
NIPSNAP1 Protein NipSnap1	IPI00304435	36019.10938	9.35	3	156.9400024	100	75.05999756	99.99972923	0.671390681	0.6969326	3
SELENBP1 53 kDa protein	IPI00745729	57664.26953	6.03	3	122.3199997	100	48.38000107	99.87393123	0.671347102	0.5708795	3
CALR Protein	IPI00794237	19298.58008	4.47	4	199.644455	100	67.76000214	99.99854586	0.667621437	0.232172	5
RPL28 Ribosomal protein L28 variant (Fragment)	IPI00816097	11793.78027	10.42	1	64.56999969	99.99696885	64.56999969	99.99696885	0.663855491	0	1
MTCH2 Mitochondrial carrier homolog 2	IPI00003833	35542.96875	8.25	4	147.0400085	100	42.33000183	99.49229966	0.663473899	0.3389921	4
KRT18 Keratin, type I cytoskeletal 18	IPI00784347	51196.89844	5.34	15	897.7000122	100	157.1699982	100	0.658860386	0.3229556	16
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	26915.57031	5.15	4	180.1600037	100	55.77999878	99.97705924	0.656672586	0.2613248	4
TXNDC5;MUTED thioredoxin domain containing 5 isoform 2	IPI00395646	48461.78125	5.77	8	427.9144592	100	124.4400024	100	0.655687571	0.2581076	8
ATP5B ATP synthase subunit beta, mitochondrial precursor	IPI00303476	59980.98828	5.26	15	1113.828857	100	133.5500031	100	0.654245025	0.2564786	16
SORD Sorbitol dehydrogenase	IPI00216057	42378.10938	8.23	2	84.18000031	100	46.40999985	99.80156985	0.654096842	0.6565632	2
H6PD GDH/6PGL endoplasmic bifunctional protein precursor	IPI00607861	93328.71875	6.84	4	199.3499908	100	69.16000366	99.99894657	0.653421097	0.1725092	4
COX6C Cytochrome c oxidase polypeptide VIc precursor	IPI00015972	9927.879883	10.38	4	213.6199951	100	79.45999908	99.99990169	0.650299096	0.3014299	4
RPL4 60S ribosomal protein L4	IPI00003918	56250.17969	11.07	2	110.6888809	100	60.06000137	99.99143736	0.643630448	0.1652094	2
FLJ21963 hypothetical protein LOC79611	IPI00002245	81861.02344	8.84	4	171.519989	100	60.43000031	99.99213665	0.637623756	0.5362779	4
hCG_1640785 hypothetical protein LOC401206	IPI00401105	17395.9707	10.06	2	96.19000244	100	58.09999847	99.98655355	0.635795235	5.92E-02	2
ACOT1 Acyl-coenzyme A thioesterase 1	IPI00333838	49306.28906	6.9	2	108.1200027	100	55.54000092	99.97575582	0.633956785	0.1934598	2
CALR 37 kDa protein	IPI00793605	41138.14063	4.55	9	613.4599609	100	119.5299988	100	0.633365462	0.2472835	10
ATP5O ATP synthase O subunit, mitochondrial precursor	IPI00007611	26090.96094	9.97	3	136.8300018	100	59.06000137	99.98922028	0.633134907	0.5895055	3
TBCA Tubulin-specific chaperone A	IPI00217236	15052.96973	5.25	1	80.80999756	99.99992795	80.80999756	99.99992795	0.632750341	0	1
VDP General vesicular transport factor p115	IPI00743314	117492.7188	4.85	1	117.6399994	100	117.6399994	100	0.631387915	0	1
BAAT Bile acid CoA:amino acid N-acyltransferase	IPI00017819	48856.32031	6.49	2	115.2200012	100	75.95999908	99.99977991	0.628377233	0.4548838	2

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PARK7 Protein DJ-1	IPI00298547	22464.75	6.33	5	252.5	100	69.95999908	99.99912379	0.624540853	0.2164835	6
SUCLG1 succinate-CoA ligase, GDP-forming, alpha subunit	IPI00759493	39717.12109	9.01	4	317.9500122	100	103.5100021	100	0.624498481	0.2163542	4
PSMA4 Proteasome subunit beta type	IPI00789638	30677.13086	6.91	1	72.26000214	99.99948405	72.26000214	99.99948405	0.621435134	0	1
RRBP1 Isoform 1 of Ribosome-binding protein 1	IPI00220967	178629.8125	8.73	9	593.3644409	100	128	100	0.620036407	0.2720343	9
HADHA Trifunctional enzyme subunit alpha, mitochondrial precursor	IPI00031522	93913.70313	9.16	18	1015.214417	100	86.76999664	100	0.618746666	0.3539562	19
MAOA Amine oxidase [flavin-containing] A	IPI00008483	65674.00781	7.94	4	194.8500061	100	56.27000046	99.9795069	0.617648444	0.5761415	4
TPI1 Isoform 1 of Triosephosphate isomerase	IPI00465028	34025.98828	5.65	9	789.1199951	100	118.0400009	100	0.614538423	0.2342444	9
GSTO1 Glutathione transferase omega-1	IPI00019755	31234.35938	6.23	3	140.8699951	100	65.12999725	99.99733555	0.610431327	0.1127696	3
HSPA5 HSPA5 protein	IPI00003362	81398.29688	5.07	25	2094.601318	100	141.3300018	100	0.609786135	0.3513689	28
PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904	82667.8125	4.96	19	1037.39563	100	115.0999985	100	0.609272723	0.3742005	19
SLC25A3 Isoform B of Phosphate carrier protein, mitochondrial precursor	IPI00215777	44188.96875	9.43	2	86.86000061	100	54.77000046	99.97105273	0.606985706	0.146756	2
CSTB Cystatin-B	IPI00021828	12618.79004	6.96	3	223.1999969	100	95.09999847	100	0.605079798	0.1317777	3
GPI Glucose-6-phosphate isomerase	IPI00027497	68475.72656	8.43	4	201.3800049	100	83.58000183	100	0.603494576	0.1654314	4
GGTLA1 Isoform 2 of Gamma-glutamyltransferase 5 precursor	IPI00339373	61051.73828	7.67	2	115.5200043	100	73.97000122	99.99965198	0.598232936	0.2437469	2
- 14 kDa protein	IPI00455040	16069.75977	8.86	1	85.73000336	100	85.73000336	100	0.596104915	0.2578946	2
PSMB4 Proteasome subunit beta type 4 precursor	IPI00555956	30095.63086	5.72	1	63.95000076	99.99650371	63.95000076	99.99650371	0.595278334	0	1
AKR1A1 Alcohol dehydrogenase	IPI00220271	39850.12891	6.32	8	335.4844055	100	64.26999664	99.99675206	0.594544498	0.3388224	8
PRDX4 Protein	IPI00639945	19604.41992	5.56	2	143.9100037	100	78.26000214	99.9998704	0.593714379	8.47E-02	2
PRDX6 Peroxiredoxin-6	IPI00220301	27847.49023	6	10	643.0400391	100	128.3000031	100	0.592424759	0.4994095	10
CMPK cytidylate kinase	IPI00219953	29138.61914	8.14	4	270.5400085	100	93.48000336	100	0.589409251	0.2379775	4
LMAN1 ERGIC-53 protein precursor	IPI00026530	62207.39063	6.3	4	274.3800049	100	128.4499969	100	0.587250838	7.27E-02	4
PSMA3 Isoform 1 of Proteasome subunit alpha type 3	IPI00419249	31335.35938	5.19	1	66.55000305	99.99807865	66.55000305	99.99807865	0.587213411	0	1
PDIA4 Protein	IPI00852792	21271.91992	8.33	6	305.4400024	100	86.51000214	100	0.585293111	0.1233382	6

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MAT1A S-adenosylmethionine synthetase isoform type-1	IPI00021772	47392.28906	5.86	5	238.8744507	100	86.52999878	100	0.584329845	0.3511509	5
HSPA9 Stress-70 protein, mitochondrial precursor	IPI00007765	81497.46094	5.87	15	1009.074463	100	120.0699997	100	0.582349001	0.3419179	15
FTL Ferritin light chain	IPI00852596	21925.33984	5.51	5	342.6799927	100	92.97000122	100	0.578543496	0.2297759	5
HYOU1 Hypoxia up-regulated protein 1 precursor	IPI00000877	122683.2188	5.16	7	415.25	100	80.76000214	99.99992712	0.571204972	0.3064075	7
- 25 kDa protein	IPI00412122	28146.10938	5.48	1	71.98999786	99.99945096	71.98999786	99.99945096	0.569920376	0	1
SDHB Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondria	IPI00294911	35997.07813	9.03	2	70.75	99.99926952	41.16999817	99.33685604	0.569495287	3.25E-02	2
FKBP2 FK506-binding protein 2 precursor	IPI00002535	17649.5293	9.24	4	248.9899902	100	92.48999786	100	0.568843863	0.1313032	4
HINT1 Histidine triad nucleotide-binding protein 1	IPI00239077	15325.28027	6.43	3	246.1499939	100	98.5	100	0.559835694	0.5945098	3
MAOB Amine oxidase [flavin-containing] B	IPI00328156	63747.53125	7.2	3	113.6699982	100	42.02999878	99.4559889	0.559769523	0.1652405	3
HADHB Trifunctional enzyme beta subunit, mitochondrial precursor	IPI00022793	56777.03906	9.45	8	446.4799805	100	85.72000122	100	0.554907365	0.1521809	8
RPLP2 60S acidic ribosomal protein P2	IPI00008529	13242.07031	4.42	1	94.69000244	100	94.69000244	100	0.549054121	0	1
- CALRETICULIN=CALCIUM binding protein (Fragment)	IPI00383751	26354.40039	4.45	5	398.019989	100	119.5299988	100	0.548444226	0.2686494	5
AK3 GTP:AMP phosphotransferase	IPI00478236	20052.85938	8.73	2	117.5599976	100	72.27999878	99.99948642	0.547042121	0.3086591	2
EIF3S10 EIF3S10 protein (Fragment)	IPI00386403	51034.98047	6.24	1	62.02000046	99.99454735	62.02000046	99.99454735	0.54692606	0	1
CBR1 Carbonyl reductase [NADPH] 1	IPI00295386	33322.12891	8.55	7	415.6700134	100	96.26000214	100	0.545126887	0.3470988	7
CNDP2 53 kDa protein	IPI00646632	58467.37891	5.66	12	831.8200073	100	143.2700043	100	0.543299371	0.2616244	12
PPIF Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor	IPI00026519	24750.41992	9.48	2	94.19999695	100	56.33000183	99.97978809	0.53960438	0.2276606	2
CYP4F2 Cytochrome P450 4F2	IPI00019160	63921.05859	6.6	2	96.68000031	100	53.95000076	99.96503709	0.537991178	2.33E-02	2
CRYZ Quinone oxidoreductase	IPI00000792	38778.89063	8.56	4	282.1300049	100	136.2400055	100	0.537260357	0.193974	5
HDHD3 Haloacid dehalogenase-like hydrolase domain-containing protein 3	IPI00009931	29030.5293	6.21	2	145.4799957	100	83.97000122	100	0.532809137	0.5128546	2
C5orf33 hypothetical protein LOC133686 isoform 1	IPI00845432	52310.35156	8.46	2	125.7099991	100	74.59999847	99.99969897	0.531246871	7.35E-02	2
ALDOC 16 kDa protein	IPI00789171	18438.7207	7.74	3	225.0944519	100	119.3600006	100	0.529430692	1.3628115	3
- 24 kDa protein	IPI00747151	25497.4707	8.59	1	70.16999817	99.99916515	70.16999817	99.99916515	0.52294488	0	1

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ETFB Isoform 2 of Electron transfer flavoprotein subunit beta	IPI00556451	41287.32813	6.78	6	258.9599915	100	50.45999908	99.92190779	0.520850789	0.5893814	6
ALDH1L1 Formyltetrahydrofolate dehydrogenase isoform a variant	IPI00793673	109020.6328	5.63	3	135.6988831	100	64.37000275	99.996826	0.520285275	8.18E-02	3
TGM2 Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2	IPI00294578	82951.92188	5.11	9	502.7399902	100	71.41999817	99.99937395	0.518355287	0.1696458	9
ARG1 Isoform 2 of Arginase-1	IPI00398768	39380.19922	6.72	3	109.0600052	100	42.08000183	99.46221653	0.517708326	9.18E-03	3
MDH1 Malate dehydrogenase, cytoplasmic	IPI00291005	41195.46094	6.91	2	88.31999969	100	53.47999954	99.96104101	0.515299458	0.1197618	2
UNQ501 MBC3205	IPI00063130	22277.99023	8.91	1	78.47000122	99.99987652	78.47000122	99.99987652	0.51330587	0	1
PECI Peroxisomal 3,2-trans-enoyl-CoA isomerase	IPI00639841	48775.80078	9.13	3	167.6699982	100	69.70999908	99.99907187	0.512863655	0.3277265	3
AKR7A3 Aflatoxin B1 aldehyde reductase member 3	IPI00293721	39376.69141	6.67	4	184.1999969	100	59.41999817	99.9900778	0.510574105	0.4268619	4
EHHADH Peroxisomal bifunctional enzyme	IPI00216164	86466.10156	9.22	5	201.9244385	100	47.52999878	99.84667684	0.509688146	0.315607	5
PGM1 Isoform 1 of Phosphoglucomutase-1	IPI00219526	66969.02344	6.3	9	556.8944092	100	84.62000275	100	0.506107448	0.4262223	9
NNT NAD(P) transhydrogenase, mitochondrial precursor	IPI00337541	123493.2578	8.31	6	286.5700073	100	70.95999908	99.999304	0.505580126	0.4705573	6
ASL argininosuccinate lyase isoform 3	IPI00607563	52220	5.82	3	204.2899933	100	104.8399963	100	0.503857536	0.4147404	3
CPT2 Carnitine O-palmitoyltransferase 2, mitochondrial precursor	IPI00012912	79760.85938	8.38	3	159.0399933	100	87.09999847	100	0.503164303	0.2232465	3
LDHAL6A L-lactate dehydrogenase A-like 6A	IPI00148061	40792.55078	6.51	2	83.77999878	100	53.88999939	99.9645507	0.502956422	8.89E-02	2
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	58388.32813	6.3	11	675.194397	100	86.12999725	100	0.500703053	0.5535931	11
PYGL 97 kDa protein	IPI00783313	107098.9297	6.71	7	371.960022	100	74.45999908	99.99968911	0.497331683	0.1438407	7
HSDL2 Hydroxysteroid dehydrogenase-like protein 2	IPI00414384	51500.05078	8.07	2	130.7600098	100	66.23000336	99.99793173	0.496676682	0.4643452	2
NNMT Nicotinamide N-methyltransferase	IPI00027681	33091.32031	5.56	2	81.08000183	99.9999323	48.75999832	99.88449313	0.496517605	7.75E-03	2
ADH5 Alcohol dehydrogenase class 3	IPI00746777	45140.69141	7.45	3	166.0499878	100	74.87999725	99.99971777	0.494034083	0.1671787	3
DBT Lipoamide acyltransferase component of branched-chain alpha-keto acid d	IPI00003944	59823.44141	8.71	2	95.1499939	100	60.72999954	99.99266149	0.492313503	0.3117282	2
MT1X Metallothionein-1X	IPI00008753	8279.200195	8.38	2	126.2200012	100	91.13999939	100	0.492172477	5.80E-02	2
SDHA Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondri	IPI00305166	77793.53125	7.06	7	333.210022	100	66.87000275	99.99821513	0.492049902	0.1779117	7
PCCB Hypothetical protein	IPI00387103	34520.42188	4.61	1	60.76443863	99.99271946	61.93999863	99.99444598	0.485108568	0	1

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AKR1C3 Aldo-keto reductase family 1 member C3	IPI00291483	41031.17969	8.05	6	283.6900024	100	69.58000183	99.99904367	0.483249334	0.3538979	7
AKR1B1 Aldo-keto reductase family 1, member B1 variant (Fragment)	IPI00556258	32725.51953	6.54	1	64.26999664	99.99675206	64.26999664	99.99675206	0.482063754	0	1
CAT Catalase	IPI00465436	64367.17969	6.9	9	586.8799438	100	92.09999847	100	0.474786979	0.2565191	9
HAO1 Hydroxyacid oxidase 1	IPI00006934	44682.82031	8.2	3	167.6299896	100	63.11999893	99.99576739	0.473177436	0.6801375	3
RPS5 40S ribosomal protein S5	IPI00008433	25448.32031	9.73	1	131.8699951	100	131.8699951	100	0.467551933	0	1
P4HB Protein disulfide-isomerase precursor	IPI00010796	64315.26953	4.76	22	1451.75	100	133.8200073	100	0.467384977	0.2417369	26
SDHALP2 SDHALP2 protein	IPI00479656	17968.10938	6.14	2	89.30999756	100	49.00999832	99.89095449	0.464925415	0.2353338	2
KIAA1598 Protein KIAA1598	IPI00448751	84444.75781	5.37	1	59.45999908	99.99016877	59.45999908	99.99016877	0.456801315	0	1
FIS1 Mitochondrial fission 1 protein	IPI00007052	19709.33008	8.84	1	81.41000366	99.99993725	81.41000366	99.99993725	0.452613816	0	1
TXN Thioredoxin	IPI00216298	13831.92969	4.82	5	406.0899963	100	113.0999985	100	0.452153751	0.1138242	6
DCXR 26 kDa protein	IPI00797249	27252.58984	8.33	6	363.5799866	100	103.5100021	100	0.451098867	0.2391219	6
HSD17B4 Peroxisomal multifunctional enzyme type 2	IPI00019912	88068.99219	8.96	7	440.2000122	100	115.1399994	100	0.447403755	0.2228602	7
CYCS Cytochrome c	IPI00465315	14569.42969	9.59	4	228.3599854	100	82.93000031	100	0.446292709	0.2908261	5
PGRMC2 Membrane-associated progesterone receptor component 2	IPI00005202	28072.17969	5.2	2	75.04000092	99.99972798	41.04000092	99.3167061	0.444895348	9.14E-03	2
UGDH UDP-glucose 6-dehydrogenase	IPI00031420	60869.64844	6.73	4	301.5299988	100	154.0599976	100	0.443838373	0.2453099	4
UGT2B17 similar to UDP glycosyltransferase 2 family, polypeptide B17	IPI00787638	68438.74219	8.79	2	91.8944397	100	60.18000031	99.99167072	0.443274951	6.83E-02	2
- 105 kDa protein	IPI00794900	115433.2422	7.3	8	472.1400146	100	131.25	100	0.442075944	0.1335476	8
METTL7B Methyltransferase-like protein 7B precursor	IPI00090807	30474.44922	8.71	1	60.75999832	99.99271201	60.75999832	99.99271201	0.439943059	0	1
BLVRB Flavin reductase	IPI00783862	23637.61914	7.13	2	102.4599991	100	55.20999908	99.97384181	0.437948024	0.1534966	2
UGP2 Isoform 1 of UTP--glucose-1-phosphate uridylyltransferase	IPI00329331	63091.28906	8.16	8	568.944458	100	147.1399994	100	0.435690072	0.4773601	9
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	68931.10156	5.7	20	1502.262207	100	123.1399994	100	0.435211153	0.3046954	21
AKR1C1 Aldo-keto reductase family 1 member C1	IPI00029733	41021.35156	8.02	6	241.8600006	100	53.34000015	99.95976467	0.432017835	0.2402605	7
DPYS Dihydropyrimidinase	IPI00028910	62048.10938	6.81	4	167.8000031	100	59.40999985	99.99005493	0.426515067	0.4923917	4

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ACO1 Iron-responsive element-binding protein 1	IPI00008485	105951.1797	6.23	3	127.9100037	100	50.13999939	99.91593646	0.421511923	0.121285	3
NDUFAB1 Acyl carrier protein, mitochondrial precursor	IPI00022442	18696.14063	4.82	2	99.81999969	100	69.06999969	99.99892451	0.416408516	9.25E-02	2
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	12902.16992	6.28	6	307.9400024	100	76.55000305	99.99980786	0.416223911	0.1516635	6
BBS1 36 kDa protein	IPI00163204	37530.44922	5.61	1	84.76999664	100	84.76999664	100	0.414734087	0	1
MDH2 Malate dehydrogenase, mitochondrial precursor	IPI00291006	39765.08984	8.92	14	1037.274414	100	150.6799927	100	0.414058784	0.317633	14
PCK2 mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor	IPI00797038	74784.85938	7.57	9	426.3299866	100	77.48000336	99.9998449	0.412111629	0.2924395	9
DAK Dihydroxyacetone kinase	IPI00551024	63392.42188	7.12	5	420.7399902	100	139.7299957	100	0.411491523	0.2505309	5
UGT2B4 38 kDa protein	IPI00790652	41813.85156	8.87	3	156.7900085	100	63.72000122	99.99631356	0.408036132	7.35E-02	3
NUDT5 20 kDa protein	IPI00644292	21952.84961	4.67	1	63.74000168	99.9963305	63.74000168	99.9963305	0.406545142	0	1
BDH1 D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	IPI00025341	41766.75	9.11	4	167.8944397	100	55.20000076	99.97378152	0.405912975	0.6647343	4
ALDH7A1 similar to antiquitin	IPI00786942	63780.78125	8.25	2	98.63000488	100	56	99.97819241	0.405701998	0.1373031	2
GSTK1 GSTK1 protein	IPI00440703	33653.75	8.85	3	200.2200012	100	111.8600006	100	0.400309423	0.123865	3
QPRT 17 kDa protein	IPI00853023	17914	7.71	2	99.80999756	100	50.66999817	99.92559402	0.399128949	8.66E-02	2
HPD 40 kDa protein	IPI00795913	44884.14063	5.93	2	96.68000031	100	51.13999939	99.93322595	0.395293092	2.09E-02	2
GOT2 Aspartate aminotransferase, mitochondrial precursor	IPI00018206	52087.64844	9.14	6	410.4400024	100	114.9899979	100	0.388856325	0.7726941	6
DLD Dihydrolipoyl dehydrogenase, mitochondrial precursor	IPI00015911	60048.35938	7.59	3	227.0699921	100	97.73999786	100	0.38787513	3.14E-02	3
AOX1 Hypothetical protein AOX1	IPI00743616	161854.2031	6.78	7	314.460022	100	69.88999939	99.99910955	0.384738214	0.5064496	7
PC Pyruvate carboxylase, mitochondrial precursor	IPI00299402	138358.0469	6.37	14	833.0643921	100	124.8099976	100	0.381866588	0.3174893	15
PGRMC1 Membrane-associated progesterone receptor component 1	IPI00220739	23621.98047	4.56	3	158.6699982	100	67.40000153	99.99842018	0.380648405	8.75E-02	4
CYP2C8 45 kDa protein	IPI00843846	49430.42188	8.91	3	113.8300018	100	49.99000168	99.91298233	0.377500435	0.2503743	3
GRHPR GRHPR protein (Fragment)	IPI00550682	39375.17188	5.95	5	322.0844421	100	83.84999847	100	0.373163588	7.17E-02	5
DDT D-dopachrome decarboxylase	IPI00293867	13515.79004	6.71	4	253.4144287	100	94.47000122	100	0.372595582	0.1602614	4
SUCLG2 Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precurso	IPI00096066	51941.89844	6.15	4	220.0744324	100	85.44000244	100	0.372578738	0.1055257	4

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IDH1 Isocitrate dehydrogenase [NADP] cytoplasmic	IPI00027223	52332.01172	6.53	20	1224.219971	100	119.0899963	100	0.371284695	0.3252229	22
AK2 Isoform 2 of Adenylate kinase isoenzyme 2, mitochondrial	IPI00218988	28472.61914	7.71	2	114.4199982	100	74.33000183	99.99967966	0.371215308	4.60E-02	2
NDUFA8 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	IPI00219034	22908.26953	7.57	2	67.58000183	99.99848432	37.61000061	98.49475368	0.371043246	0.17215	2
AIFM1 Isoform 3 of Apoptosis-inducing factor 1, mitochondrial precursor	IPI00157908	72532.10938	9.03	3	189.1499939	100	83.56999969	100	0.365634308	0.1958388	3
ETFA Electron transfer flavoprotein subunit alpha, mitochondrial precursor	IPI00010810	39221.92969	8.62	6	617.0400391	100	160.8500061	100	0.365613685	0.2496209	6
C11orf54 Isoform 1 of Ester hydrolase C11orf54	IPI00072044	39108.89844	6.23	3	114.8199997	100	51.54999924	99.93924141	0.365387713	0.3496618	3
UGT2B7 similar to UDP-glucuronosyltransferase 2B7 precursor	IPI00787584	65314.41016	8.41	3	156.1900024	100	63.72000122	99.99631356	0.363973307	1.60E-02	3
ACADM Hypothetical protein DKFZp686M24262	IPI00513827	55018.78906	7.94	4	198.9900208	100	78.05000305	99.99986398	0.360475383	0.2337433	4
ADH4 Alcohol dehydrogenase 4	IPI00218899	45828.03125	8.25	7	400.5299988	100	66.34999847	99.99798809	0.358736954	0.2629936	7
HEBP1 Heme-binding protein 1	IPI00148063	23623.80078	5.71	1	69.61000061	99.99905025	69.61000061	99.99905025	0.358457876	0	1
HMGCL 19 kDa protein	IPI00514407	21853.41016	8.9	1	84.47000122	100	84.47000122	100	0.354256427	0	1
MMAB 19 kDa protein	IPI00789857	20551.83008	8.35	1	65.26000214	99.99741413	65.26000214	99.99741413	0.353921027	0	1
AKR1C4 Aldo-keto reductase family 1 member C4	IPI00289524	41137.30859	6.71	4	209.4100037	100	85.11000061	100	0.35353642	0.1544949	5
FH Isoform Cytoplasmic of Fumarate hydratase, mitochondrial precursor	IPI00759715	55071.17188	6.9	6	367.5100098	100	102.4300003	100	0.34768382	0.1348362	6
NDUFA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	IPI00011770	10562.08984	9.42	2	124.0700073	100	79.23000336	99.99989634	0.346702423	0.1037811	2
SHMT1 Isoform 2 of Serine hydroxymethyltransferase, cytosolic	IPI00220668	53489.17969	7.59	3	156.6000061	100	61.22000122	99.99344447	0.346055904	0.2422681	3
CYP2C19 Cytochrome P-450 II C (Fragment)	IPI00657852	44746.01953	6.82	2	118.9400024	100	88.41999817	100	0.345569668	0.4025501	2
COQ9 Isoform 1 of Ubiquinone biosynthesis protein COQ9, mitochondrial precu	IPI00470631	37064.78125	5.61	1	67.43000031	99.99843106	67.43000031	99.99843106	0.345135936	0	1
HRSP12 Ribonuclease UK114	IPI00005038	15826.7998	8.74	2	120.2600021	100	64.97000122	99.99723556	0.341223093	0.3068584	2
IDH2 Isocitrate dehydrogenase [NADP], mitochondrial precursor	IPI00011107	56573.30859	8.88	14	762.2543945	100	96.51999664	100	0.341202068	0.2383263	14
KHK Isoform C of Ketohexokinase	IPI00216136	35220.62891	5.91	3	149.0999908	100	66.41999817	99.99802026	0.339159113	0.2756871	3
ACADSB Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	IPI00024623	52051.67969	6.53	1	96.27999878	100	96.27999878	100	0.332672295	0	1
REEP6 Receptor expression-enhancing protein 6	IPI00647161	22153.98047	8.74	2	74.77999878	99.99971119	42.90999985	99.55577024	0.330600878	4.33E-02	2

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CA2 11 kDa protein	IPI00790885	13118.76953	6.21	1	62.36999893	99.99496954	62.36999893	99.99496954	0.323903626	0	1
DCI Isoform 2 of 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor	IPI00398758	32932.46875	9.07	2	155.4400024	100	107.9400024	100	0.321668831	1.64E-03	2
SULT1A1 Sulfotransferase 1A1	IPI00300026	47814.69922	8.61	4	259.4599915	100	90.48999786	100	0.32107992	0.0301411	4
- 14 kDa protein	IPI00788848	15907.24023	5.24	6	409.9299927	100	109.0899963	100	0.31290784	0.4417834	8
HINT2 Histidine triad nucleotide-binding protein 2	IPI00000335	18349.41992	9.2	2	157.0400085	100	106.8899994	100	0.312402428	7.69E-02	2
MPST 3-mercaptopyruvate sulfurtransferase	IPI00165360	34971.80078	6.13	6	463.2999878	100	120.7699966	100	0.312284959	0.1463331	6
MUT Methylmalonyl-CoA mutase, mitochondrial precursor	IPI00024934	90636.34375	6.48	2	138.7799988	100	70.55999756	99.99923685	0.309162517	0.0773756	2
CYP2E1 Cytochrome P450 2E1	IPI00007282	61500.80078	8.27	6	325.3300171	100	83.15000153	100	0.308502048	0.134847	6
GLUD2 Glutamate dehydrogenase 2, mitochondrial precursor	IPI00027146	66855.89844	8.63	14	868.5100098	100	91.33000183	100	0.307026697	0.2244148	16
HGD Homogentisate 1,2-dioxygenase	IPI00303174	54236.85938	6.54	4	178.1199951	100	54.11999893	99.96637922	0.299588774	0.2729922	4
PRDX3 peroxiredoxin 3 isoform b	IPI00374151	27924.48047	7.04	2	94.25999451	100	53.47999954	99.96104101	0.298945492	0.1000014	2
SYNE1 Isoform 6 of Nesprin-1	IPI00247297	1110045.75	5.37	2	73.52999878	99.99961487	38.04000092	98.63664943	0.297039021	0.4586662	2
PCCA Propionyl-CoA carboxylase alpha chain, mitochondrial precursor	IPI00749503	84435.1875	6.63	1	70.95999908	99.999304	70.95999908	99.999304	0.295062418	0	1
ACSL1 Isoform 1 of Long-chain-fatty-acid--CoA ligase 1	IPI00012728	85201.29688	6.81	12	630.9400024	100	74.62999725	99.99970104	0.293741983	0.2570779	12
GOT1 Aspartate aminotransferase, cytoplasmic	IPI00219029	49570.83984	6.52	10	557.289978	100	113.0500031	100	0.2926514	0.2706112	10
ALDH1A1 Retinal dehydrogenase 1	IPI00218914	60949.39063	6.3	12	719.000061	100	110.4499969	100	0.290227758	0.2263165	12
CYP2C9 Cytochrome P450 2C9	IPI00007219	61374.14063	8.13	4	221.5744476	100	88.41999817	100	0.288484806	0.1349634	4
GLYAT Isoform 1 of Glycine N-acyltransferase	IPI00402759	37221.21094	8.38	5	228.9199982	100	60.38999939	99.99206389	0.287525761	0.2955587	5
GPT Alanine aminotransferase 1	IPI00217458	57510.32813	6.77	2	94.12999725	100	50.70999908	99.9262762	0.286613913	4.94E-02	2
CES2 carboxylesterase 2 isoform 1	IPI00332828	72247.0625	6.03	6	326.3399963	100	70.5	99.99922624	0.286079516	0.2414844	6
ALDH1B1 Aldehyde dehydrogenase X, mitochondrial precursor	IPI00103467	62178.58984	6.36	7	347.1100159	100	90.43000031	100	0.282611964	4.55E-02	7
HMGCS2 Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor	IPI00008934	61333.76953	8.4	7	376.6199951	100	68.63999939	99.99881257	0.280766378	0.3340166	7
SOD2 manganese superoxide dismutase isoform A precursor	IPI00847322	27176.83984	8.35	6	411.9299927	100	108.4899979	100	0.276495281	0.122785	6

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ADH1B Alcohol dehydrogenase 1B	IPI00473031	45270.91016	8.63	11	833.9199829	100	112.0500031	100	0.27629345	0.2674934	12
HSPE1 10 kDa heat shock protein, mitochondrial	IPI00220362	12653.11035	8.89	8	512.7800293	100	121.5500031	100	0.275587996	0.3499906	9
ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria	IPI00024990	63211.07813	8.72	10	597.8944092	100	104.8199997	100	0.274465854	0.3391284	10
PBLD Phenazine biosynthesis-like domain-containing protein	IPI00024896	34011.42969	6.06	4	184.2044373	100	69.19999695	99.99895622	0.274403441	0.2858152	4
HADH Isoform 2 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precu	IPI00298406	47125.23047	9.34	6	308.7999878	100	94.25	100	0.272927407	0.2151241	6
SULT2A1 Bile salt sulfotransferase	IPI00216133	37496.32813	5.71	6	313.2400208	100	77.77999878	99.99985525	0.269711938	0.1925289	6
GLUD1 Glutamate dehydrogenase 1, mitochondrial precursor	IPI00016801	66531.63281	7.66	22	1490.390015	100	102.2799988	100	0.266607767	0.2283993	26
PEBP1 Phosphatidylethanolamine-binding protein 1	IPI00219446	23439.92969	7.01	9	647.960022	100	165.8999939	100	0.26364018	0.2639601	10
AGXT Serine--pyruvate aminotransferase	IPI00009367	46426.73047	8.61	7	443.6300049	100	108.9800034	100	0.259148698	0.2721108	7
BPHL Isoform 1 of Valacyclovir hydrolase precursor	IPI00384428	35828.30078	9.2	1	56.84999847	99.98206886	56.84999847	99.98206886	0.257112176	0	1
ALDH4A1 Aldehyde dehydrogenase 4 family, member A1	IPI00647328	65056.12109	7.62	12	672.9599609	100	89.19999695	100	0.245762516	0.3755329	12
FAH 33 kDa protein	IPI00793664	34681.60938	7.12	1	66.23000336	99.99793173	66.23000336	99.99793173	0.245705652	0	1
ATP5J ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6 i	IPI00456008	15010.11035	9.13	2	98.88000488	100	66.26000214	99.99794597	0.244694405	3.56E-02	2
EPHX1 Epoxide hydrolase 1	IPI00009896	57419.37891	6.77	6	416.4100037	100	115.6900024	100	0.244295105	0.2625821	6
ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	IPI00001539	46153.96875	8.32	13	806.8499756	100	112.5899963	100	0.241474675	0.3840297	15
ASS1 Argininosuccinate synthase	IPI00020632	56147.66016	8.6	7	328.0799866	100	86.38999939	100	0.237150573	0.1111469	7
ADH1C Alcohol dehydrogenase 1C	IPI00465343	45428	8.63	8	557.8399658	100	112.0500031	100	0.233706519	0.1666589	10
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	61418.91016	8.17	8	483.8100281	100	97.55999756	100	0.232547633	0.1376939	8
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	35335.42969	8.34	11	725.0244751	100	117.2699966	100	0.228598609	8.07E-02	11
DECR1 2,4-dienoyl-CoA reductase, mitochondrial precursor	IPI00003482	40019.14844	9.35	6	396.3300171	100	118.2300034	100	0.227500448	0.2551874	6
ACAA1 3-ketoacyl-CoA thiolase, peroxisomal precursor	IPI00012828	47604.07031	8.76	5	363.3999939	100	87.47000122	100	0.225956191	0.2714067	5
ALDH2 Mitochondrial aldehyde dehydrogenase 2 variant (Fragment)	IPI00792207	61065.96094	6.63	12	825.8099365	100	129.7400055	100	0.22356672	0.2002954	12
ADH1A Alcohol dehydrogenase 1A	IPI00218896	45320.80859	8.26	11	854.6399536	100	112.0500031	100	0.223111218	0.1572152	13

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OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	43936.05859	8.75	9	582.0244751	100	100.9300003	100	0.21814725	0.1763961	9
ACSM2B Xenobiotic/medium-chain fatty acid:CoA ligase	IPI00829974	70410.38281	8.36	3	136.0899963	100	65.75	99.99769002	0.213410661	0.1161195	3
ACY1 Aminoacylase-1	IPI00009268	48344.23047	5.77	3	160.7599945	100	69.59999847	99.99904806	0.208000035	0.1310792	3
BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101	49946.23828	6.58	4	231.9644318	100	77.41999817	99.99984274	0.20537631	0.1194301	4
DBI Isoform 2 of Acyl-CoA-binding protein	IPI00218836	13802.13965	5.41	4	264.3900146	100	74.29000092	99.9996767	0.202358612	4.69E-02	4
TST Thiosulfate sulfurtransferase	IPI00216293	35752.05859	6.77	9	494.0644531	100	114.8700027	100	0.191628658	0.3068047	9
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	48966.78125	6.61	13	925.1099243	100	124.5800018	100	0.181071629	0.2690773	14
ACAT1 Acetyl-CoA acetyltransferase, mitochondrial precursor	IPI00030363	49865.05859	8.98	10	774.1512451	100	142.6399994	100	0.180414216	0.1351051	10
SOD1 Superoxide dismutase	IPI00783680	17838.08984	5.7	3	179.8999939	100	103.1699982	100	0.179158867	1.74E-02	3
CYB5A Isoform 1 of Cytochrome b5	IPI00397860	16616.71094	4.88	5	468.7200012	100	207.6499939	100	0.172427966	0.129543	6
GSTA1 Glutathione S-transferase A1	IPI00657682	29261.05078	8.91	6	323.1300049	100	75.59999847	99.99976088	0.170434962	6.13E-02	6
UGT1A6;UGT1A1 UDP-glucuronosyltransferase 1-1 precursor	IPI00434346	64522.89063	8.19	6	414.5	100	138.9700012	100	0.169831398	0.1352742	6
RDH16 Microsomal NAD+-dependent retinol dehydrogenase 4 variant (Fragment)	IPI00555683	23832.68945	7.67	2	90.88000488	100	50.58000183	99.92403607	0.163466662	2.16E-02	2
CPS1 Isoform 1 of Carbamoyl-phosphate synthase [ammonia], mitochondrial pre	IPI00011062	180875.9531	6.3	60	4232.14502	100	178.3600006	100	0.161998939	0.125535	67
SCP2 sterol carrier protein 2 isoform 2	IPI00433347	61608.94141	6.25	5	295.2000122	100	87.93000031	100	0.150105606	0.1123207	6
CES1 carboxylesterase 1 isoform c precursor	IPI00607693	68199.60938	6.15	14	1068.299927	100	163.9700012	100	0.129009922	0.2464198	18
FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	41289.14844	6.54	9	801.2800293	100	129.6499939	100	0.12365205	0.1118413	9
FTCD Isoform C of Formimidoyltransferase-cyclodeaminase	IPI00218976	64571.53125	5.24	4	181.164444	100	56.90000153	99.98227413	0.122899469	9.49E-02	4
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	43462.35156	8	11	842.4343872	100	111.0599976	100	0.109515469	9.45E-02	12

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio * (117/116)	iTRAQ Standard Deviation * (117/116)	iTRAQ Peptides (117/116)
DHRS2 dehydrogenase/reductase (SDR family) member 2 isoform 2	IPI00218235	32245.88	9.21	1	77.96	99.99986	77.96	99.99986	8.116348	0	1
IFITM1 Interferon-induced transmembrane protein 1	IPI00300620	14931.44	7.78	2	192.54	100	112.53	100	5.683454	1.274800253	3
S100P Protein S100-P	IPI00017526	12023.44	4.75	1	102.4	100	102.4	100	5.408724	0	1
GALK1 Galactokinase	IPI00019383	43765.66	6.04	5	300.38	100	107.09	100	3.351021	1.05369088	5
STIP1 STIP1 protein	IPI00479946	77915.94	7.81	4	188.13	100	51.07	99.93214	3.203762	0.905269245	4
ACSL4 Isoform Short of Long-chain-fatty-acid--CoA ligase 4	IPI00219897	83902.51	8.33	2	81.3	99.99994	41.33	99.36084	2.970697	0.904314362	2
KHSRP KH-type splicing regulatory protein	IPI00479786	77908.45	6.85	2	131.3244	100	86.68	100	2.902571	4.42E-02	2
PTGES3 19 kDa protein	IPI00789101	21682.36	4.76	2	124.17	100	78.92	99.99989	2.883691	1.632853953	2
APEX1 DNA-(apurinic or apyrimidinic site) lyase	IPI00215911	40174.54	8.33	2	152.4845	100	105.41	100	2.781259	0.850952924	2
MMAB 19 kDa protein	IPI00789857	20551.83	8.35	1	65.26	99.99741	65.26	99.99741	2.728747	0	1
QPRT 17 kDa protein	IPI00853023	17914	7.71	2	99.81	100	50.67	99.92559	2.681702	0.973237627	2
FUS Fus-like protein (Fragment)	IPI00260715	55689.03	9.46	3	246.29	100	123.67	100	2.652173	2.866567511	3
IGF2BP2 Insulin-like growth factor 2 mRNA-binding protein 2	IPI00180983	67944.93	8.22	1	68.97	99.9989	68.97	99.9989	2.644223	0	1
IGF2BP3 64 kDa protein	IPI00746216	71308.52	9.12	1	68.97	99.9989	68.97	99.9989	2.644223	0	1
FASN Fatty acid synthase	IPI00847250	287598.8	5.99	31	1696.97	100	130.32	100	2.63146	1.461603758	33
NPM1 Isoform 1 of Nucleophosmin	IPI00549248	37589.32	4.64	6	394.85	100	102.45	100	2.608175	0.650576875	6
TBCA Tubulin-specific chaperone A	IPI00217236	15052.97	5.25	1	80.81	99.99993	80.81	99.99993	2.417026	0	1
TPR nuclear pore complex-associated protein TPR	IPI00742682	292969.3	4.97	1	59.56	99.99039	59.56	99.99039	2.380934	0	1

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PSAT1 Isoform 1 of Phosphoserine aminotransferase	IPI00001734	44751.16	7.56	3	186.26	100	63.97	99.99652	2.361067	0.485296108	3
NCL Isoform 1 of Nucleolin	IPI00604620	89719.57	4.6	10	590.42	100	103.39	100	2.35832	0.725253152	11
FAM10A5 Protein FAM10A5	IPI00168839	46431.76	4.96	2	154.95	100	80.66	99.99993	2.335872	0.198524374	2
TXNL1 37 kDa protein	IPI00642032	39663.04	4.75	2	144.23	100	83.67	100	2.290523	7.27E-02	2
DAK Dihydroxyacetone kinase	IPI00551024	63392.42	7.12	5	420.74	100	139.73	100	2.277686	0.804440242	5
PSMC3 26S protease regulatory subunit 6A	IPI00018398	54730.94	5.13	3	120.4	100	56.71	99.98148	2.267275	0.496768465	3
OTUB1 Hypothetical protein DKFZp564E242	IPI00000581	34180.75	4.9	1	95.68	100	95.68	100	2.25772	0	1
NSFL1C Isoform 3 of NSFL1 cofactor p47	IPI00397571	43383.75	5.04	2	186.57	100	138.32	100	2.23658	0.702191788	2
TMEM4 Isoform 1 of MIR-interacting saposin-like protein precursor	IPI00443909	22355.31	4.81	4	204.83	100	70.02	99.99914	2.231083	0.558819258	4
SURF4 Surfeit 4	IPI00399142	22555.05	8.88	1	122.17	100	122.17	100	2.231041	0	1
SARS Seryl-tRNA synthetase	IPI00514587	68889.06	6.64	3	133.2244	100	49.54	99.90348	2.230443	0.131915472	3
HMGB1 High mobility group protein B1	IPI00419258	31352.76	5.62	2	186.3544	100	96.87	100	2.226229	0.499710104	2
FDPS Farnesyl diphosphate synthase	IPI00101405	51970.89	5.83	4	255.56	100	89.23	100	2.224157	0.354233649	4
- Farnesyl pyrophosphate synthetase like-4 protein (Fragment)	IPI00382869	42840.9	4.87	4	208.4	100	59.83	99.99097	2.224157	0.354233649	4
PTBP1 polypyrimidine tract-binding protein 1 isoform a	IPI00183626	64630.35	9.21	2	118.7	100	69.21	99.99896	2.202798	2.230870686	2
CKAP4 CKAP4 protein (Fragment)	IPI00433214	72955.87	9.34	10	674.2145	100	99.14	100	2.182461	1.06568519	10
CYB5R3 Isoform 2 of NADH-cytochrome b5 reductase 3	IPI00446235	34240.61	7.15	4	242.4844	100	67.37	99.99841	2.170853	0.497140991	4
HSPB1 Heat shock protein beta-1	IPI00025512	23966.67	5.98	7	399.99	100	122.59	100	2.169555	0.625755716	7
C14orf156 SRA stem-loop-interacting RNA-binding protein, mitochondrial prec	IPI00009922	13395.59	10.25	1	58.13	99.98665	58.13	99.98665	2.165553	0	1

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HNRPA3 Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	IPI00419373	42922.9	9.1	4	374.23	100	178.18	100	2.161781	2.005034332	5
NAP1L1 43 kDa protein	IPI00789029	47959.44	4.45	2	114.35	100	72.49	99.99951	2.161538	0.458023477	2
C20orf77 Uncharacterized protein C20orf77	IPI00009659	41289.62	5.73	1	88.33	100	88.33	100	2.133475	0	1
HNRPA1 Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	IPI00465365	37003.55	9.27	8	431.01	100	96.29	100	2.123985	1.316034294	8
CLINT1 Isoform 2 of Clathrin interactor 1	IPI00397519	73929.33	6.01	1	62.57	99.9952	62.57	99.9952	2.117071	0	1
RPS20 16 kDa protein	IPI00794659	18149.66	9.4	3	153.96	100	77.06	99.99983	2.108564	0.166026648	3
HSP90AB1 Heat shock protein HSP 90-beta	IPI00414676	94433.06	4.97	30	1951.044	100	115.03	100	2.10582	1.133342242	33
FBL rRNA 2'-O-methyltransferase fibrillarin	IPI00025039	36735.73	10.18	1	66.78	99.99818	66.78	99.99818	2.081688	0	1
EIF4H;LOC653994 Isoform Short of Eukaryotic translation initiation factor 4	IPI00220894	26958.75	7.79	1	69.79	99.99909	69.79	99.99909	2.075839	0	1
TRIM28 Isoform 2 of Transcription intermediary factor 1-beta	IPI00438230	85861.79	5.67	2	159.17	100	106.35	100	2.071946	0.38268805	2
PA2G4 41 kDa protein	IPI00794875	47417.53	6.82	4	233.85	100	79.52	99.9999	2.056473	0.194280156	4
FKBP5 51 kDa protein	IPI00743671	59312.21	5.79	1	71.46	99.99938	71.46	99.99938	2.052584	0	1
ERH Enhancer of rudimentary homolog	IPI00029631	13541.16	5.63	2	135.75	100	96.53	100	2.01877	2.21E-02	2
GLUD2 Glutamate dehydrogenase 2, mitochondrial precursor	IPI00027146	66855.9	8.63	14	868.51	100	91.33	100	2.01456	0.690186734	16
- 12 kDa protein	IPI00455557	13102.08	4.68	1	141.93	100	141.93	100	2.013059	0	1
PPIF Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor	IPI00026519	24750.42	9.48	2	94.2	100	56.33	99.97979	2.007303	0.252235228	2
- 14 kDa protein	IPI00455040	16069.76	8.86	1	85.73	100	85.73	100	2.005748	0.37585395	2
VDP General vesicular transport factor p115	IPI00743314	117492.7	4.85	1	117.64	100	117.64	100	1.990942	0	1
GTPBP9 Isoform 1 of Putative GTP-binding protein 9	IPI00290416	51379.9	7.64	3	187.21	100	107.89	100	1.982881	1.538214011	3

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C20orf3 47 kDa protein	IPI00479431	49085.11	5.82	5	261.48	100	76.8	99.99982	1.981541	0.85135387	6
HNRPM Isoform 2 of Heterogeneous nuclear ribonucleoprotein M	IPI00383296	79706.9	8.94	3	279.67	100	137.03	100	1.97323	6.85E-02	3
RBMX Heterogeneous nuclear ribonucleoprotein G	IPI00304692	44322.6	10.06	3	148.1644	100	70.51	99.99923	1.969061	0.635847241	3
GLUD1 Glutamate dehydrogenase 1, mitochondrial precursor	IPI00016801	66531.63	7.66	22	1490.39	100	102.28	100	1.96862	0.778631523	26
MATR3 100 kDa protein	IPI00789551	110688.3	5.71	2	94.50999	100	54.48	99.96905	1.965559	0.430775403	2
G3BP2 Isoform B of Ras GTPase-activating protein-binding protein 2	IPI00179890	53856.43	5.27	1	59.41	99.99005	59.41	99.99005	1.960587	0	1
CBX3;LOC653972 Chromobox protein homolog 3	IPI00297579	24680.73	5.23	1	86.04	100	86.04	100	1.955106	0	1
PDIA4 Protein	IPI00852792	21271.92	8.33	6	305.44	100	86.51	100	1.942883	0.386784921	6
ANXA7 Isoform 2 of Annexin A7	IPI00021771	52673.88	6.25	1	77.57	99.99985	77.57	99.99985	1.896483	0	1
HSPA5 HSPA5 protein	IPI00003362	81398.3	5.07	25	2094.601	100	141.33	100	1.893627	0.578454857	28
SRP14 8 kDa protein	IPI00789296	8752.33	10.03	1	74.84	99.99972	74.84	99.99972	1.89354	0	1
PCNA Proliferating cell nuclear antigen	IPI00021700	31474.52	4.57	2	83.99	100	42.64	99.52728	1.889842	0.295297168	2
HSPA1A;HSPA1B Heat shock 70 kDa protein 1	IPI00304925	77583.7	5.48	16	1055.449	100	136.35	100	1.88948	0.592831967	16
CSNK2A1 Casein kinase 2 alpha isoform	IPI00741317	49134.26	7.75	2	79.91	99.99991	50.46	99.92191	1.87337	0.942411045	2
DBI Isoform 2 of Acyl-CoA-binding protein	IPI00218836	13802.14	5.41	4	264.39	100	74.29	99.99968	1.863641	0.401583004	4
PGRMC1 Membrane-associated progesterone receptor component 1	IPI00220739	23621.98	4.56	3	158.67	100	67.4	99.99842	1.862146	0.759477078	4
ENO2 6 kDa protein	IPI00790892	6040.03	4.89	2	192.91	100	120.04	100	1.857822	0.059837972	2
SYNCRIP Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q	IPI00402182	72162.18	8.69	3	180.86	100	72.37	99.9995	1.856331	0.111875671	3
HNRPD Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	IPI00220684	37704.56	8.23	3	179.56	100	79.04	99.99989	1.850698	0.266793997	4

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PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904	82667.81	4.96	19	1037.396	100	115.1	100	1.848238	0.567886386	19
HSPE1 10 kDa heat shock protein, mitochondrial	IPI00220362	12653.11	8.89	8	512.78	100	121.55	100	1.838326	0.496969681	9
HSP90AB4P Heat shock protein 90Bd	IPI00555565	66222.18	4.65	7	425.64	100	103.38	100	1.82908	0.515599005	7
EEF1D EEF1D protein	IPI00064086	31512.7	4.81	3	248.12	100	102.39	100	1.827388	0.794367927	3
CALR Protein	IPI00794237	19298.58	4.47	4	199.6445	100	67.76	99.99855	1.826623	0.693486095	5
NONO Non-POU domain-containing octamer-binding protein	IPI00304596	58321.69	9.01	5	213.7645	100	52.49	99.95107	1.816619	0.813877767	5
SET Isoform 2 of Protein SET	IPI00301311	35108.06	4.12	2	111.17	100	80.1	99.99992	1.811698	1.45E-02	2
SLC9A3R1 26 kDa protein	IPI00794755	27862.19	5.12	2	63.97	99.99652	34.14	96.65337	1.792776	0.808381027	2
LOC388885 similar to 40S ribosomal protein S10	IPI00398673	21722.75	10.07	3	177.39	100	75.55	99.99976	1.789744	8.83E-02	4
MARCKS Myristoylated alanine-rich C-kinase substrate	IPI00219301	35850.28	4.47	1	96.12	100	96.12	100	1.786437	0	1
BCAP31 21 kDa protein	IPI00639976	22905.45	8.94	3	135.63	100	58.35	99.98731	1.781957	8.11E-02	3
HINT1 Histidine triad nucleotide-binding protein 1	IPI00239077	15325.28	6.43	3	246.15	100	98.5	100	1.780588	0.151964705	3
SNTB1 Isoform 2 of Beta-1-syntrophin	IPI00216858	44616.67	9.13	1	76.84	99.99982	76.84	99.99982	1.777718	0	1
SSBP1 Single-stranded DNA-binding protein, mitochondrial precursor	IPI00029744	18545.23	9.59	4	205.8	100	80.23	99.99992	1.776709	0.395526114	4
LRPPRC Leucine-rich PPR motif-containing protein	IPI00783271	173604.2	5.81	3	161.8344	100	90.87	100	1.772152	0.158238098	3
RPS5 40S ribosomal protein S5	IPI00008433	25448.32	9.73	1	131.87	100	131.87	100	1.765033	0	1
GART Isoform Long of Trifunctional purine biosynthetic protein adenosine-3	IPI00025273	118791.7	6.26	2	73.77	99.99964	40.43	99.21367	1.756357	1.38970177	2
ARHGDIA 28 kDa protein	IPI00794402	30709	4.94	3	278.6	100	103.19	100	1.753555	0.205291349	3
TNS3 tensin 3	IPI00658152	166503.4	6.34	1	74.55	99.9997	74.55	99.9997	1.746249	0	1

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SCAMP3 Isoform 2 of Secretory carrier-associated membrane protein 3	IPI00306383	37073.83	7.53	2	113.18	100	68.44	99.99876	1.740391	0.615517983	2
PSMC4 Isoform 2 of 26S protease regulatory subunit 6B	IPI00216770	47172.91	5.13	2	158.72	100	82	99.99995	1.729491	0.142667124	2
SUMO3 Small ubiquitin-related modifier 3 precursor	IPI00299147	12971.92	5.32	1	84.76	100	84.76	100	1.724582	0	1
FUBP1 Isoform 2 of Far upstream element-binding protein 1	IPI00644386	73175.53	7.74	3	119.72	100	45.82	99.7727	1.722625	0.762020841	3
hCG_1983058 hypothetical protein LOC644820	IPI00414723	28320.82	4.59	3	204.67	100	102.79	100	1.719594	0.234989385	3
DYNLL1 Dynein light chain 1, cytoplasmic	IPI00019329	12081.3	6.89	2	84.43	100	45.15	99.73478	1.7156	0.532056398	2
HNRPH3 Isoform 2 of Heterogeneous nuclear ribonucleoprotein H3	IPI00216492	36558.57	6.36	3	217.61	100	79.33	99.9999	1.713307	0.307083478	3
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	68931.1	5.7	20	1502.262	100	123.14	100	1.706832	0.645225253	21
HSP90AB2P Heat shock protein 90Bb	IPI00455599	57370.48	5.09	7	487.28	100	115.03	100	1.703505	1.2086136	7
HNRPU heterogeneous nuclear ribonucleoprotein U isoform a	IPI00644079	101350.8	5.76	5	259.68	100	70.44	99.99922	1.700977	0.485240655	5
UNQ501 MBC3205	IPI00063130	22277.99	8.91	1	78.47	99.99988	78.47	99.99988	1.699668	0	1
EPN1 Isoform 2 of Epsin-1	IPI00027082	63516.05	4.72	1	76.00444	99.99978	77.18	99.99983	1.693141	0	1
HNRPH1 HNRPH1 protein	IPI00479191	53875.41	6.33	6	476.8544	100	147.84	100	1.687383	0.247768208	7
KTN1 Isoform 2 of Kinectin	IPI00337736	174519.1	5.57	1	83.1	100	83.1	100	1.681124	0	1
PAICS phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazol	IPI00815732	53853.99	7.86	1	58.78	99.9885	58.78	99.9885	1.675603	0	1
ACADSB Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	IPI00024623	52051.68	6.53	1	96.28	100	96.28	100	1.665971	0	1
TRAP1 57 kDa protein	IPI00646055	62264.06	7.21	2	107.73	100	72.46	99.99951	1.657248	0.159156973	2
PRKCSH Glucosidase 2 beta subunit precursor	IPI00792916	64937.08	4.34	7	400.6145	100	84.15	100	1.657127	0.27690097	7
HDGF Hepatoma-derived growth factor	IPI00514127	32181.3	4.77	2	149.2345	100	79.9	99.99991	1.655977	0.480126294	2

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HNRPA2B1 Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	IPI00414696	38478.16	8.67	11	701.1544	100	149.74	100	1.654907	0.667179288	14
CARHSP1 Calcium-regulated heat stable protein 1	IPI00304409	17218.17	8.41	1	118.63	100	118.63	100	1.651572	0	1
CS citrate synthase precursor, isoform b	IPI00383539	50469.26	6.74	3	123.77	100	48.24	99.8698	1.650204	0.366873294	3
AHCY Adenosylhomocysteinase	IPI00012007	52465.54	5.92	5	320.44	100	110.51	100	1.644259	0.536537307	5
UGDH UDP-glucose 6-dehydrogenase	IPI00031420	60869.65	6.73	4	301.53	100	154.06	100	1.64181	0.385711854	4
ACAT2 Acetyl-CoA acetyltransferase, cytosolic	IPI00291419	44906.64	6.47	2	119.53	100	77.04	99.99983	1.639922	0.134287615	2
HNRPL heterogeneous nuclear ribonucleoprotein L isoform b	IPI00465225	54634.78	7.22	5	330.81	100	90.86	100	1.639068	0.134492532	5
IDH1 Isocitrate dehydrogenase [NADP] cytoplasmic	IPI00027223	52332.01	6.53	20	1224.22	100	119.09	100	1.638322	0.480172835	22
CANX Calnexin precursor	IPI00020984	75958.54	4.47	5	448.2	100	143.5	100	1.635756	0.2436979	5
STOML2 Stomatin-like protein 2	IPI00334190	41194.49	6.88	3	128.49	100	57.02	99.98276	1.63369	0.125496948	3
TALDO1 Transaldolase	IPI00744692	42118.9	6.36	6	370.35	100	90.9	100	1.615755	0.500075798	6
DDAH1 NG,NG-dimethylarginine dimethylaminohydrolase 1	IPI00220342	34258.2	5.53	2	109.41	100	57.08	99.98299	1.614278	0.3032966	2
HNRPF Heterogeneous nuclear ribonucleoprotein F	IPI00003881	48367.08	5.38	4	221.84	100	109.75	100	1.614241	0.263521125	4
NEDD8 NEDD8 precursor	IPI00020008	10506.17	7.98	2	117.32	100	82.3	99.99995	1.604795	0.333918402	2
CPNE1 53 kDa protein	IPI00852917	56975.76	5.52	2	119.5	100	86.37	100	1.603542	0.558504462	2
HNRPK Isoform 1 of Heterogeneous nuclear ribonucleoprotein K	IPI00216049	54486.72	5.39	7	439.3044	100	100.52	100	1.603353	0.329250983	8
HNRPH2 Heterogeneous nuclear ribonucleoprotein H'	IPI00026230	51910.53	5.89	6	436.94	100	147.84	100	1.602494	0.202341491	7
PRKDC Isoform 2 of DNA-dependent protein kinase catalytic subunit	IPI00376215	508806.4	6.81	1	84.68	100	84.68	100	1.602127	0	1
THOC4 THO complex subunit 4	IPI00328840	29269.14	11.05	1	65.82	99.99773	65.82	99.99773	1.600807	0	1

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HYOU1 Hypoxia up-regulated protein 1 precursor	IPI00000877	122683.2	5.16	7	415.25	100	80.76	99.99993	1.596622	0.291051514	7
PRDX5 Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial pre	IPI00759663	19174.23	6.73	7	503.33	100	102.28	100	1.594821	0.34485222	7
ENO1 Isoform alpha-enolase of Alpha-enolase	IPI00465248	53031.82	7.01	13	948.2799	100	120.04	100	1.593619	0.393030526	14
PPA1 Inorganic pyrophosphatase	IPI00015018	37183.51	5.54	4	233	100	85.52	100	1.589989	0.305972064	4
LRRC59 Leucine-rich repeat-containing protein 59	IPI00396321	40703.35	9.61	2	108.83	100	67.67	99.99852	1.583628	0.170878201	2
GANAB Isoform 3 of Neutral alpha-glucosidase AB precursor	IPI00441414	99842.16	5.43	10	542.05	100	98.09	100	1.576707	0.662601733	10
NHP2L1 NHP2-like protein 1	IPI00026167	15932.73	8.72	2	77.66	99.99985	40.93	99.29918	1.576307	3.51E-02	2
LMAN1 ERGIC-53 protein precursor	IPI00026530	62207.39	6.3	4	274.38	100	128.45	100	1.575437	0.558641857	4
TUFM Tu translation elongation factor, mitochondrial	IPI00027107	54583.72	7.26	8	492.99	100	83.39	100	1.574182	0.523401455	8
RAB1B Ras-related protein Rab-1B	IPI00008964	24743.49	5.55	2	152.77	100	94.93	100	1.567831	6.51E-02	2
EML4 Echinoderm microtubule-associated protein-like 4	IPI00001466	119213.9	5.88	3	137.95	100	58.02	99.9863	1.565598	0.196987592	3
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	12902.17	6.28	6	307.94	100	76.55	99.99981	1.560138	0.35801258	6
CALR 37 kDa protein	IPI00793605	41138.14	4.55	9	613.46	100	119.53	100	1.553994	0.565188592	10
PKM2 58 kDa protein	IPI00784179	63980.44	7.95	7	317.2	100	69.29	99.99898	1.552805	0.559380621	7
BBS1 36 kDa protein	IPI00163204	37530.45	5.61	1	84.77	100	84.77	100	1.548378	0	1
HIST3H2A Histone H2A type 3	IPI00031562	16129.2	11.05	4	278.61	100	136.37	100	1.527993	1.838326044	5
TXNDC4 Thioredoxin domain-containing protein 4 precursor	IPI00401264	50287.66	5.09	3	152.75	100	61.98	99.9945	1.525827	0.221070086	3
LGALS3BP Galectin-3-binding protein precursor	IPI00023673	68905.43	5.13	4	212.23	100	94.05	100	1.524065	0.483049366	4
PDHB Isoform 2 of Pyruvate dehydrogenase E1 component subunit beta, mitocho	IPI00549885	40188.14	5.64	1	87.01	100	87.01	100	1.521515	0	1

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ORM1 Alpha-1-acid glycoprotein 1 precursor	IPI00022429	25840.99	4.93	3	261.89	100	106.51	100	1.518155	0.195547928	3
- 30 kDa protein	IPI00472119	35896.37	9.78	2	117.09	100	62.35	99.99495	1.514896	0.448702155	3
PSMC6 26S protease regulatory subunit S10B	IPI00021926	48839.51	7.1	2	81.4	99.99994	49.15	99.89441	1.514194	0.372385952	2
TCP1 T-complex protein 1 isoform b	IPI00550591	48598.41	7.59	1	69.89	99.99911	69.89	99.99911	1.513879	0	1
SFPQ Isoform Long of Splicing factor, proline- and glutamine-rich	IPI00010740	81090.11	9.45	5	249.9644	100	65.47	99.99754	1.513022	0.525013457	5
LOC650157 similar to peptidylprolyl isomerase A isoform 1	IPI00397191	33761.59	8.81	2	82.82	100	43.78	99.63641	1.512371	7.49E-02	2
KHK Isoform C of Ketohexokinase	IPI00216136	35220.63	5.91	3	149.1	100	66.42	99.99802	1.512131	0.302536224	3
TPI1 Isoform 1 of Triosephosphate isomerase	IPI00465028	34025.99	5.65	9	789.12	100	118.04	100	1.511496	0.337702507	9
FKBP2 FK506-binding protein 2 precursor	IPI00002535	17649.53	9.24	4	248.99	100	92.49	100	1.508774	0.203341714	4
NUTF2 Nuclear transport factor 2	IPI00009901	15615.19	5.1	2	94.17	100	59.1	99.98932	1.50731	7.12E-02	2
GLUL Glutamine synthetase	IPI00010130	45423.51	6.43	3	119.39	100	54.91	99.97197	1.506461	0.341273291	3
VCP Transitional endoplasmic reticulum ATPase	IPI00022774	96730.26	5.14	11	709.2844	100	131.79	100	1.504756	0.635821248	11
DC2 DC2 protein	IPI00183603	17773.97	9.23	1	58.11	99.98658	58.11	99.98658	1.503055	0	1
SNRP70 Isoform 3 of U1 small nuclear ribonucleoprotein 70 kDa	IPI00219484	21454.14	7.82	1	58.11444	99.9866	59.29	99.98978	1.502094	0	1
HSP90AA1 Isoform 1 of Heat shock protein HSP 90-alpha	IPI00784295	96593.69	4.94	23	1505.42	100	111.49	100	1.501396	0.621281343	24
FUBP3 similar to Far upstream element-binding protein 3	IPI00787451	79292.07	7.66	3	139.23	100	64.51	99.99693	1.495295	0.146739834	3
HIST1H4E;HIST1H4I;HIST1H4D;HIST1H4L;HIS	IPI00453473	13088.62	11.36	8	485.67	100	97.44	100	1.494903	1.142172159	8
RPLP0 60S acidic ribosomal protein P0	IPI00556485	30148.59	8.36	5	272.26	100	88.81	100	1.492038	0.137492582	5
PDIA3 55 kDa protein	IPI00657680	62595.52	6.42	19	1476.589	100	180.79	100	1.485737	0.401478807	19

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DYNC1I2 Isoform 2B of Cytoplasmic dynein 1 intermediate chain 2	IPI00302712	77936.73	5.1	1	66.86	99.99821	66.86	99.99821	1.477568	0	1
ST6GAL1 CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,6-sialyltransfer	IPI00013887	52461.07	9.13	1	60.91	99.99296	60.91	99.99296	1.477349	0	1
NDUFAB1 Acyl carrier protein, mitochondrial precursor	IPI00022442	18696.14	4.82	2	99.82	100	69.07	99.99892	1.473742	0.794458187	2
RBP4 Retinol binding protein 4, plasma	IPI00480192	24933.3	5.77	2	131.66	100	77.71	99.99985	1.46757	0.155541368	2
GC Vitamin D-binding protein precursor	IPI00555812	60697.33	5.4	4	192.0644	100	72.72	99.99954	1.467332	0.381322567	4
RAB1A Isoform 2 of Ras-related protein Rab-1A	IPI00334174	17664.9	8.31	2	127.42	100	94.93	100	1.466815	3.85E-02	2
HSPA6 Heat shock 70 kDa protein 6	IPI00339269	77112.71	5.81	7	454.35	100	136.35	100	1.463043	0.416231736	7
RPS12 ribosomal protein S12	IPI00847579	17275.7	6.81	4	256.74	100	75.25	99.99974	1.458107	0.363088768	4
FKBP1A Peptidyl-prolyl cis-trans isomerase	IPI00647507	12759.03	9.17	1	86.05	100	86.05	100	1.45756	0	1
ILF3 Isoform 1 of Interleukin enhancer-binding factor 3	IPI00298788	105105.9	8.86	3	157.97	100	88.36	100	1.450929	0.149340225	3
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	48966.78	6.61	13	925.1099	100	124.58	100	1.449792	0.394704318	14
GLO1 Lactoylglutathione lyase	IPI00220766	23684.52	5.12	2	116.1	100	81.76	99.99994	1.447161	4.53E-03	2
GANAB Isoform 2 of Neutral alpha-glucosidase AB precursor	IPI00011454	114201.4	5.82	10	543.91	100	99.95	100	1.444169	0.67004354	10
RBM8A Isoform 2 of RNA-binding protein 8A	IPI00216659	21665.93	5.64	1	111.56	100	111.56	100	1.441316	0	1
C4B;C4A complement component 4B preproprotein	IPI00418163	205105.3	6.89	4	163.0944	100	49.3	99.898	1.439727	0.474018827	5
TMEM137;RBM14 Isoform 1 of RNA-binding protein 14	IPI00013174	72467.21	9.68	2	99.5	100	62.55	99.99517	1.43784	0.257140254	2
RPS19 40S ribosomal protein S19	IPI00215780	18354.82	10.31	5	286.71	100	71.07	99.99932	1.436251	0.659909237	5
TUBB2A Tubulin beta-2A chain	IPI00013475	52501.16	4.78	14	1052.6	100	144.42	100	1.435768	0.339544095	17
APOE Apolipoprotein E precursor	IPI00021842	38239.99	5.65	5	346.6	100	121.81	100	1.43088	0.382995122	5

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DHX9 ATP-dependent RNA helicase A	IPI00844578	151431.7	6.41	5	250.1689	100	62.77	99.99541	1.427903	0.430959438	6
ALDOA Fructose-bisphosphate aldolase A	IPI00465439	43651.63	8.3	10	774.1444	100	120.53	100	1.416858	0.335537113	10
HSPA9 Stress-70 protein, mitochondrial precursor	IPI00007765	81497.46	5.87	15	1009.074	100	120.07	100	1.415962	0.378491562	15
EPRS glutamyl-prolyl tRNA synthetase	IPI00013452	193228.7	7.02	3	163.07	100	69.7	99.99907	1.412832	0.553671278	3
- Tubulin alpha-4 chain	IPI00017454	29152.96	8.65	2	128.92	100	87.98	100	1.411732	0.287330388	3
HIST1H2BI;HIST1H2BG;HIST1H2BF;HIST1H2	IPI00020101	16921.91	10.31	4	270.07	100	102.54	100	1.410981	1.132346264	11
NUCB2 Nucleobindin-2 precursor	IPI00009123	57484.05	5.03	1	71.38	99.99937	71.38	99.99937	1.410131	0	1
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	20345.11	7.68	12	787.22	100	111.95	100	1.406229	0.18767621	13
PKLR Pyruvate kinase L	IPI00743713	67899.97	7.6	3	140.97	100	69.29	99.99898	1.403681	0.422885812	3
TUBA1B Similar to Tubulin alpha-ubiquitous chain	IPI00792677	49578.06	4.96	11	934.15	100	165.24	100	1.402998	0.289282015	13
COX4I1 COX4I1 protein	IPI00645361	10672.9	8.64	3	152.15	100	79.16	99.99989	1.39885	0.134378939	3
SPTBN1 275 kDa protein	IPI00794135	301224.9	5.39	9	435.7833	100	78.25	99.99987	1.397295	0.370967714	9
RAC1 Isoform B of Ras-related C3 botulinum toxin substrate 1 precursor	IPI00219675	26798.57	8.87	3	112.21	100	44.46	99.68911	1.395561	0.225921787	3
EEF1G 50 kDa protein	IPI00747497	55012.56	6.27	6	316.8	100	80.36	99.99992	1.39508	0.586863381	6
- CALRETICULIN=CALCIUM binding protein (Fragment)	IPI00383751	26354.4	4.45	5	398.02	100	119.53	100	1.3932	0.277544399	5
LOC387934 similar to Fatty acid-binding protein, epidermal	IPI00398985	17565.75	6.73	1	39.02	98.91205	39.02	98.91205	1.392871	0.157424435	2
TUBB3 Tubulin beta-3 chain	IPI00013683	53216.46	4.83	11	828.32	100	144.42	100	1.392038	0.330335933	12
EIF5A Isoform 1 of Eukaryotic translation initiation factor 5A-1	IPI00411704	19021.62	5.08	2	152.85	100	109.25	100	1.391198	1.15E-02	2
ACTR3 Actin-like protein 3	IPI00028091	51165.27	5.61	3	120.81	100	47.51	99.84597	0.701903	0.119161603	3

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ACADVL Isoform 2 of Very-long-chain specific acyl-CoA dehydrogenase, mitoch	IPI00178744	78527.98	9.06	4	235.86	100	98.33	100	0.701365	0.090502638	4
ECGF1 46 kDa protein	IPI00853163	47964.33	5.35	2	117.02	100	58.99	99.98905	0.698404	5.60E-02	2
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00472282	42025.16	5.89	6	267.5244	100	76.52	99.99981	0.697195	0.194921023	6
DDT D-dopachrome decarboxylase	IPI00293867	13515.79	6.71	4	253.4144	100	94.47	100	0.692719	0.121928998	4
IGHA2 Hypothetical protein DKFZp686C02218 (Fragment)	IPI00642017	57449.88	6.67	9	571.69	100	134.44	100	0.691445	0.271456836	11
ARPC2 Actin-related protein 2/3 complex subunit 2	IPI00005161	38147.87	6.84	5	198.3944	100	52.09	99.94635	0.688874	0.129551102	5
UGT2B17 similar to UDP glycosyltransferase 2 family, polypeptide B17	IPI00787638	68438.74	8.79	2	91.89444	100	60.18	99.99167	0.688679	2.71E-03	2
MYH14 Isoform 5 of Myosin-14	IPI00029818	180709	6.27	4	274.0744	100	91.21	100	0.686569	0.178596024	4
ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	IPI00001539	46153.97	8.32	13	806.85	100	112.59	100	0.685317	0.267825128	15
MAOB Amine oxidase [flavin-containing] B	IPI00328156	63747.53	7.2	3	113.67	100	42.03	99.45599	0.682675	0.125183749	3
TGM2 Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2	IPI00294578	82951.92	5.11	9	502.74	100	71.42	99.99937	0.682383	9.89E-02	9
RPL15 60S ribosomal protein L15	IPI00470528	26815.37	11.62	2	70.00999	99.99913	36.48	98.04743	0.681934	7.83E-03	2
CMPK cytidylate kinase	IPI00219953	29138.62	8.14	4	270.54	100	93.48	100	0.681848	0.115295593	4
FTH1 Ferritin heavy chain	IPI00554521	23366.52	5.3	2	106.55	100	61.44	99.99377	0.681325	2.13E-02	2
IGHG2 Hypothetical protein DKFZp686I04196 (Fragment)	IPI00399007	50615.94	7.63	7	463.82	100	116.61	100	0.680102	0.157849765	8
IGKV1-5 IGKV1-5 protein	IPI00419424	28320.14	6.3	7	651.95	100	142.8	100	0.679636	0.219329006	8
SUCLG2 Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precurso	IPI00096066	51941.9	6.15	4	220.0744	100	85.44	100	0.67762	0.228063193	4
KRT10 57 kDa protein	IPI00383111	60122.17	5.09	5	241.6945	100	88.54	100	0.676783	0.483507052	5
BDH1 D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	IPI00025341	41766.75	9.11	4	167.8944	100	55.2	99.97378	0.676488	0.250267262	4

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PSMB8 Isoform 1 of Proteasome subunit beta type 8 precursor	IPI00000783	32050.75	7.63	3	121.4744	100	52.95	99.95598	0.672558	8.47E-02	3
VIL2 Ezrin	IPI00843975	77526.5	5.94	10	409.8789	100	54.4	99.96848	0.671655	0.168730878	10
AK2 Isoform 2 of Adenylate kinase isoenzyme 2, mitochondrial	IPI00218988	28472.62	7.71	2	114.42	100	74.33	99.99968	0.671124	0.329889139	2
RPN2 Ribophorin II	IPI00383680	72001.89	5.7	1	68.18	99.99868	68.18	99.99868	0.666749	0	1
- Tryptophanyl-tRNA synthetase (Fragment)	IPI00383754	12867.94	4.57	1	62.81444	99.99546	63.99	99.99654	0.666069	0	1
SAMHD1 SAM domain and HD domain-containing protein 1	IPI00294739	79521.29	6.69	6	352.84	100	97.97	100	0.66562	0.143595716	6
WARS tryptophanyl-tRNA synthetase isoform b	IPI00412737	53848.83	6.03	4	175.08	100	63.99	99.99654	0.663253	0.104148107	4
REEP6 Receptor expression-enhancing protein 6	IPI00647161	22153.98	8.74	2	74.78	99.99971	42.91	99.55577	0.657825	0.225167377	2
PFKM CDNA FLJ44241 fis, clone THYMU3008436, highly similar to 6- phosphofru	IPI00465179	101419	8.2	1	56.62	99.98109	56.62	99.98109	0.657176	0	1
UGT1A6;UGT1A1 UDP-glucuronosyltransferase 1-1 precursor	IPI00434346	64522.89	8.19	6	414.5	100	138.97	100	0.654575	8.34E-02	6
MYL6 17 kDa protein	IPI00744444	18920.58	4.54	5	482.35	100	131.7	100	0.654376	9.17E-02	6
SCP2 sterol carrier protein 2 isoform 2	IPI00433347	61608.94	6.25	5	295.2	100	87.93	100	0.652468	0.251202315	6
ACSL1 Isoform 1 of Long-chain-fatty-acid--CoA ligase 1	IPI00012728	85201.3	6.81	12	630.94	100	74.63	99.9997	0.649322	0.19003652	12
ANXA5 Annexin A5	IPI00329801	39272.76	4.94	12	753.39	100	105.29	100	0.642168	0.13563291	12
VCL Isoform 2 of Vinculin	IPI00307162	135558.8	5.5	4	257.6245	100	114.57	100	0.640453	0.192074125	4
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	58388.33	6.3	11	675.1944	100	86.13	100	0.63822	0.182095833	11
HBA2;HBA1 Alpha 2 globin variant (Fragment)	IPI00853068	17045.17	8.72	7	511.84	100	111.39	100	0.636739	0.18846872	18
COL6A3 alpha 3 type VI collagen isoform 4 precursor	IPI00072918	345401	6.48	31	1747.335	100	110.05	100	0.635751	0.184333935	33
SELENBP1 53 kDa protein	IPI00745729	57664.27	6.03	3	122.32	100	48.38	99.87393	0.634818	0.40816821	3

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HSPG2 Basement membrane-specific heparan sulfate proteoglycan core protein	IPI00024284	487110.2	6.06	7	277.0344	100	54.73	99.97078	0.628273	0.103642933	7
APCS Serum amyloid P-component precursor	IPI00022391	27335.36	6.1	1	71.68	99.99941	71.68	99.99941	0.628142	0	1
PRSS1 Trypsin-1 precursor	IPI00011694	29161.24	6.08	1	72.37	99.9995	72.37	99.9995	0.625513	0	1
DPYS Dihydropyrimidinase	IPI00028910	62048.11	6.81	4	167.8	100	59.41	99.99005	0.625205	0.13935343	4
SERPINB1 Leukocyte elastase inhibitor	IPI00027444	47127.14	5.9	2	93.14	100	57.5	99.98456	0.62469	3.39E-02	2
TPM3 Isoform 2 of Tropomyosin alpha-3 chain	IPI00218319	32655.08	4.75	8	477.68	100	83.34	100	0.622066	0.210648367	8
RPS8 Ribosomal protein S8	IPI00645201	26370.43	10.37	3	165.55	100	79.85	99.99991	0.620291	4.82E-02	3
A1BG 41 kDa protein	IPI00644018	42068.62	5.5	2	68.49001	99.99877	38.83	98.8634	0.618897	0.315866261	2
VIM Vimentin	IPI00418471	56977.44	5.06	23	1567.599	100	114.66	100	0.615189	0.101542696	26
HIST1H1D Histone H1.3	IPI00217466	31265.18	11.02	2	105.92	100	71.89	99.99944	0.614181	0.443048711	2
SERPINC1 SERPINC1 protein	IPI00844156	32447.11	9.03	4	201.36	100	94.71	100	0.611658	0.229837544	4
- 2,3-bisphosphoglycerate mutase variant (Fragment)	IPI00556284	18558.81	6.59	1	74.07	99.99966	74.07	99.99966	0.611022	0	1
HAO1 Hydroxyacid oxidase 1	IPI00006934	44682.82	8.2	3	167.63	100	63.12	99.99577	0.610558	0.181927901	3
ACO1 Iron-responsive element-binding protein 1	IPI00008485	105951.2	6.23	3	127.91	100	50.14	99.91594	0.608357	0.278000872	3
CYP2C9 Cytochrome P450 2C9	IPI00007219	61374.14	8.13	4	221.5744	100	88.42	100	0.607689	0.176628552	4
CYP4F2 Cytochrome P450 4F2	IPI00019160	63921.06	6.6	2	96.68	100	53.95	99.96504	0.605442	0.102014877	2
SDHALP2 SDHALP2 protein	IPI00479656	17968.11	6.14	2	89.31	100	49.01	99.89095	0.605028	7.06E-02	2
FTL Ferritin light chain	IPI00852596	21925.34	5.51	5	342.68	100	92.97	100	0.604866	0.285684049	5
UGT2B4 38 kDa protein	IPI00790652	41813.85	8.87	3	156.79	100	63.72	99.99631	0.601034	0.127610949	3

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SDHA Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondri	IPI00305166	77793.53	7.06	7	333.21	100	66.87	99.99822	0.597194	0.1018256	7
COL6A1 Collagen alpha-1(VI) chain precursor	IPI00291136	117302.5	5.26	7	492.52	100	110.47	100	0.596963	0.196301422	7
HP Haptoglobin precursor	IPI00641737	52573.75	6.28	12	821.32	100	109.96	100	0.595825	0.246621022	14
CFB Isoform 2 of Complement factor B precursor (Fragment)	IPI00218508	74644.81	6.11	2	87.4	100	46.91	99.82315	0.595396	2.05E-02	2
PDLIM1 PDZ and LIM domain protein 1	IPI00010414	39729.32	6.56	2	80.33	99.99992	44.73	99.70785	0.590328	0.034100893	2
TPM3 tropomyosin 3 isoform 1	IPI00183968	38592.34	4.68	6	309.06	100	59.88	99.99108	0.588914	0.212695527	6
ANXA2 Annexin A2	IPI00455315	43516.27	7.57	14	874.8489	100	104.63	100	0.586426	0.175738381	14
HBD;HBB Hemoglobin subunit delta	IPI00473011	17865.5	7.85	10	760.98	100	137.29	100	0.586287	0.335604919	15
JUP JUP protein	IPI00789324	87025.11	5.75	1	63.87	99.99644	63.87	99.99644	0.583532	0	1
HMOX1 33 kDa protein	IPI00747450	35080.3	8.72	1	58.81	99.98858	58.81	99.98858	0.58319	0	1
SOD2 manganese superoxide dismutase isoform A precursor	IPI00847322	27176.84	8.35	6	411.93	100	108.49	100	0.575455	8.79E-02	6
- 105 kDa protein	IPI00794900	115433.2	7.3	8	472.14	100	131.25	100	0.574426	0.209541582	8
MYH10 Isoform 2 of Myosin-10	IPI00479307	260063.2	5.46	9	456.8056	100	104.78	100	0.570376	0.119983918	9
PCK2 mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor	IPI00797038	74784.86	7.57	9	426.33	100	77.48	99.99984	0.568484	0.131935747	9
ARPC3 12 kDa protein	IPI00796102	13215.08	8.52	2	81.87	99.99994	48.82	99.88608	0.567455	0.220480228	2
ARPC4 actin related protein 2/3 complex subunit 4 isoform b	IPI00607772	10554.03	6.84	2	87.74	100	56.98	99.9826	0.565852	0.13081302	2
SULT1A1 Sulfotransferase 1A1	IPI00300026	47814.7	8.61	4	259.46	100	90.49	100	0.565421	0.176021316	4
ASL argininosuccinate lyase isoform 3	IPI00607563	52220	5.82	3	204.29	100	104.84	100	0.564032	0.088061989	3
TBXAS1 TBXAS1 protein	IPI00329700	56407.3	6.62	1	55.38	99.97485	55.38	99.97485	0.563432	0	1

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HBB Hemoglobin subunit beta	IPI00654755	17808.5	6.75	13	1126.75	100	137.29	100	0.55043	0.289334126	21
ACAA1 3-ketoacyl-CoA thiolase, peroxisomal precursor	IPI00012828	47604.07	8.76	5	363.4	100	87.47	100	0.544761	0.173943854	5
C9 Complement component C9 precursor	IPI00022395	69800.94	5.43	2	92.00999	100	59.51	99.99028	0.54388	0.140533504	2
EPHX1 Epoxide hydrolase 1	IPI00009896	57419.38	6.77	6	416.41	100	115.69	100	0.539358	0.242105233	6
LUM 23 kDa protein	IPI00794403	25919.61	8.52	3	212.92	100	92.41	100	0.537598	0.232048266	3
RCN3 Reticulocalbin-3 precursor	IPI00101037	38766.2	4.74	2	105.19	100	56.11	99.97874	0.532264	3.48E-02	2
DECR1 2,4-dienoyl-CoA reductase, mitochondrial precursor	IPI00003482	40019.15	9.35	6	396.33	100	118.23	100	0.529786	0.251894093	6
- Histone 2, H3, pseudogene 2	IPI00455457	17482.8	11.27	3	114.46	100	39.31	98.98233	0.524354	0.137984864	4
COQ9 Isoform 1 of Ubiquinone biosynthesis protein COQ9, mitochondrial precu	IPI00470631	37064.78	5.61	1	67.43	99.99843	67.43	99.99843	0.524271	0	1
BGN CDNA FLJ35635 fis, clone SPLEN2011805, highly similar to	IPI00385748	39528	6.31	4	198.66	100	68.31	99.99872	0.523345	4.99E-02	4
PYGL 97 kDa protein	IPI00783313	107098.9	6.71	7	371.96	100	74.46	99.99969	0.520886	0.164573999	7
GRHPR GRHPR protein (Fragment)	IPI00550682	39375.17	5.95	5	322.0844	100	83.85	100	0.515825	8.73E-02	5
CYP2E1 Cytochrome P450 2E1	IPI00007282	61500.8	8.27	6	325.33	100	83.15	100	0.51508	0.222385191	6
COTL1 Coactosin-like protein	IPI00017704	18043.27	5.54	2	102.95	100	53.81	99.96389	0.51042	2.03E-02	2
CPT2 Carnitine O-palmitoyltransferase 2, mitochondrial precursor	IPI00012912	79760.86	8.38	3	159.04	100	87.1	100	0.507829	0.11397982	3
HIST3H3 Histone H3.1t	IPI00216402	17606.75	11.13	4	167.82	100	54.76	99.97099	0.507048	0.154111767	4
HBD Hemoglobin Lepore-Baltimore (Fragment)	IPI00829896	12794.05	6.17	8	558.48	100	137.29	100	0.505955	0.265737318	11
ILK Integrin-linked protein kinase	IPI00013219	55688.24	8.3	1	72.62	99.99953	72.62	99.99953	0.504729	0	1
TPM1 Isoform 1 of Tropomyosin alpha-1 chain	IPI00014581	38351.24	4.69	5	245.24	100	59.88	99.99108	0.501231	9.45E-02	5

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EHHADH Peroxisomal bifunctional enzyme	IPI00216164	86466.1	9.22	5	201.9244	100	47.53	99.84668	0.499493	0.178942445	5
TPM4 Isoform 1 of Tropomyosin alpha-4 chain	IPI00010779	32340.88	4.67	8	475.27	100	102.98	100	0.499185	0.114128738	8
ACADM Hypothetical protein DKFZp686M24262	IPI00513827	55018.79	7.94	4	198.99	100	78.05	99.99986	0.497914	0.203373166	4
COL14A1 Isoform 3 of Collagen alpha-1(XIV) chain precursor	IPI00402215	195722	5.16	2	73.09	99.99957	37.04	98.28364	0.493378	0.10057905	2
HRSP12 Ribonuclease UK114	IPI00005038	15826.8	8.74	2	120.26	100	64.97	99.99724	0.492397	5.39E-02	2
KRT18 Keratin, type I cytoskeletal 18	IPI00784347	51196.9	5.34	15	897.7	100	157.17	100	0.488946	0.247254128	16
CYP2C19 Cytochrome P-450 II C (Fragment)	IPI00657852	44746.02	6.82	2	118.94	100	88.42	100	0.488141	1.88E-02	2
ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria	IPI00024990	63211.08	8.72	10	597.8944	100	104.82	100	0.487955	0.140569611	10
ANXA1 Annexin A1	IPI00218918	43626.43	6.57	4	350.32	100	118.41	100	0.486535	2.52E-02	4
UGT2B7 similar to UDP-glucuronosyltransferase 2B7 precursor	IPI00787584	65314.41	8.41	3	156.19	100	63.72	99.99631	0.483175	0.147785731	3
EIF3S10 EIF3S10 protein (Fragment)	IPI00386403	51034.98	6.24	1	62.02	99.99455	62.02	99.99455	0.483123	0	1
ACY1 Aminoacylase-1	IPI00009268	48344.23	5.77	3	160.76	100	69.6	99.99905	0.483065	0.113414817	3
LGALS4 Galectin-4	IPI00009750	38026.42	9.21	2	73.83	99.99964	38.64	98.81257	0.482033	1.06E-02	2
PCCA Propionyl-CoA carboxylase alpha chain, mitochondrial precursor	IPI00749503	84435.19	6.63	1	70.96	99.9993	70.96	99.9993	0.480116	0	1
CA2 11 kDa protein	IPI00790885	13118.77	6.21	1	62.37	99.99497	62.37	99.99497	0.479285	0	1
CLU clusterin isoform 1	IPI00400826	62857.9	6.24	2	108.4644	100	77.81	99.99986	0.479094	0.13083983	2
RPL28 Ribosomal protein L28 variant (Fragment)	IPI00816097	11793.78	10.42	1	64.57	99.99697	64.57	99.99697	0.478027	0	1
BPHL Isoform 1 of Valacyclovir hydrolase precursor	IPI00384428	35828.3	9.2	1	56.85	99.98207	56.85	99.98207	0.466649	0	1
CYBB Cytochrome b-245 heavy chain	IPI00218646	71069.92	8.9	1	91.33	100	91.33	100	0.464571	0	1

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AGXT Serine--pyruvate aminotransferase	IPI00009367	46426.73	8.61	7	443.63	100	108.98	100	0.463747	0.132866654	7
CALD1 Isoform 2 of Caldesmon	IPI00218694	76226.47	6.37	4	247.66	100	99.24	100	0.461506	0.100982558	4
SYNE1 Isoform 6 of Nesprin-1	IPI00247297	1110046	5.37	2	73.53	99.99961	38.04	98.63665	0.460492	0.762836942	2
KRT8 Keratin, type II cytoskeletal 8	IPI00554648	58423.63	5.52	24	1611.229	100	113.78	100	0.456955	0.147398673	28
LSP1 50 kDa protein	IPI00554652	54843.82	5.42	1	87.08	100	87.08	100	0.45249	0	1
NNMT Nicotinamide N-methyltransferase	IPI00027681	33091.32	5.56	2	81.08	99.99993	48.76	99.88449	0.448786	0.165526567	2
FLNA Filamin-A	IPI00333541	305957.4	5.7	17	991.5889	100	112.07	100	0.444513	0.155661707	17
S100A8 Protein S100-A8	IPI00007047	12745.89	6.51	5	246.9645	100	57.89	99.98589	0.443812	0.096007318	5
- Myosin-reactive immunoglobulin heavy chain variable region (Fragment)	IPI00783024	15665.44	9.65	1	91.43	100	91.43	100	0.44369	0	1
COL1A2 Collagen alpha-2(I) chain precursor	IPI00304962	136968	9.08	2	150.8	100	86.65	100	0.438417	0.316445597	2
TST Thiosulfate sulfurtransferase	IPI00216293	35752.06	6.77	9	494.0645	100	114.87	100	0.438076	0.124298096	9
GLYAT Isoform 1 of Glycine N-acyltransferase	IPI00402759	37221.21	8.38	5	228.92	100	60.39	99.99206	0.436126	0.652411828	5
GPT Alanine aminotransferase 1	IPI00217458	57510.33	6.77	2	94.13	100	50.71	99.92628	0.434113	0.079601726	2
- 24 kDa protein	IPI00747151	25497.47	8.59	1	70.17	99.99917	70.17	99.99917	0.428561	0	1
ANXA4 annexin IV	IPI00793199	39558.52	5.84	8	555.35	100	105.99	100	0.425466	0.112760284	8
ANXA6 Annexin A6	IPI00221226	83734.25	5.42	21	1241.849	100	125.37	100	0.420811	0.13643287	22
- Transforming growth factor, beta-induced, 68kDa variant (Fragment)	IPI00556324	27690.46	5.33	1	77.8	99.99986	77.8	99.99986	0.41926	0	1
ADH1A Alcohol dehydrogenase 1A	IPI00218896	45320.81	8.26	11	854.64	100	112.05	100	0.41916	0.104487349	13
ALDH1A1 Retinal dehydrogenase 1	IPI00218914	60949.39	6.3	12	719.0001	100	110.45	100	0.41621	0.127074898	12

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AKR7A3 Aflatoxin B1 aldehyde reductase member 3	IPI00293721	39376.69	6.67	4	184.2	100	59.42	99.99008	0.413547	0.126146405	4
ANXA6 annexin VI isoform 2	IPI00002459	83137.9	5.46	21	1294.119	100	125.37	100	0.40972	0.127442597	22
APOL2 Apolipoprotein-L2	IPI00220007	53133.3	8.51	1	63.72	99.99631	63.72	99.99631	0.409376	0	1
LOC651249 similar to ribosomal protein L34	IPI00741167	17426.44	11.43	1	56.18	99.97908	56.18	99.97908	0.408956	0	1
KRT77 Keratin 77	IPI00376379	65018.72	5.63	3	169.07	100	75.44	99.99975	0.404868	0.199432703	3
ADH1C Alcohol dehydrogenase 1C	IPI00465343	45428	8.63	8	557.84	100	112.05	100	0.400889	0.108360674	10
UGP2 Isoform 1 of UTP--glucose-1-phosphate uridylyltransferase	IPI00329331	63091.29	8.16	8	568.9445	100	147.14	100	0.399961	0.144804149	9
CES2 carboxylesterase 2 isoform 1	IPI00332828	72247.06	6.03	6	326.34	100	70.5	99.99923	0.394389	0.156987197	6
SULT2A1 Bile salt sulfotransferase	IPI00216133	37496.33	5.71	6	313.24	100	77.78	99.99986	0.391405	0.225741218	6
BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101	49946.24	6.58	4	231.9644	100	77.42	99.99984	0.385061	0.278986279	4
FTCD Isoform C of Formimidoyltransferase-cyclodeaminase	IPI00218976	64571.53	5.24	4	181.1644	100	56.9	99.98227	0.377616	0.218450347	4
S100A9 Protein S100-A9	IPI00027462	15007.73	5.71	5	473.76	100	143.73	100	0.369881	8.68E-02	8
HGD Homogentisate 1,2-dioxygenase	IPI00303174	54236.86	6.54	4	178.12	100	54.12	99.96638	0.369873	0.156767155	4
LTF 73 kDa protein	IPI00789477	80974.52	8.2	3	104.18	100	36.65	98.12238	0.364365	0.28617315	4
CYP2C8 45 kDa protein	IPI00843846	49430.42	8.91	3	113.83	100	49.99	99.91298	0.35808	0.101332587	3
KRT79 keratin 6L	IPI00241841	62350.57	6.75	4	193.81	100	53.43	99.96059	0.356146	6.87E-02	4
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	43462.35	8	11	842.4344	100	111.06	100	0.355333	0.145519469	12
MGC29506 hypothetical protein LOC51237	IPI00102821	21677.3	5.37	3	150.71	100	61.25	99.99349	0.354631	0.16533242	3
ADH1B Alcohol dehydrogenase 1B	IPI00473031	45270.91	8.63	11	833.92	100	112.05	100	0.353893	0.104848203	12

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RDH16 Microsomal NAD+-dependent retinol dehydrogenase 4 variant (Fragment)	IPI00555683	23832.69	7.67	2	90.88	100	50.58	99.92404	0.344116	0.151259497	2
HPD 40 kDa protein	IPI00795913	44884.14	5.93	2	96.68	100	51.14	99.93323	0.3348	0.060868391	2
EMILIN1 EMILIN-1 precursor	IPI00013079	109415.5	5.1	2	136.28	100	92.22	100	0.324485	0.253628339	2
FMO3 Dimethylaniline monooxygenase [N-oxide-forming] 3	IPI00329033	66260.83	7.9	2	79.89	99.99991	46.26	99.7946	0.322228	0.177796806	2
LYZ Lysozyme C precursor	IPI00019038	17902.36	9.38	2	128.17	100	92.78	100	0.317979	9.71E-03	2
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1	5.6	4	270.47	100	104.88	100	0.310772	0.278080462	4
KRT19 Keratin, type I cytoskeletal 19	IPI00479145	46225.38	5.04	7	341.17	100	83.98	100	0.310013	0.213561586	7
FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	41289.15	6.54	9	801.28	100	129.65	100	0.295678	0.09865427	9
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	43936.06	8.75	9	582.0245	100	100.93	100	0.287102	0.160531926	9
TAGLN Transgelin	IPI00216138	25234.73	8.87	5	302.45	100	89.48	100	0.278881	0.196635935	5
PRELP Prolargin precursor	IPI00020987	46264.34	9.47	3	116.91	100	45.85	99.77426	0.263424	0.081221483	3
KRT7 keratin 7	IPI00847342	55144.71	5.4	7	342.8644	100	71.24	99.99935	0.261428	0.130869413	7
CPS1 Isoform 1 of Carbamoyl-phosphate synthase [ammonia], mitochondrial pre	IPI00011062	180876	6.3	60	4232.145	100	178.36	100	0.253138	0.129906658	67
GSTP1 Glutathione S-transferase P	IPI00219757	25397.22	5.43	3	164.34	100	66.2	99.99792	0.240001	8.24E-02	3
MT1X Metallothionein-1X	IPI00008753	8279.2	8.38	2	126.22	100	91.14	100	0.236027	7.92E-02	2
ADH4 Alcohol dehydrogenase 4	IPI00218899	45828.03	8.25	7	400.53	100	66.35	99.99799	0.225796	0.110771993	7
GSTA1 Glutathione S-transferase A1	IPI00657682	29261.05	8.91	6	323.13	100	75.6	99.99976	0.200662	0.132825039	6
DEFA3 Neutrophil defensin 3 precursor	IPI00021827	10946.22	5.71	4	150.51	100	42.83	99.54751	0.189988	7.66E-02	4
GGTLA1 Isoform 2 of Gamma-glutamyltransferase 5 precursor	IPI00339373	61051.74	7.67	2	115.52	100	73.97	99.99965	0.12845	6.01E-02	2

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio * (115/114)	iTRAQ Standard Deviation * (115/114)	iTRAQ Peptides (115/114)
S100P Protein S100-P	IPI00017526	12023.44043	4.75	1	101.6399994	100	101.6399994	100	40.23634604	0	1
DEFA3 Neutrophil defensin 3 precursor	IPI00021827	10946.21973	5.71	2	79.36999512	99.99989493	42.93000031	99.53710435	5.655948762	2.27782103	2
KYNU Kynureninase	IPI00003818	58348.64844	6.56	2	79.53443909	99.99989883	49.52000046	99.89849602	4.692876773	1.3306637	2
NAP1L1 43 kDa protein	IPI00789029	47959.44141	4.45	1	81.54000092	99.99993625	81.54000092	99.99993625	4.640823499	0	1
FKBP11 Peptidyl-prolyl cis-trans isomerase	IPI00789642	11840.12988	4.57	1	75.73999786	99.99975763	75.73999786	99.99975763	4.017763302	0	1
FN1 fibronectin 1 isoform 2 preproprotein	IPI00845263	280315.25	5.36	12	578.178833	100	63.74000168	99.99615866	3.531886193	1.83779318	12
S100A9 Protein S100-A9	IPI00027462	15007.73047	5.71	6	494.4100037	100	132.7700043	100	3.484993538	1.19194646	7
PKM2 Isoform M2 of Pyruvate kinase isozymes M1/M2	IPI00479186	63832.46094	7.96	5	268.1099854	100	64.05000305	99.9964233	3.400636445	1.2030494	5
S100A8 Protein S100-A8	IPI00007047	12745.88965	6.51	7	387.7444458	100	89.33999634	100	3.278518778	0.88095252	7
OAT Ornithine aminotransferase, mitochondrial precursor	IPI00022334	52956.57813	6.57	5	187.0099945	100	50.66999817	99.92210971	3.161515407	2.11094382	5
ANXA2 Annexin A2	IPI00455315	43516.26953	7.57	13	743.098877	100	107.2300034	100	3.015991858	1.08767905	13
LSP1 50 kDa protein	IPI00554652	54843.82031	5.42	1	86.51000214	100	86.51000214	100	2.970087632	0	1
RAB10 Ras-related protein Rab-10	IPI00016513	25878.90039	8.59	2	116.5700073	100	66.44000244	99.99793708	2.946380773	3.61E-02	2
LYZ Lysozyme C precursor	IPI00019038	17902.35938	9.38	1	100.2799988	100	100.2799988	100	2.828595693	0	1
RAN 26 kDa protein	IPI00792352	29358.91016	8.51	3	148.1800079	100	65.41000366	99.99738493	2.814809077	0.90425406	3
NCL Isoform 1 of Nucleolin	IPI00604620	89719.57031	4.6	7	396.3299866	100	98.73000336	100	2.739876053	0.71469586	7
FGB Fibrinogen beta chain precursor	IPI00298497	61772.66016	8.54	10	824.0500488	100	112.4199982	100	2.67215264	0.43245668	10
EPRS glutamyl-prolyl tRNA synthetase	IPI00013452	193228.6875	7.02	1	84.54000092	100	84.54000092	100	2.444217283	0	1
- CD68 antigen variant (Fragment)	IPI00555602	45637.91016	5.46	7	506.2999573	100	110.8199997	100	2.439592015	1.07046531	7
LRPPRC Leucine-rich PPR motif-containing protein	IPI00783271	173604.2344	5.81	3	131.5700073	100	52.22000122	99.94548914	2.417892896	0.50393709	3
VDAC2 Isoform 2 of Voltage-dependent anion-selective channel protein 2	IPI00216024	39125.44922	5.87	2	84.83999634	100	51.18000031	99.9307399	2.412844048	0.41265082	2

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ANXA1 Annexin A1	IPI00218918	43626.42969	6.57	1	108.3600006	100	108.3600006	100	2.407393515	0	1
XRCC6 70 kDa protein	IPI00465430	78696.84375	6.23	1	75.5	99.99974386	75.5	99.99974386	2.30637601	0	1
MPO Isoform H14 of Myeloperoxidase precursor	IPI00236554	77088.74219	9.3	5	226.0499878	100	60.97000122	99.99273086	2.273772136	0.56255613	5
VDAC1 Voltage-dependent anion-selective channel protein 1	IPI00216308	34589.96094	8.62	4	193.3000031	100	67.54000092	99.99839866	2.267978913	0.34978132	4
HNRPA1 Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	IPI00465365	37003.55078	9.27	6	422.5299683	100	136.6399994	100	2.251334172	0.75876352	6
- Tubulin alpha-4 chain	IPI00017454	29152.96094	8.65	2	131.2900085	100	81.88999939	99.99994119	2.2283067	1.68040825	2
PARP1 Poly [ADP-ribose] polymerase 1	IPI00449049	131945.8906	8.99	2	112.7200012	100	61.18999863	99.99308992	2.227703364	1.51E-02	2
HNRPU heterogeneous nuclear ribonucleoprotein U isoform a	IPI00644079	101350.8203	5.76	2	139.6900024	100	95.94999695	100	2.213805437	1.15410684	2
- 140 kDa protein	IPI00829641	149651.875	7.92	3	160.5400085	100	83.95999908	100	2.21151654	0.92627	3
HNRPA3 Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	IPI00419373	42922.89844	9.1	4	315.1900024	100	130.0800018	100	2.201613582	0.94041803	4
LDHA Isoform 1 of L-lactate dehydrogenase A chain	IPI00217966	41071.75	8.44	11	548.0044556	100	90.72000122	100	2.182228249	1.1573262	13
SRP14 8 kDa protein	IPI00789296	8752.330078	10.03	1	72.80999756	99.99952414	72.80999756	99.99952414	2.132435525	0	1
ARHGDIB 13 kDa protein	IPI00791712	14875.75977	4.69	1	115.5199966	100	115.5199966	100	2.119406881	0	1
NPM1 Isoform 1 of Nucleophosmin	IPI00549248	37589.32031	4.64	5	307.6300049	100	90.95999908	100	2.105772827	1.22049752	5
NME1;NME2 Nucleoside diphosphate kinase	IPI00604590	36163.17969	8.7	6	297.3177795	100	84.93000031	100	2.099593129	0.47884558	7
DAZAP1 Isoform 2 of DAZ-associated protein 1	IPI00335930	43470.07813	8.48	1	64.5	99.99677535	64.5	99.99677535	2.065011936	0	1
SFPQ Isoform Long of Splicing factor, proline- and glutamine-rich	IPI00010740	81090.10938	9.45	3	132.9244385	100	59.66999817	99.99019419	2.056983513	0.32448831	3
PIR Pirin	IPI00012575	35353.58984	6.42	1	74.86000061	99.99970319	74.86000061	99.99970319	2.042476028	0	1
SERPINB1 Leukocyte elastase inhibitor	IPI00027444	47127.14063	5.9	2	82.28999329	99.99994636	43.00999832	99.54555294	2.040612093	0.40635151	2
FGG Isoform Gamma-A of Fibrinogen gamma chain precursor	IPI00219713	55011.35938	5.7	6	289.0100098	100	83.04000092	100	1.977503577	0.46164369	6
VDAC3 Isoform 2 of Voltage-dependent anion-selective channel protein 3	IPI00294779	35078.69141	8.85	2	101.1999969	100	67.54000092	99.99839866	1.972251928	8.82E-02	2
LTF 73 kDa protein	IPI00789477	80974.52344	8.2	5	280.190033	100	96.54000092	100	1.953068244	0.76455	5
GCS1 Mannosyl-oligosaccharide glucosidase	IPI00328170	95022.89844	8.97	1	66.54000092	99.99798403	66.54000092	99.99798403	1.942659433	0	1

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ANXA5 Annexin A5	IPI00329801	39272.76172	4.94	11	673.6500244	100	106.3700027	100	1.938948157	0.80183947	12
ATIC Bifunctional purine biosynthesis protein PURH	IPI00289499	70461.78906	6.27	1	68.58999634	99.99874257	68.58999634	99.99874257	1.910925303	0	1
FGA Isoform 2 of Fibrinogen alpha chain precursor	IPI00029717	76032.28906	8.23	13	754.3845215	100	103.9300003	100	1.907973728	0.65248423	13
TRAP1 57 kDa protein	IPI00646055	62264.05859	7.21	3	134.484436	100	63.25	99.99569985	1.856870167	0.30569297	3
EIF4A2 Isoform 2 of Eukaryotic initiation factor 4A-II	IPI00409717	49956.14063	5.33	5	368.4299927	100	110.8199997	100	1.856681192	0.90093675	5
RBM8A Isoform 2 of RNA-binding protein 8A	IPI00216659	21665.92969	5.64	1	110.5999985	100	110.5999985	100	1.841043432	0	1
ENO1 Isoform alpha-enolase of Alpha-enolase	IPI00465248	53031.82031	7.01	13	858.4200439	100	103.6800003	100	1.837945632	0.60812758	13
CYCS Cytochrome c	IPI00465315	14569.42969	9.59	3	129.1799927	100	50.18999863	99.91300721	1.835758251	0.61747588	3
HSP90AB1 Heat shock protein HSP 90-beta	IPI00414676	94433.0625	4.97	16	937.8744507	100	123.5299988	100	1.834798629	1.47029804	16
HIST1H1B Histone H1.5	IPI00217468	32071.38086	10.91	1	82.69000244	100	82.69000244	100	1.827931132	0	1
RPS3 40S ribosomal protein S3	IPI00011253	29833.74023	9.68	2	107.6399994	100	63.56999969	99.99600531	1.811035884	0.10588164	2
YWHAZ 14-3-3 protein zeta/delta	IPI00021263	30890.03906	4.73	5	383.1744385	100	145.25	100	1.804757089	0.47506278	5
AKR1C2 Aldo-keto reductase family 1 member C2	IPI00005668	40922.30078	7.13	7	332.8800049	100	67.13999939	99.99824417	1.799855965	0.39685595	7
TAGLN2 24 kDa protein	IPI00647915	26448.48047	8.41	5	371.7800293	100	109.5999985	100	1.776599994	0.43976564	5
HBD Hemoglobin Lepore-Baltimore (Fragment)	IPI00829896	12794.0498	6.17	10	823.6199951	100	135.2899933	100	1.768347913	1.83684612	14
ANXA4 annexin IV	IPI00793199	39558.51953	5.84	10	580.6400146	100	98.5	100	1.761418999	0.36346861	10
LOC648517 similar to Aldo-keto reductase family 1 member C1 (20-alpha-hydro	IPI00736657	35442.78906	9.01	8	367.0599976	100	67.13999939	99.99824417	1.7561367	0.39402092	8
ALDOA Fructose-bisphosphate aldolase A	IPI00465439	43651.62891	8.3	8	464.7644348	100	91.27999878	100	1.754176549	2.77238867	10
ANPEP Aminopeptidase N	IPI00221224	116417.4531	5.31	3	121.6444397	100	47.11999893	99.82360623	1.737489174	0.20878212	3
TUBA1B Similar to Tubulin alpha-ubiquitous chain	IPI00792677	49578.05859	4.96	11	909.7099609	100	189.2799988	100	1.736879731	0.68109527	11
HSPD1 60 kDa heat shock protein, mitochondrial precursor	IPI00784154	68931.10156	5.7	20	1487.047852	100	122.9300003	100	1.726014269	0.52819537	21
TUBA1C Tubulin alpha-1C chain	IPI00218343	53295.64844	4.96	11	902.5899658	100	189.2799988	100	1.721939678	0.6665395	11
TES Isoform 2 of Testin	IPI00216425	54398.51953	7.82	1	62.75	99.99517516	62.75	99.99517516	1.716490873	0	1

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EEF1D EEF1D protein	IPI00064086	31512.69922	4.81	1	61.41999817	99.99344635	61.41999817	99.99344635	1.704492486	0	1
LOC651249 similar to ribosomal protein L34	IPI00741167	17426.43945	11.43	1	63.43000031	99.99587444	63.43000031	99.99587444	1.698519277	0	1
SURF4 Surfeit 4	IPI00399142	22555.05078	8.88	1	84.88999939	100	84.88999939	100	1.698050758	0	1
BID Isoform 2 of BH3-interacting domain death agonist	IPI00420084	27815.5	6.6	1	63.70000076	99.99612311	63.70000076	99.99612311	1.695282857	0	1
DHX9 ATP-dependent RNA helicase A	IPI00844578	151431.7344	6.41	2	125.0699997	100	84.93000031	100	1.693805514	4.51E-02	2
HSP90AB4P Heat shock protein 90Bd	IPI00555565	66222.17969	4.65	4	185.1100006	100	65.5	99.99743857	1.693231561	0.42897494	4
SLC25A6 ADP/ATP translocase 3	IPI00291467	36341.51953	9.76	3	130.4300079	100	45.47000122	99.7420812	1.691653624	0.96579841	3
CAP1 Adenylyl cyclase-associated protein	IPI00639931	58646.21094	8.24	3	171.0299988	100	64.97000122	99.9971061	1.689643119	6.75E-02	3
SFRS6 Isoform SRP55-1 of Splicing factor, arginine/serine-rich 6	IPI00012345	43543.78906	11.42	1	62.56999969	99.99497098	62.56999969	99.99497098	1.685175714	0	1
A2M Alpha-2-macroglobulin precursor	IPI00478003	177285.7656	6	1	64.80000305	99.99699058	64.80000305	99.99699058	1.684446549	0	1
- Elongation factor 1-alpha	IPI00472724	57485.78125	9.15	11	619.9900513	100	98.19999695	100	1.684017092	0.99996512	11
CYB5R3 Isoform 2 of NADH-cytochrome b5 reductase 3	IPI00446235	34240.60938	7.15	2	83.68000031	100	45.75	99.75818506	1.676020818	1.07142586	2
SCAMP3 Isoform 2 of Secretory carrier-associated membrane protein 3	IPI00306383	37073.82813	7.53	1	74.31999969	99.99966389	74.31999969	99.99966389	1.674427209	0	1
HNRPD Isoform 1 of Heterogeneous nuclear ribonucleoprotein D0	IPI00028888	43300.76953	7.62	1	61.63000107	99.99375571	61.63000107	99.99375571	1.665540796	0	1
CCT6A T-complex protein 1 subunit zeta	IPI00027626	64980.16016	6.23	3	191.0099945	100	72.08999634	99.99943833	1.654769131	0.20476942	3
AKR1C3 Aldo-keto reductase family 1 member C3	IPI00291483	41031.17969	8.05	8	375.8299866	100	75.91000366	99.99976693	1.638678638	0.27903921	8
GGH Gamma-glutamyl hydrolase precursor	IPI00023728	39719.46875	6.67	1	76.79000092	99.99980968	76.79000092	99.99980968	1.638211502	0	1
EEF2 Elongation factor 2	IPI00186290	105563.6484	6.41	9	569.8599854	100	92.70999908	100	1.63796065	0.47411814	9
PRPH Isoform 2 of Peripherin	IPI00793184	57006.82031	5.37	3	156.3800049	100	79.87999725	99.99990657	1.635023363	0.65868075	3
CCT5 T-complex protein 1 subunit epsilon	IPI00010720	66337.35156	5.45	3	116.5	100	49.31999969	99.89371226	1.632359398	0.52687739	3
HNRPAB Isoform 1 of Heterogeneous nuclear ribonucleoprotein A/B	IPI00329355	41002.28906	9.04	2	128.6999969	100	76.25	99.99978448	1.627511624	0.45616132	2
GBP2 GBP2 protein	IPI00848358	76021.07813	5.54	2	149.1199951	100	78.18000031	99.99986181	1.617173448	0.49661472	2
TPM4 Isoform 1 of Tropomyosin alpha-4 chain	IPI00010779	32340.88086	4.67	6	300.9244385	100	67.69000244	99.99845303	1.610324042	0.27509382	6

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HSPA1A;HSPA1B heat shock 70kDa protein 1A	IPI00845339	77569.67969	5.48	8	467.5700073	100	108.4400024	100	1.610013732	0.4043797	9
IGHM IGHM protein	IPI00761159	57955.55078	7.53	7	659.9499512	100	145.9700012	100	1.607670332	0.2879175	7
PAH Phenylalanine-4-hydroxylase	IPI00017579	56707.82031	6.15	3	108.75	100	42.02999878	99.43051374	1.607557869	0.33676117	3
LOC388720 similar to ubiquitin and ribosomal protein S27a precursor	IPI00397808	21877.69922	9.53	5	241.3300018	100	71.72000122	99.99938838	1.598765136	0.27485976	5
YWHAQ 14-3-3 protein theta	IPI00018146	30857.03906	4.68	5	286.6499939	100	84.48000336	100	1.596827686	0.5329611	5
IGHM Hypothetical protein DKFZp686I15212	IPI00418153	62655.28125	8.39	6	368.1600037	100	106.2600021	100	1.592659183	0.28961092	6
PGK1 Phosphoglycerate kinase 1	IPI00169383	51100.66016	8.3	10	557.4400024	100	126.5299988	100	1.591460347	0.50224922	10
PGD 53 kDa protein	IPI00747533	59047.51953	7.12	2	91.66000366	100	56.13999939	99.97789537	1.591106481	7.22E-02	2
ENO2 6 kDa protein	IPI00790892	6040.029785	4.89	2	132.8199921	100	69.55999756	99.99899427	1.586576046	0.35880554	2
CSTB Cystatin-B	IPI00021828	12618.79004	6.96	3	174.1700134	100	80.15000153	99.9999122	1.584769495	0.35237289	3
EEA1 Early endosome antigen 1	IPI00329536	188351.2031	5.53	1	85.29000092	100	85.29000092	100	1.57496379	0	1
S100A6 Protein S100-A6	IPI00027463	11659.54004	5.33	2	82.44999695	99.9999483	42.25	99.45864378	1.572958585	0.08777251	2
hCG_1983058 hypothetical protein LOC644820	IPI00414723	28320.82031	4.59	2	72.51000214	99.9994901	41.93000031	99.4172489	1.56746945	8.67E-03	2
RPS15A 40S ribosomal protein S15a	IPI00221091	16650.17969	10.14	4	149.6844482	100	42.88999939	99.53282113	1.565600561	0.75437269	4
TUBB2C Tubulin beta-2C chain	IPI00007752	52471.19141	4.79	11	856.9400024	100	137.6199951	100	1.553050345	0.39021271	12
RPSA Ribosomal protein SA	IPI00413108	35158.85156	4.79	3	193.9499969	100	93.75	100	1.552697286	0.3425397	3
NNMT Nicotinamide N-methyltransferase	IPI00027681	33091.32031	5.56	3	126.7999954	100	49.5	99.89802749	1.547437455	0.13483723	3
RPS9 40S ribosomal protein S9	IPI00221088	25503.88086	10.66	3	100.0800018	100	34.77000046	96.96971774	1.545288791	0.33977197	3
VCP 89 kDa protein	IPI00843748	96637.15625	5.11	6	403.6600037	100	118.0100021	100	1.544496827	0.45154559	6
MICA;HLA-A;HLA-A29.1;LOC730410;HLA-B;HLA-C HLA class I histocompatibility a	IPI00743359	42850.23828	6.08	4	261.714447	100	114.8199997	100	1.538966325	0.20137721	4
IGHG1 Hypothetical protein DKFZp686K03196	IPI00423464	57631.46875	8.84	7	672.1300049	100	145.9700012	100	1.536762236	0.33813475	8
CCT8 T-complex protein 1 subunit theta	IPI00784090	66090.99219	5.42	3	201.7700043	100	77.19000244	99.99982643	1.534328958	0.31682746	3
CLTC Isoform 2 of Clathrin heavy chain 1	IPI00455383	203165.7031	5.48	7	374.2944336	100	72.31999969	99.9994673	1.533775747	0.37413328	7

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LCP1 Plastin-2	IPI00010471	77185.35938	5.2	4	214.0899963	100	67.23000336	99.99828018	1.530250449	0.47229128	4
CGN cingulin	IPI00844508	149111.4844	5.44	1	105.4199982	100	105.4199982	100	1.52996065	0	1
HNRPR HNRPR protein	IPI00644055	77880.99219	8.23	1	69.23000336	99.99891487	69.23000336	99.99891487	1.521588961	0	1
SERPINA1 Alpha-1-antitrypsin precursor	IPI00553177	51885.51172	5.37	8	536.2144775	100	93.48000336	100	1.515431271	0.51969802	9
AKR1B10 Aldo-keto reductase family 1 member B10	IPI00105407	41078.28125	7.12	1	88.87000275	100	88.87000275	100	1.515356027	0	1
HBB Hemoglobin subunit beta	IPI00654755	17808.5	6.75	14	1269.130005	100	145.1799927	100	1.500962849	1.56622786	21
SEC31A Isoform 4 of Protein transport protein Sec31A	IPI00515103	138953.7344	7.03	3	202.0288849	100	108.2099991	100	1.492981784	0.23469306	3
RPS11 40S ribosomal protein S11	IPI00025091	21725.32031	10.31	4	187.0144501	100	61.61000061	99.99372689	1.484909805	0.46446499	4
VIM Vimentin	IPI00418471	56977.44141	5.06	19	1256.898926	100	125.4199982	100	1.481563112	0.5452161	20
FLNA Filamin-A	IPI00333541	305957.375	5.7	4	183.8144531	100	78.55000305	99.99987309	1.480824959	0.12603579	4
HNRPK Isoform 2 of Heterogeneous nuclear ribonucleoprotein K	IPI00216746	54394.67969	5.19	5	290.8244324	100	93.43000031	100	1.479497297	0.25413331	5
HSPE1 10 kDa heat shock protein, mitochondrial	IPI00220362	12653.11035	8.89	7	409.6900024	100	77.38999939	99.99983424	1.47886066	0.45362892	10
HIST3H3 Histone H3.1t	IPI00216402	17606.75	11.13	3	130.5899963	100	55.20999908	99.97261686	1.474411807	0.55639164	4
TUBB3 Tubulin beta-3 chain	IPI00013683	53216.46094	4.83	6	471.5099792	100	137.6199951	100	1.473849954	0.42758433	6
RPLP0 60S acidic ribosomal protein P0	IPI00556485	30148.58984	8.36	3	186.7600098	100	102.8300018	100	1.466852709	0.2231332	3
HSPA9 Stress-70 protein, mitochondrial precursor	IPI00007765	81497.46094	5.87	15	986.6744385	100	109.8600006	100	1.464667288	0.35211581	15
SOD2 manganese superoxide dismutase isoform A precursor	IPI00847322	27176.83984	8.35	4	250.8299866	100	106.5299988	100	1.458499803	0.1274883	4
HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein	IPI00003865	78958.95313	5.37	19	1172.518921	100	118.0299988	100	1.457466781	0.19748925	20
HSPA6 Heat shock 70 kDa protein 6	IPI00339269	77112.71094	5.81	4	242.6499939	100	108.4400024	100	1.456474203	0.50558929	4
IMMT Isoform 3 of Mitochondrial inner membrane protein	IPI00470829	88364.21094	6.31	3	203.4599915	100	118.0100021	100	1.455046869	0.4387022	3
LONP1 Lon protease homolog	IPI00334291	109879.3125	6.11	1	60.88000107	99.99257865	60.88000107	99.99257865	1.453515138	0	1
LOC388474 similar to 60S ribosomal protein L7a isoform 1	IPI00397676	35921.55078	10.56	2	110.7600021	100	65.65000153	99.99752553	1.44962134	0.13118665	2
TUBB Tubulin beta chain	IPI00011654	52311.16016	4.78	11	868.8900146	100	137.6199951	100	1.448838709	0.42741624	12

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GAPDH 32 kDa protein	IPI00795257	35122.30859	7.15	9	681.6244507	100	125.5100021	100	1.444394465	0.6921141	11
EIF4G3 Isoform 1 of Eukaryotic translation initiation factor 4 gamma 3	IPI00646377	194311.3594	5.27	2	77.37999725	99.99983386	42.93999863	99.5381688	1.441493245	0.3527914	2
EIF4G1 eukaryotic translation initiation factor 4 gamma, 1 isoform 2	IPI00384463	180908.9531	5.15	2	77.37999725	99.99983386	42.93999863	99.5381688	1.441493245	0.3527914	2
LRRC59 Leucine-rich repeat-containing protein 59	IPI00396321	40703.35156	9.61	2	92.43000031	100	53.86999893	99.96271937	1.431699177	0.22145403	2
HNRPA2B1 Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	IPI00414696	38478.16016	8.67	9	617.2045288	100	98.65000153	100	1.42512171	0.43173685	9
TUBB2A Tubulin beta-2A chain	IPI00013475	52501.16016	4.78	10	789.3699951	100	137.6199951	100	1.424005608	0.45586438	10
PGAM1;hCG_2015138;hCG_2015269 Phosphoglycerate mutase 1	IPI00549725	31614.14063	6.67	7	446.2199707	100	107.1299973	100	1.417457639	0.22217796	7
CAPZB Capping protein (Actin filament) muscle Z-line, beta	IPI00642256	32963.14844	6.45	1	66.66999817	99.99804348	66.66999817	99.99804348	1.416327825	0	1
CS citrate synthase precursor, isoform b	IPI00383539	50469.26172	6.74	3	103.6500015	100	41.40000153	99.34161038	1.413529273	0.243629	3
HNRPH1 HNRPH1 protein	IPI00479191	53875.41016	6.33	4	242.1444397	100	98.52999878	100	1.411382222	0.29803979	5
SERPINB6 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), me	IPI00749398	46902.42188	5.18	1	68.01000214	99.99856291	68.01000214	99.99856291	1.402886894	0	1
AKR1C4 Aldo-keto reductase family 1 member C4	IPI00289524	41137.30859	6.71	9	401.6599731	100	58.08000183	99.98585891	1.400143536	0.61510333	9
CECR5 Isoform 2 of Cat eye syndrome critical region protein 5 precursor	IPI00011511	48531.94141	8.38	1	74.34443665	99.99966577	75.51999664	99.99974503	1.399957442	0	1
FDPS Farnesyl diphosphate synthase	IPI00101405	51970.89063	5.83	4	248.4599915	100	95.16000366	100	1.399024093	0.16645783	4
- Farnesyl pyrophosphate synthetase like-4 protein (Fragment)	IPI00382869	42840.89844	4.87	4	193.3499908	100	64.5	99.99677535	1.399024093	0.16645783	4
ACTG1;PSPHL Actin, cytoplasmic 2	IPI00021440	44922.05859	5.31	12	1109.289917	100	201.4199982	100	1.396114576	0.43270713	16
TUFM Tu translation elongation factor, mitochondrial	IPI00027107	54583.71875	7.26	4	308.5100098	100	122.0599976	100	1.395068417	0.24038387	4
HIST1H2BL Histone H2B type 1-L	IPI00018534	16967.94922	10.31	3	228.8099976	100	83.56999969	100	1.390187918	0.31217616	6
ALDH16A1 Aldehyde dehydrogenase family 16 member A1	IPI00217920	87917.74219	6.35	1	69.54000092	99.99898962	69.54000092	99.99898962	0.704649331	0	1
KRT19 Keratin, type I cytoskeletal 19	IPI00479145	46225.37891	5.04	3	156.2599945	100	74.25	99.99965843	0.702913876	0.27132037	3
HINT1 Histidine triad nucleotide-binding protein 1	IPI00239077	15325.28027	6.43	4	271.1199951	100	93.84999847	100	0.694546912	0.31450495	4
ANXA6 Annexin A6	IPI00221226	83734.25	5.42	19	1154.843384	100	125.3199997	100	0.689011052	0.15549822	20
RRBP1 Isoform 1 of Ribosome-binding protein 1	IPI00220967	178629.8125	8.73	10	699.1489258	100	153.6300049	100	0.681721589	0.29181371	10

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ETFA 24 kDa protein	IPI00792673	27117.09961	8.77	3	323.25	100	171.9499969	100	0.681023593	6.04E-02	3
AIFM1 Isoform 3 of Apoptosis-inducing factor 1, mitochondrial precursor	IPI00157908	72532.10938	9.03	3	201.6999969	100	84.58000183	100	0.675976301	0.03010373	3
IVD Isovaleryl-CoA dehydrogenase, mitochondrial precursor	IPI00789848	50635.03906	8.26	1	67.91999817	99.99853282	67.91999817	99.99853282	0.67514055	0	1
MAT1A S-adenosylmethionine synthetase isoform type-1	IPI00021772	47392.28906	5.86	7	343.9044495	100	85.58000183	100	0.674515954	0.20885323	7
PRDX6 Peroxiredoxin-6	IPI00220301	27847.49023	6	7	553.1099854	100	135.1600037	100	0.670006318	0.14634367	9
TPP1 Isoform 3 of Tripeptidyl-peptidase 1 precursor	IPI00554538	62032.14844	5.94	2	109.1300049	100	63.86000061	99.99626334	0.665062502	3.49E-02	2
ALDOC Fructose-bisphosphate aldolase C	IPI00418262	42921.51172	6.41	4	230.3299866	100	93.37999725	100	0.663793434	1.93179501	5
COL6A3 alpha 3 type VI collagen isoform 3 precursor	IPI00072917	345457.3438	6.47	5	209.8300018	100	48.81999969	99.8807432	0.660029095	0.3098978	5
METTL7A Methyltransferase-like protein 7A precursor	IPI00022300	30730.71094	8.7	1	80.56999969	99.9999203	80.56999969	99.9999203	0.654776006	0	1
C20orf3 47 kDa protein	IPI00479431	49085.10938	5.82	3	150.3199921	100	73.56999969	99.99960053	0.654149855	0.36393537	3
GOT2 Aspartate aminotransferase, mitochondrial precursor	IPI00018206	52087.64844	9.14	5	367.2200012	100	119.5299988	100	0.651164633	0.21199404	5
CNDP2 53 kDa protein	IPI00646632	58467.37891	5.66	3	151.1600037	100	80.83999634	99.9999251	0.648711939	0.17050558	4
ECGF1 46 kDa protein	IPI00853163	47964.32813	5.35	2	130.519989	100	71.16999817	99.9993058	0.648360665	2.60E-02	2
ANXA6 annexin VI isoform 2	IPI00002459	83137.89844	5.46	19	1164.003418	100	125.3199997	100	0.646942837	0.21120628	20
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	58388.32813	6.3	7	411.1499939	100	94.19999695	100	0.645682469	0.21323231	7
DBI Isoform 2 of Acyl-CoA-binding protein	IPI00218836	13802.13965	5.41	4	343.3599854	100	130.8300018	100	0.644849195	6.64E-02	4
AK3 GTP:AMP phosphotransferase	IPI00478236	20052.85938	8.73	1	71.87999725	99.9994105	71.87999725	99.9994105	0.635505382	0	1
SORBS2 sorbin and SH3 domain containing 2 isoform 2	IPI00477577	135030.8438	8.56	2	95.86999512	100	49.09000015	99.88793161	0.627740832	6.40E-02	2
MPST 3-mercaptopyruvate sulfurtransferase	IPI00165360	34971.80078	6.13	6	372.3500061	100	95.98999786	100	0.617491497	0.13543009	6
FKBP2 FK506-binding protein 2 precursor	IPI00002535	17649.5293	9.24	2	124.6399994	100	67.98999786	99.99855628	0.617181936	7.07E-02	2
APOL2 Apolipoprotein-L2	IPI00220007	53133.30078	8.51	1	65.41000366	99.99738493	65.41000366	99.99738493	0.617178306	0	1
AGL Isoform 6 of Glycogen debranching enzyme	IPI00219066	185998.375	6.26	1	99.05999756	100	99.05999756	100	0.615164517	0	1
ETFB Isoform 2 of Electron transfer flavoprotein subunit beta	IPI00556451	41287.32813	6.78	2	97.86999512	100	52.68999863	99.95108036	0.614864636	0.10488794	2

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SHMT1 Isoform 2 of Serine hydroxymethyltransferase, cytosolic	IPI00220668	53489.17969	7.59	5	269.2744446	100	91.13999939	100	0.613920569	0.1930788	5
HIST1H4E;HIST1H4I;HIST1H4D;HIST1H4L;HI	IPI00453473	13088.62012	11.36	5	283.0400085	100	77.05000305	99.99982074	0.61365226	0.28387805	5
CRYZ 32 kDa protein	IPI00647366	34670.82031	8.59	3	265.25	100	146.3999939	100	0.610146609	6.18E-02	3
ACADVL Isoform 2 of Very-long-chain specific acyl-CoA dehydrogenase, mitoch	IPI00178744	78527.97656	9.06	1	62.61999893	99.99502855	62.61999893	99.99502855	0.609980795	0	1
MAOA Amine oxidase [flavin-containing] A	IPI00008483	65674.00781	7.94	2	124.6600037	100	76.56999969	99.99979979	0.609599101	0.30991958	2
GANAB Isoform 2 of Neutral alpha-glucosidase AB precursor	IPI00011454	114201.4219	5.82	3	219.8099976	100	90.94999695	100	0.605711468	0.48512432	3
KRT6C Keratin, type II cytoskeletal 6E	IPI00299145	64682.71875	8.09	5	238.7044373	100	72.30999756	99.99946607	0.603040128	0.22529676	9
PCBD1 Pterin-4-alpha-carbinolamine dehydratase	IPI00218568	12902.16992	6.28	2	91.15000153	100	46.02000046	99.77276089	0.602768593	7.88E-02	3
ARG1 Isoform 2 of Arginase-1	IPI00398768	39380.19922	6.72	5	296.6099854	100	90.51999664	100	0.602516819	0.40541004	5
CPT2 Carnitine O-palmitoyltransferase 2, mitochondrial precursor	IPI00012912	79760.85938	8.38	2	125.5344391	100	90.81999969	100	0.600058824	0.0176979	2
ECH1 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor	IPI00011416	38661.62109	8.16	3	157.1300049	100	67.40000153	99.9983462	0.599050576	0.15897946	3
MMAB 19 kDa protein	IPI00789857	20551.83008	8.35	1	79.16000366	99.99988972	79.16000366	99.99988972	0.598837173	0	1
NNT NAD(P) transhydrogenase, mitochondrial precursor	IPI00337541	123493.2578	8.31	4	196.3399963	100	54.20000076	99.96544722	0.592528015	0.18616118	4
ESD 28 kDa protein	IPI00641040	31266.09961	6.29	2	101.8099976	100	53.38000107	99.95826667	0.581659385	9.54E-02	2
APOC3 13 kDa protein	IPI00657670	13861.62012	7.9	1	87.90000153	100	87.90000153	100	0.579910736	0	1
ALDH1A1 Retinal dehydrogenase 1	IPI00218914	60949.39063	6.3	12	713.7700195	100	116.6299973	100	0.578332914	0.1194347	12
KRT2 Keratin, type II cytoskeletal 2 epidermal	IPI00021304	71239.86719	8.07	4	220.1000061	100	94.55000305	100	0.572341326	0.24365179	5
IDH2 Isocitrate dehydrogenase [NADP], mitochondrial precursor	IPI00011107	56573.30859	8.88	9	502.694458	100	96.40000153	100	0.567220576	0.24940713	9
C10orf125 Isoform 2 of Protein fucU homolog	IPI00845372	15786.78027	5.2	1	62.58000183	99.99498255	62.58000183	99.99498255	0.563223822	0	1
PC Pyruvate carboxylase, mitochondrial precursor	IPI00299402	138358.0469	6.37	10	617.9589233	100	111.5699997	100	0.562111522	0.13899065	10
BLVRB Flavin reductase	IPI00783862	23637.61914	7.13	2	88.80000305	100	45.20000076	99.72553748	0.550305624	7.75E-02	2
PGRMC2 Membrane-associated progesterone receptor component 2	IPI00005202	28072.17969	5.2	2	69.91999817	99.99907427	35.86999893	97.64775131	0.550024064	0.19902442	2
CYP2E1 Cytochrome P450 2E1	IPI00007282	61500.80078	8.27	3	160.9400024	100	67.26000214	99.99829202	0.549634246	6.73E-02	3

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KRT8 Keratin, type II cytoskeletal 8	IPI00554648	58423.62891	5.52	24	1435.693359	100	100.5199966	100	0.547577073	0.15645338	29
UGT1A6;UGT1A1 UDP-glucuronosyltransferase 1-1 precursor	IPI00434346	64522.89063	8.19	4	242.1600037	100	71.58000183	99.99936834	0.544811534	0.35430489	4
ALDH1L1 Formyltetrahydrofolate dehydrogenase isoform a variant	IPI00793673	109020.6328	5.63	3	147.3144379	100	74.08999634	99.99964561	0.544043307	0.12086434	3
ACOT1 Acyl-coenzyme A thioesterase 1	IPI00333838	49306.28906	6.9	1	61.61999893	99.99374131	61.61999893	99.99374131	0.542283078	0	1
CARHSP1 Calcium-regulated heat stable protein 1	IPI00304409	17218.16992	8.41	1	110.0899963	100	110.0899963	100	0.529035039	0	1
CBR1 Carbonyl reductase [NADPH] 1	IPI00295386	33322.12891	8.55	6	352.3799744	100	92.18000031	100	0.527179228	0.14029558	7
KRT79 keratin 6L	IPI00241841	62350.57031	6.75	4	183.3800049	100	53.36999893	99.95817045	0.524329572	0.17357955	6
EHHADH 8 kDa protein	IPI00797006	7706.140137	7.98	1	123.75	100	123.75	100	0.517959632	0	1
KRT18 Keratin, type I cytoskeletal 18	IPI00784347	51196.89844	5.34	10	499.8800049	100	94.44000244	100	0.514990657	0.1401707	11
- 105 kDa protein	IPI00794900	115433.2422	7.3	8	417.8933411	100	89.48000336	100	0.514639671	0.27958476	8
CA2 Carbonic anhydrase 2	IPI00218414	32874.30859	6.87	3	201.8099976	100	84.37000275	100	0.512735983	0.17527702	3
DDAH1 NG,NG-dimethylarginine dimethylaminohydrolase 1	IPI00220342	34258.19922	5.53	2	108.3199997	100	58.36999893	99.98677233	0.510362221	2.45E-02	2
LTB4DH NADP-dependent leukotriene B4 12-hydroxydehydrogenase	IPI00292657	40639.17188	8.45	3	185.1399994	100	117.6699982	100	0.505252763	5.70E-02	3
AADAC Arylacetamide deacetylase	IPI00383879	49123.19141	8.75	1	85.05444336	100	86.23000336	100	0.499872173	0	1
GBE1 1,4-alpha-glucan-branching enzyme	IPI00296635	85817.03906	5.87	2	116.2600021	100	84.94000244	100	0.49849675	0.28628799	2
ACADSB Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	IPI00024623	52051.67969	6.53	2	138.4299927	100	98.23999786	100	0.495981717	2.66E-03	2
COL6A1 Collagen alpha-1(VI) chain precursor	IPI00291136	117302.5391	5.26	3	153.4899902	100	65.18000031	99.99724271	0.492355307	2.15E-02	3
DECR1 2,4-dienoyl-CoA reductase, mitochondrial precursor	IPI00003482	40019.14844	9.35	6	406.9900208	100	109.6900024	100	0.482946102	0.10661875	6
DBT Lipoamide acyltransferase component of branched-chain alpha-keto acid d	IPI00003944	59823.44141	8.71	2	128.5700073	100	67.80000305	99.99849172	0.47688215	0.27668581	2
AOX1 Hypothetical protein AOX1	IPI00743616	161854.2031	6.78	6	257.3444519	100	61.47000122	99.99352137	0.471897485	0.13755349	6
BAAT Bile acid CoA:amino acid N-acyltransferase	IPI00017819	48856.32031	6.49	2	116.8099976	100	76.13999939	99.99977895	0.466311126	0.20207701	2
SELENBP1 53 kDa protein	IPI00745729	57664.26953	6.03	3	126.8199921	100	50.59000015	99.92066166	0.466066698	0.13756307	4
ACY1 Aminoacylase-1	IPI00009268	48344.23047	5.77	4	189.5	100	56.45000076	99.97941821	0.461514946	0.13039517	4

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PEBP1 Phosphatidylethanolamine-binding protein 1	IPI00219446	23439.92969	7.01	8	666.8200684	100	204.1799927	100	0.455580886	8.44E-02	10
AKR1A1 Alcohol dehydrogenase	IPI00220271	39850.12891	6.32	7	365.5299988	100	75.26000214	99.9997293	0.446235402	0.20608501	7
DDT D-dopachrome decarboxylase	IPI00293867	13515.79004	6.71	4	227.5544586	100	85.11000061	100	0.443694155	0.16289988	5
SOD1 Superoxide dismutase	IPI00783680	17838.08984	5.7	5	344.0400085	100	116.3600006	100	0.443442842	2.62E-02	5
AKR7A3 Aflatoxin B1 aldehyde reductase member 3	IPI00293721	39376.69141	6.67	2	120.7200012	100	64.08000183	99.99644792	0.441910448	0.16800398	2
MT1X Metallothionein-1X	IPI00008753	8279.200195	8.38	2	112.3200073	100	69.55000305	99.99899195	0.437214488	1.86E-02	2
MSRA 22 kDa protein	IPI00794951	23445.88086	7.12	1	63.38000107	99.99582667	63.38000107	99.99582667	0.437150277	0	1
MAOB Amine oxidase [flavin-containing] B	IPI00328156	63747.53125	7.2	2	114.8800049	100	76.56999969	99.99979979	0.435525758	3.38E-02	2
H1F0 Histone H1.0	IPI00550239	29058.99023	10.84	1	83.52999878	100	83.52999878	100	0.434374598	0	1
SULT1A1 Sulfotransferase 1A1	IPI00300026	47814.69922	8.61	8	371.8500061	100	58.77999878	99.98796397	0.428086325	0.1453276	8
FMO3 Dimethylaniline monooxygenase [N-oxide-forming] 3	IPI00329033	66260.82813	7.9	2	70.88999939	99.99925957	35.97999954	97.70658222	0.423598756	0.10390954	2
ALDH1B1 Aldehyde dehydrogenase X, mitochondrial precursor	IPI00103467	62178.58984	6.36	4	218.4100037	100	85.26000214	100	0.423091895	0.16238105	4
FABP1 FABP1 protein (Fragment)	IPI00010290	18729.4707	9.52	6	401.8299866	100	115.1399994	100	0.421102419	0.12676313	8
DCXR 26 kDa protein	IPI00797249	27252.58984	8.33	6	300.9799805	100	66.70999908	99.99806142	0.415402358	0.16535472	6
KHK Isoform C of Ketohexokinase	IPI00216136	35220.62891	5.91	2	70.70999908	99.99922824	38.38999939	98.68331105	0.406444734	0.59471182	2
SLC27A5 Bile acyl-CoA synthetase	IPI00016827	78658.29688	7.81	2	95.38443756	100	63.79999924	99.99621136	0.400170634	0.21630523	2
SUCLG2 Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precurso	IPI00096066	51941.89844	6.15	3	178.3399963	100	82.91999817	100	0.39865757	9.98E-02	3
ALDH4A1 Aldehyde dehydrogenase 4 family, member A1	IPI00647328	65056.12109	7.62	11	583.0700073	100	90.26000214	100	0.398635216	0.12948829	11
GPT Alanine aminotransferase 1	IPI00217458	57510.32813	6.77	3	149.25	100	55.59000015	99.97491101	0.389697007	9.07E-02	3
CES2 carboxylesterase 2 isoform 1	IPI00332828	72247.0625	6.03	4	187.6900024	100	61.81999969	99.994023	0.384695375	0.10745092	4
ACAT1 Acetyl-CoA acetyltransferase, mitochondrial precursor	IPI00030363	49865.05859	8.98	12	863.3612061	100	137.1499939	100	0.383968946	0.15479506	12
AGXT Serine--pyruvate aminotransferase	IPI00009367	46426.73047	8.61	7	477.230011	100	109.4599991	100	0.382934742	0.11484164	7
CAT Catalase	IPI00465436	64367.17969	6.9	11	824.2300415	100	192.7100067	100	0.382488232	0.2462603	11

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MUT Methylmalonyl-CoA mutase, mitochondrial precursor	IPI00024934	90636.34375	6.48	3	233.6299896	100	92.87999725	100	0.380012262	0.1363373	3
HADH Isoform 2 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precu	IPI00298406	47125.23047	9.34	5	257.5	100	93.91999817	100	0.375892732	0.19763108	5
GLUD1 Glutamate dehydrogenase 1, mitochondrial precursor	IPI00016801	66531.63281	7.66	18	1232.970093	100	136.3500061	100	0.362815548	0.13767236	18
FAH Fumarylacetoacetase	IPI00031708	49546.46094	6.46	2	102.3799973	100	60.52999878	99.99195579	0.360432164	0.14794561	2
PGRMC1 Membrane-associated progesterone receptor component 1	IPI00220739	23621.98047	4.56	3	148.1399994	100	71.30999756	99.99932782	0.345808356	4.93E-02	3
EMILIN1 EMILIN-1 precursor	IPI00013079	109415.4531	5.1	1	85.91000366	100	85.91000366	100	0.339293112	0	1
PGM1 Phosphoglucomutase 1	IPI00844159	66935.90625	6.2	3	219.4700012	100	99.80999756	100	0.335838047	0.12900664	3
UNQ501 MBC3205	IPI00063130	22277.99023	8.91	1	76.41000366	99.99979228	76.41000366	99.99979228	0.335543292	0	1
EHHADH Peroxisomal bifunctional enzyme	IPI00216164	86466.10156	9.22	4	181.9944458	100	66.52999878	99.99797939	0.332709624	7.79E-02	4
GRHPR Glyoxylate reductase/hydroxypyruvate reductase	IPI00037448	38271.94141	7.01	9	660.7544556	100	124.4100037	100	0.332157018	0.18319711	9
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	26915.57031	5.15	2	143.4600067	100	84.76000214	100	0.332096264	2.32E-02	2
ACADM Hypothetical protein DKFZp686M24262	IPI00513827	55018.78906	7.94	4	224.1999969	100	80.98000336	99.99992748	0.331354423	0.11825541	4
ABHD14B 22 kDa protein	IPI00747859	23098.53906	5.43	2	132.9299927	100	95.76000214	100	0.33040402	1.44E-02	2
ALDH9A1 aldehyde dehydrogenase 9A1	IPI00479877	61023.67188	6.23	1	94.34999847	100	94.34999847	100	0.329797256	0	1
PYGL 97 kDa protein	IPI00783313	107098.9297	6.71	6	311.1499939	100	92.09999847	100	0.326806301	8.33E-02	6
DPYS Dihydropyrimidinase	IPI00028910	62048.10938	6.81	5	259.3899841	100	66.80000305	99.99810118	0.32675151	0.13511939	5
TST Thiosulfate sulfurtransferase	IPI00216293	35752.05859	6.77	8	607.8144531	100	112.8000031	100	0.326622253	0.15826975	8
PCK2 mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor	IPI00797038	74784.85938	7.57	14	810.9899902	100	106.5	100	0.324551656	0.23101197	15
HRSP12 Ribonuclease UK114	IPI00005038	15826.7998	8.74	3	173.8899994	100	66.15000153	99.99779462	0.315552751	1.99E-02	3
PBLD Phenazine biosynthesis-like domain-containing protein	IPI00024896	34011.42969	6.06	2	97.97444153	100	66.58000183	99.99800252	0.314278123	0.32667903	2
HMGCS2 Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor	IPI00008934	61333.76953	8.4	10	557.3499756	100	85.23999786	100	0.310037574	0.19317026	10
CYP3A4 Cytochrome P450 3A4	IPI00465138	63244.41016	8.27	2	113.3099976	100	81.01999664	99.99992814	0.309043153	0.40584699	2
IL11RA 13 kDa protein	IPI00167641	14096.79004	7.79	1	71.41000366	99.99934312	71.41000366	99.99934312	0.308006069	0	1

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ACSL1 Isoform 1 of Long-chain-fatty-acid--CoA ligase 1	IPI00012728	85201.29688	6.81	9	591.6699829	100	121.4400024	100	0.306841859	0.12173862	9
HAGH Hydroxyacylglutathione hydrolase	IPI00745553	32141.91016	6.86	1	99.62999725	100	99.62999725	100	0.299084827	0	1
SCP2 sterol carrier protein 2 isoform 2	IPI00433347	61608.94141	6.25	6	310.5844421	100	81.47000122	99.99993521	0.294671263	0.10145713	6
SORD Sorbitol dehydrogenase	IPI00216057	42378.10938	8.23	4	222.5700073	100	103.6699982	100	0.294242325	7.91E-02	4
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	35335.42969	8.34	11	716.5599365	100	112.2799988	100	0.290538942	0.14422899	11
ALDH2 Mitochondrial aldehyde dehydrogenase 2 variant (Fragment)	IPI00792207	61065.96094	6.63	13	856.2000122	100	106.4499969	100	0.281163211	0.17237171	14
UGP2 Isoform 1 of UTP--glucose-1-phosphate uridylyltransferase	IPI00329331	63091.28906	8.16	11	732.9788818	100	138	100	0.264200699	0.14168397	11
ACSM2A LOC123876 protein	IPI00644771	70304.24219	8.34	4	186.1400146	100	59.06999969	99.98874143	0.260675229	0.13408905	4
FTCD Isoform A of Formimidoyltransferase-cyclodeaminase	IPI00001441	62321.57813	5.58	7	389.1799927	100	74.90000153	99.99970591	0.25786259	0.16292638	7
SULT2A1 Bile salt sulfotransferase	IPI00216133	37496.32813	5.71	7	352.8500061	100	83.44000244	100	0.256433902	0.11572872	7
FTL Ferritin light chain	IPI00852596	21925.33984	5.51	3	199.7999878	100	75.77999878	99.99975985	0.246255634	5.16E-02	3
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	43936.05859	8.75	7	420.2844543	100	104.0899963	100	0.244630453	0.12134267	7
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	61418.91016	8.17	5	293.1699829	100	83.61000061	100	0.243131937	7.60E-02	5
BDH1 D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	IPI00025341	41766.75	9.11	3	143.5244446	100	56.22999954	99.97834874	0.228818222	0.26459057	3
CYB5A Isoform 1 of Cytochrome b5	IPI00397860	16616.71094	4.88	6	524.5899658	100	227.2200012	100	0.227018513	4.56E-02	6
ACAA1 3-ketoacyl-CoA thiolase, peroxisomal precursor	IPI00012828	47604.07031	8.76	4	349.6000061	100	110.1999969	100	0.225431545	9.10E-02	4
ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	IPI00001539	46153.96875	8.32	11	707.7799683	100	138.3200073	100	0.220514994	0.14814864	11
ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria	IPI00024990	63211.07813	8.72	8	555.3644409	100	94.58999634	100	0.215647272	0.17281552	8
ACSM2B Acyl-CoA synthetase medium-chain family member 2	IPI00329444	70450.35938	8.5	4	169.4700012	100	55.27000046	99.97299258	0.205965148	9.91E-02	4
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1406	5.6	1	95.41999817	100	95.41999817	100	0.205684898	0	1
CYP2C8 45 kDa protein	IPI00843846	49430.42188	8.91	4	229.0500031	100	64.80999756	99.9969975	0.204592735	0.10040232	4
CYP2C9 Cytochrome P450 2C9	IPI00007219	61374.14063	8.13	3	186.4799957	100	79.30999756	99.99989347	0.194452276	6.02E-02	3
CYP3A5 Cytochrome P450 3A5	IPI00025831	63206.64063	8.86	2	116.9899979	100	81.08999634	99.99992929	0.193498805	0.08675896	2

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FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	41289.14844	6.54	9	692.1900024	100	123.7600021	100	0.190802158	0.22849112	9
BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101	49946.23828	6.58	14	768.6488647	100	125.2300034	100	0.180062713	0.10995276	16
ADH4 Alcohol dehydrogenase 4	IPI00218899	45828.03125	8.25	9	690.5800171	100	116.8899994	100	0.178223351	0.13288805	9
UGT2B7 similar to UDP-glucuronosyltransferase 2B7 precursor	IPI00787584	65314.41016	8.41	4	214.0400085	100	74.30999756	99.99966311	0.177838805	8.30E-02	4
LOC554235 29 kDa protein	IPI00419903	29217.00977	6.5	1	109.6800003	100	109.6800003	100	0.176564177	0	1
CYP2C19 Cytochrome P-450 II C (Fragment)	IPI00657852	44746.01953	6.82	2	118.1800003	100	61.59000015	99.99369793	0.176431233	4.66E-02	2
EPHX1 Epoxide hydrolase 1	IPI00009896	57419.37891	6.77	6	468	100	112.0899963	100	0.176255207	0.14702675	7
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	48966.78125	6.61	16	1090.650024	100	136.7899933	100	0.175484401	0.17455749	18
GGTLA1 Isoform 2 of Gamma-glutamyltransferase 5 precursor	IPI00339373	61051.73828	7.67	1	74.33999634	99.99966543	74.33999634	99.99966543	0.16565382	0	1
CYP1A2 Isoform 1 of Cytochrome P450 1A2	IPI00719591	62467.67188	9.18	1	76.54000092	99.9997984	76.54000092	99.9997984	0.158577674	0	1
DAK Dihydroxyacetone kinase	IPI00551024	63392.42188	7.12	5	521.5	100	156.3899994	100	0.150961653	9.81E-02	6
GLYAT Isoform 1 of Glycine N-acyltransferase	IPI00402759	37221.21094	8.38	3	135.8099976	100	57.43000031	99.98357584	0.150897903	0.33367253	3
ADH1A Alcohol dehydrogenase 1A	IPI00218896	45320.80859	8.26	11	859.1099854	100	121.3399963	100	0.13377832	0.1133497	12
UGT2B17 UDP-glucuronosyltransferase 2B17 precursor	IPI00026932	67707.59375	8.76	1	66.90000153	99.99814441	66.90000153	99.99814441	0.129522258	0	1
CPS1 Isoform 1 of Carbamoyl-phosphate synthase [ammonia], mitochondrial pre	IPI00011062	180875.9531	6.3	60	4328.580078	100	149.0200043	100	0.12154383	0.14185499	70
CYP2A6 Cytochrome P450 2A6	IPI00299568	61083.51172	9.24	3	171.6900024	100	90.04000092	100	0.112595776	7.90E-02	3
ADH1B Alcohol dehydrogenase 1B	IPI00473031	45270.91016	8.63	11	826.0499268	100	121.3399963	100	0.109795835	5.04E-02	12
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	43462.35156	8	12	865.0800171	100	112.6500015	100	0.109708808	0.10960813	16
GSTA2 Glutathione S-transferase A2	IPI00745233	29104	8.51	8	439.5299683	100	84.43000031	100	0.105112377	0.13296491	9
ADH1C Alcohol dehydrogenase 1C	IPI00465343	45428	8.63	7	533.5999756	100	121.3399963	100	9.83E-02	4.07E-02	8
RDH16 Retinol dehydrogenase 16	IPI00289551	38852.73828	8.83	4	219.2744446	100	69.81999969	99.99905271	9.14E-02	6.35E-02	4
CES1 carboxylesterase 1 isoform c precursor	IPI00607693	68199.60938	6.15	20	1418.180054	100	199.9900055	100	8.93E-02	0.10970959	21

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Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Total Ion Score	Total Ion Score C.I. %	Best Ion Score	Best Ion Score C.I. %	Avg iTRAQ ratio * (117/116)	iTRAQ Standard Deviation * (117/116)	iTRAQ Peptides (117/116)
NAP1L1 43 kDa protein	IPI00789029	47959.44141	4.45	1	81.54000092	99.99993625	81.54000092	99.99993625	5.354643197	0	1
S100P Protein S100-P	IPI00017526	12023.44043	4.75	1	101.6399994	100	101.6399994	100	5.317678828	0	1
DEFA3 Neutrophil defensin 3 precursor	IPI00021827	10946.21973	5.71	2	79.36999512	99.99989493	42.93000031	99.53710435	4.761464395	0.359685876	2
AKR1B10 Aldo-keto reductase family 1 member B10	IPI00105407	41078.28125	7.12	1	88.87000275	100	88.87000275	100	4.072898589	0	1
SCAMP3 Isoform 2 of Secretory carrier-associated membrane protein 3	IPI00306383	37073.82813	7.53	1	74.31999969	99.99966389	74.31999969	99.99966389	3.61504749	0	1
FKBP11 Peptidyl-prolyl cis-trans isomerase	IPI00789642	11840.12988	4.57	1	75.73999786	99.99975763	75.73999786	99.99975763	3.544819338	0	1
RAN 26 kDa protein	IPI00792352	29358.91016	8.51	3	148.1800079	100	65.41000366	99.99738493	3.003883752	1.305086144	3
S100A9 Protein S100-A9	IPI00027462	15007.73047	5.71	6	494.4100037	100	132.7700043	100	2.998110678	0.532129617	7
HNRPA1 Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	IPI00465365	37003.55078	9.27	6	422.5299683	100	136.6399994	100	2.986286635	1.354563121	6
EEA1 Early endosome antigen 1	IPI00329536	188351.2031	5.53	1	85.29000092	100	85.29000092	100	2.966948037	0	1
CKAP4 CKAP4 protein (Fragment)	IPI00433214	72955.86719	9.34	7	489.9144287	100	113.2300034	100	2.901862073	0.896562266	7
ANXA5 Annexin A5	IPI00329801	39272.76172	4.94	11	673.6500244	100	106.3700027	100	2.824878454	0.84201029	12
ARHGDIA 9 kDa protein	IPI00791180	10974.86035	6.73	1	67.66999817	99.99844588	67.66999817	99.99844588	2.771813654	0	1
RBM8A Isoform 2 of RNA-binding protein 8A	IPI00216659	21665.92969	5.64	1	110.5999985	100	110.5999985	100	2.642653515	0	1
SFPQ Isoform Long of Splicing factor, proline-and glutamine-rich	IPI00010740	81090.10938	9.45	3	132.9244385	100	59.66999817	99.99019419	2.592366193	0.689945158	3
SEC22B Vesicle-trafficking protein SEC22b	IPI00006865	27022.99023	8.67	1	80.02999878	99.99990974	80.02999878	99.99990974	2.520517846	0	1
MPO Isoform H14 of Myeloperoxidase precursor	IPI00236554	77088.74219	9.3	5	226.0499878	100	60.97000122	99.99273086	2.510180608	0.326251497	5
S100A8 Protein S100-A8	IPI00007047	12745.88965	6.51	7	387.7444458	100	89.33999634	100	2.475471766	0.325446586	7
PARP1 Poly [ADP-ribose] polymerase 1	IPI00449049	131945.8906	8.99	2	112.7200012	100	61.18999863	99.99308992	2.46580716	0.182159232	2
TAGLN2 24 kDa protein	IPI00647915	26448.48047	8.41	5	371.7800293	100	109.5999985	100	2.4064876	0.873876626	5
HNRPU heterogeneous nuclear ribonucleoprotein U isoform a	IPI00644079	101350.8203	5.76	2	139.6900024	100	95.94999695	100	2.40615783	0.378173495	2
RBP4 Retinol binding protein 4, plasma	IPI00480192	24933.30078	5.77	1	74.86000061	99.99970319	74.86000061	99.99970319	2.284951446	0	1

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HNRPR HNRPR protein	IPI00644055	77880.99219	8.23	1	69.23000336	99.99891487	69.23000336	99.99891487	2.279460467	0	1
LTF 73 kDa protein	IPI00789477	80974.52344	8.2	5	280.190033	100	96.54000092	100	2.25547026	0.954917033	5
HNRPA3 Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	IPI00419373	42922.89844	9.1	4	315.1900024	100	130.0800018	100	2.242980749	0.877849304	4
XRCC6 70 kDa protein	IPI00465430	78696.84375	6.23	1	75.5	99.99974386	75.5	99.99974386	2.205478373	0	1
NME1;NME2 Nucleoside diphosphate kinase	IPI00604590	36163.17969	8.7	6	297.3177795	100	84.93000031	100	2.189905327	0.118405016	7
LRPPRC Leucine-rich PPR motif-containing protein	IPI00783271	173604.2344	5.81	3	131.5700073	100	52.22000122	99.94548914	2.187649552	0.290160215	3
NUMA1 Isoform 1 of Nuclear mitotic apparatus protein 1	IPI00292771	260878.9688	5.63	1	62.68999863	99.99510804	62.68999863	99.99510804	2.182246513	0	1
DAZAP1 Isoform 2 of DAZ-associated protein 1	IPI00335930	43470.07813	8.48	1	64.5	99.99677535	64.5	99.99677535	2.158285207	0	1
CYCS Cytochrome c	IPI00465315	14569.42969	9.59	3	129.1799927	100	50.18999863	99.91300721	2.123067506	0.26490132	3
- CD68 antigen variant (Fragment)	IPI00555602	45637.91016	5.46	7	506.2999573	100	110.8199997	100	2.120582746	0.61767021	7
HNRPM Isoform 2 of Heterogeneous nuclear ribonucleoprotein M	IPI00383296	79706.89844	8.94	3	202.4100037	100	80.76000214	99.99992371	2.119396315	0.3389737	3
TES Isoform 2 of Testin	IPI00216425	54398.51953	7.82	1	62.75	99.99517516	62.75	99.99517516	2.115683377	0	1
CLTC Isoform 2 of Clathrin heavy chain 1	IPI00455383	203165.7031	5.48	7	374.2944336	100	72.31999969	99.9994673	2.106781071	0.573316338	7
TUBA1B Similar to Tubulin alpha-ubiquitous chain	IPI00792677	49578.05859	4.96	11	909.7099609	100	189.2799988	100	2.092644192	0.829464211	11
HNRPD Isoform 1 of Heterogeneous nuclear ribonucleoprotein D0	IPI00028888	43300.76953	7.62	1	61.63000107	99.99375571	61.63000107	99.99375571	2.091512352	0	1
EIF4A2 Isoform 2 of Eukaryotic initiation factor 4A-II	IPI00409717	49956.14063	5.33	5	368.4299927	100	110.8199997	100	2.079646316	0.510422696	5
hCG_1983058 hypothetical protein LOC644820	IPI00414723	28320.82031	4.59	2	72.51000214	99.9994901	41.93000031	99.4172489	2.076934051	1.55E-02	2
EIF4G3 Isoform 1 of Eukaryotic translation initiation factor 4 gamma 3	IPI00646377	194311.3594	5.27	2	77.37999725	99.99983386	42.93999863	99.5381688	2.072207842	0.875534986	2
EIF4G1 eukaryotic translation initiation factor 4 gamma, 1 isoform 2	IPI00384463	180908.9531	5.15	2	77.37999725	99.99983386	42.93999863	99.5381688	2.072207842	0.875534986	2
COPB1 Coatomer subunit beta	IPI00295851	118074.4609	5.72	2	144.9900055	100	111.3700027	100	2.054938643	0.548451994	2
DDAH1 NG,NG-dimethylarginine dimethylaminohydrolase 1	IPI00220342	34258.19922	5.53	2	108.3199997	100	58.36999893	99.98677233	2.036326279	0.469373286	2
SARS Seryl-tRNA synthetase	IPI00514587	68889.0625	6.64	2	76.16000366	99.99977997	43.29000092	99.57392796	2.035821991	2.80E-03	2
TUBA1C Tubulin alpha-1C chain	IPI00218343	53295.64844	4.96	11	902.5899658	100	189.2799988	100	2.030883346	0.770038495	11

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DHX9 ATP-dependent RNA helicase A	IPI00844578	151431.7344	6.41	2	125.0699997	100	84.93000031	100	2.022986036	1.30E-02	2
LDHA Isoform 1 of L-lactate dehydrogenase A chain	IPI00217966	41071.75	8.44	11	548.0044556	100	90.72000122	100	1.99727102	0.602474115	13
HNRPA2B1 Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	IPI00414696	38478.16016	8.67	9	617.2045288	100	98.65000153	100	1.994613346	0.633092389	9
ILF3 Isoform 1 of Interleukin enhancer-binding factor 3	IPI00298788	105105.8906	8.86	1	60.95999908	99.9927141	60.95999908	99.9927141	1.993276852	0	1
HSPA5 HSPA5 protein	IPI00003362	81398.29688	5.07	25	1999.231445	100	163.1699982	100	1.966795338	0.62805506	26
PSAT1 Isoform 2 of Phosphoserine aminotransferase	IPI00219478	38754.37109	6.23	2	113.6800003	100	70.63999939	99.9992157	1.960626787	6.97E-02	2
EPRS glutamyl-prolyl tRNA synthetase	IPI00013452	193228.6875	7.02	1	84.54000092	100	84.54000092	100	1.959573623	0	1
ITGB1 integrin beta 1 isoform 1A precursor	IPI00645194	99377.10938	5.27	2	127.6600037	100	72.98000336	99.9995424	1.958134986	9.89E-02	2
P4HB Protein disulfide-isomerase precursor	IPI00010796	64315.26953	4.76	25	1679.800049	100	108.0100021	100	1.946705062	0.319952397	29
SFRS6 Isoform SRP55-1 of Splicing factor, arginine/serine-rich 6	IPI00012345	43543.78906	11.42	1	62.56999969	99.99497098	62.56999969	99.99497098	1.943484679	0	1
ENO2 6 kDa protein	IPI00790892	6040.029785	4.89	2	132.8199921	100	69.55999756	99.99899427	1.935503011	5.15E-02	2
PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	IPI00419585	20345.10938	7.68	8	570.9000244	100	112.1900024	100	1.925110441	0.367401906	10
- Tubulin alpha-4 chain	IPI00017454	29152.96094	8.65	2	131.2900085	100	81.88999939	99.99994119	1.916505669	1.443911136	2
ENO1 Isoform alpha-enolase of Alpha-enolase	IPI00465248	53031.82031	7.01	13	858.4200439	100	103.6800003	100	1.9000646	0.473431618	13
SRP14 8 kDa protein	IPI00789296	8752.330078	10.03	1	72.80999756	99.99952414	72.80999756	99.99952414	1.899110243	0	1
CS citrate synthase precursor, isoform b	IPI00383539	50469.26172	6.74	3	103.6500015	100	41.40000153	99.34161038	1.893221318	0.124340257	3
LSM8 U6 snRNA-associated Sm-like protein LSm8	IPI00219871	10684.41016	4.34	1	110.9000015	100	110.9000015	100	1.890253636	0	1
LOC388720 similar to ubiquitin and ribosomal protein S27a precursor	IPI00397808	21877.69922	9.53	5	241.3300018	100	71.72000122	99.99938838	1.87694711	0.213333592	5
TUBB Tubulin beta chain	IPI00011654	52311.16016	4.78	11	868.8900146	100	137.6199951	100	1.87335447	0.571129605	12
C20orf77 Uncharacterized protein C20orf77	IPI00009659	41289.62109	5.73	1	105	100	105	100	1.855604572	0	1
HSP90AB4P Heat shock protein 90Bd	IPI00555565	66222.17969	4.65	4	185.1100006	100	65.5	99.99743857	1.854476561	0.294067525	4
HSP90AB1 Heat shock protein HSP 90-beta	IPI00414676	94433.0625	4.97	16	937.8744507	100	123.5299988	100	1.839153005	1.318642652	16
CSTB Cystatin-B	IPI00021828	12618.79004	6.96	3	174.1700134	100	80.15000153	99.9999122	1.837122264	7.02E-02	3

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LOC388474 similar to 60S ribosomal protein L7a isoform 1	IPI00397676	35921.55078	10.56	2	110.7600021	100	65.65000153	99.99752553	1.817207124	0.212218164	2
TUBB2A Tubulin beta-2A chain	IPI00013475	52501.16016	4.78	10	789.3699951	100	137.6199951	100	1.814744718	0.524667615	10
RPS5 40S ribosomal protein S5	IPI00008433	25448.32031	9.73	1	131.6699982	100	131.6699982	100	1.813192824	0	1
RAD23B UV excision repair protein RAD23 homolog B	IPI00008223	46214.96094	4.79	2	83.91999817	100	43.49000168	99.59310443	1.808907296	1.21E-02	2
LONP1 Lon protease homolog	IPI00334291	109879.3125	6.11	1	60.88000107	99.99257865	60.88000107	99.99257865	1.786388827	0	1
MARCKS Myristoylated alanine-rich C-kinase substrate	IPI00219301	35850.28125	4.47	1	55.40000153	99.97378904	55.40000153	99.97378904	1.780808675	0.100002788	2
C20orf3 47 kDa protein	IPI00479431	49085.10938	5.82	3	150.3199921	100	73.56999969	99.99960053	1.777626703	0.446750574	3
SND1 Staphylococcal nuclease domain-containing protein 1	IPI00140420	110982.1797	6.74	2	177.9400024	100	99.43000031	100	1.71628826	2.76E-02	2
APOE Apolipoprotein E precursor	IPI00021842	38239.98828	5.65	6	311.9599915	100	94.48999786	100	1.711130757	0.434253868	6
PDIA4 Protein	IPI00852792	21271.91992	8.33	7	387.1300049	100	96.79000092	100	1.709198577	0.377748314	8
HYOU1 Hypoxia up-regulated protein 1 precursor	IPI00000877	122683.2188	5.16	5	346.3800049	100	110.9400024	100	1.708469378	0.815761529	6
HNRPH1 HNRPH1 protein	IPI00479191	53875.41016	6.33	4	242.1444397	100	98.52999878	100	1.695461744	0.630332634	5
- Elongation factor 1-alpha	IPI00472724	57485.78125	9.15	11	619.9900513	100	98.19999695	100	1.688901052	0.84945531	11
LYZ Lysozyme C precursor	IPI00019038	17902.35938	9.38	1	100.2799988	100	100.2799988	100	1.669624579	0	1
RAB10 Ras-related protein Rab-10	IPI00016513	25878.90039	8.59	2	116.5700073	100	66.44000244	99.99793708	1.659837945	0.126950874	2
PFKL Liver phosphofructokinase isoform a variant (Fragment)	IPI00742657	47091.33984	9.06	1	60.79000092	99.99242325	60.79000092	99.99242325	1.659551898	0	1
HIST1H1B Histone H1.5	IPI00217468	32071.38086	10.91	1	82.69000244	100	82.69000244	100	1.64856673	0	1
RPS9 40S ribosomal protein S9	IPI00221088	25503.88086	10.66	3	100.0800018	100	34.77000046	96.96971774	1.643004363	0.183503678	3
GPI Glucose-6-phosphate isomerase	IPI00027497	68475.72656	8.43	5	259.0899963	100	81.62999725	99.99993756	1.641240897	0.153891773	5
FASN Fatty acid synthase	IPI00847250	287598.7813	5.99	14	714.7844238	100	77.76999664	99.99984813	1.63888755	0.304767695	14
TUBB2C Tubulin beta-2C chain	IPI00007752	52471.19141	4.79	11	856.9400024	100	137.6199951	100	1.632882526	0.651222757	12
CCT6A T-complex protein 1 subunit zeta	IPI00027626	64980.16016	6.23	3	191.0099945	100	72.08999634	99.99943833	1.628877859	0.255626833	3
GC Vitamin D-binding protein precursor	IPI00555812	60697.32813	5.4	4	176.934433	100	54.16999817	99.96520769	1.627865453	0.308354931	4

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RPS15A 40S ribosomal protein S15a	IPI00221091	16650.17969	10.14	4	149.6844482	100	42.88999939	99.53282113	1.61580032	0.272314813	4
RPL3 60S ribosomal protein L3	IPI00550021	54518.5	10.19	2	99.88444519	100	50.97999954	99.92747576	1.612407395	0.191695111	2
CAP1 Adenylyl cyclase-associated protein	IPI00639931	58646.21094	8.24	3	171.0299988	100	64.97000122	99.9971061	1.598967726	0.239726056	3
CALR 37 kDa protein	IPI00793605	41138.14063	4.55	7	513.4699707	100	99.38999939	100	1.597592202	0.137498178	8
TUBB3 Tubulin beta-3 chain	IPI00013683	53216.46094	4.83	6	471.5099792	100	137.6199951	100	1.596939579	0.225825373	6
NCL Isoform 1 of Nucleolin	IPI00604620	89719.57031	4.6	7	396.3299866	100	98.73000336	100	1.59185754	0.424921781	7
HNRPK Isoform 2 of Heterogeneous nuclear ribonucleoprotein K	IPI00216746	54394.67969	5.19	5	290.8244324	100	93.43000031	100	1.588317145	0.162778656	5
TXNDC5;MUTED thioredoxin domain containing 5 isoform 2	IPI00395646	48461.78125	5.77	6	240.6944427	100	57.52999878	99.9839497	1.583554625	0.323926433	7
PFN1 Profilin-1	IPI00216691	16766.75	8.44	4	269.7099915	100	117.1699982	100	1.580040166	0.26219137	5
PSMC2 26S protease regulatory subunit 7	IPI00021435	53677.53125	5.71	2	97.81999969	100	51.79000092	99.93981572	1.570870957	0.231666377	2
STAT3 Isoform Del-701 of Signal transducer and activator of transcription 3	IPI00306436	95480.85938	5.94	1	64.27999878	99.99660779	64.27999878	99.99660779	1.569566327	0	1
CTSD Protein	IPI00853455	44335.46875	5.38	9	580.4544678	100	108.7099991	100	1.569380693	0.200497204	9
YWHAQ 14-3-3 protein theta	IPI00018146	30857.03906	4.68	5	286.6499939	100	84.48000336	100	1.561350857	0.608100336	5
PRKCSH Glucosidase 2 beta subunit precursor	IPI00792916	64937.07813	4.34	9	435.9844055	100	72.43000031	99.99948062	1.560139601	0.320582418	10
EIF3S7 Eukaryotic translation initiation factor 3 subunit 7	IPI00006181	70198.88281	5.79	1	62.22999954	99.99456145	62.22999954	99.99456145	1.555932008	0	1
GANAB Isoform 3 of Neutral alpha-glucosidase AB precursor	IPI00441414	99842.15625	5.43	3	265.9700012	100	108.1100006	100	1.550318632	0.522184336	4
SEC31A Isoform 4 of Protein transport protein Sec31A	IPI00515103	138953.7344	7.03	3	202.0288849	100	108.2099991	100	1.545340341	0.252672722	3
GDI2 GDP dissociation inhibitor 2	IPI00640006	50710.62109	5.91	3	175.6344452	100	97.18000031	100	1.5424086	0.235571788	3
HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein	IPI00003865	78958.95313	5.37	19	1172.518921	100	118.0299988	100	1.541065312	0.21576387	20
SURF4 Surfeit 4	IPI00399142	22555.05078	8.88	1	84.88999939	100	84.88999939	100	1.540865597	0	1
GAPDH 32 kDa protein	IPI00795257	35122.30859	7.15	9	681.6244507	100	125.5100021	100	1.53930271	0.595740077	11
SET Isoform 2 of Protein SET	IPI00301311	35108.05859	4.12	2	114.6800003	100	73.90000153	99.99962976	1.524080431	4.14E-02	2
PGD 53 kDa protein	IPI00747533	59047.51953	7.12	2	91.66000366	100	56.13999939	99.97789537	1.52325366	9.13E-02	2

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YWHAB Isoform Short of 14-3-3 protein beta/alpha	IPI00759832	30949.07031	4.76	5	287.6699829	100	85.5	100	1.510829485	0.537411494	5
- 140 kDa protein	IPI00829641	149651.875	7.92	3	160.5400085	100	83.95999908	100	1.510815775	0.14537548	3
RPLP0 60S acidic ribosomal protein P0	IPI00556485	30148.58984	8.36	3	186.7600098	100	102.8300018	100	1.509692828	0.124209406	3
LOC440055 similar to ribosomal protein S12	IPI00456898	17312.76953	6.43	3	182.2700043	100	68.05000305	99.99857609	1.509452355	0.18685234	3
RPS3 40S ribosomal protein S3	IPI00011253	29833.74023	9.68	2	107.6399994	100	63.56999969	99.99600531	1.507156687	0.174513325	2
ORM1 Alpha-1-acid glycoprotein 1 precursor	IPI00022429	25840.99023	4.93	3	165.4900055	100	74.91000366	99.99970658	1.501298763	0.264231189	3
FN1 fibronectin 1 isoform 2 preproprotein	IPI00845263	280315.25	5.36	12	578.178833	100	63.74000168	99.99615866	1.499239492	0.383193625	12
CALR Protein	IPI00794237	19298.58008	4.47	2	151.3444366	100	97.84999847	100	1.498239066	5.39E-02	3
EEF1G 50 kDa protein	IPI00747497	55012.55859	6.27	7	327.4299927	100	93.30000305	100	1.495115515	0.547996924	7
BID Isoform 2 of BH3-interacting domain death agonist	IPI00420084	27815.5	6.6	1	63.70000076	99.99612311	63.70000076	99.99612311	1.492463399	0	1
SERPINA1 Alpha-1-antitrypsin precursor	IPI00553177	51885.51172	5.37	8	536.2144775	100	93.48000336	100	1.492236018	0.207381492	9
HSP90B1 Endoplasmin precursor	IPI00027230	104018.3516	4.76	23	1253.778809	100	113.8899994	100	1.492211687	0.430570974	24
HDGF Hepatoma-derived growth factor	IPI00020956	30896.2793	4.7	2	76.26443481	99.9997852	41.29999924	99.32627416	1.489978144	0.235668789	2
PDIA6 Isoform 1 of Protein disulfide-isomerase A6 precursor	IPI00644989	52733.64063	4.95	6	340.7799683	100	97.93000031	100	1.487506845	0.22211049	6
MIF 12 kDa protein	IPI00790382	12661.19043	9.3	2	86.61999512	100	43.47999954	99.59216624	1.483382004	0.238005632	2
PRKDC Isoform 2 of DNA-dependent protein kinase catalytic subunit	IPI00376215	508806.4375	6.81	1	89.05999756	100	89.05999756	100	1.479186639	0	1
CFL1 24 kDa protein	IPI00784459	28091.64063	8.13	3	175.7799988	100	79.68000031	99.99990217	1.47892307	0.269690981	4
EIF5 Eukaryotic translation initiation factor 5	IPI00022648	56760.42188	5.41	1	75.93000031	99.999768	75.93000031	99.999768	1.475069702	0	1
KPNB1 Importin subunit beta-1	IPI00001639	104502.3672	4.68	2	109.4100037	100	73.15000153	99.99955997	1.474064583	0.180898279	2
HSP90AA1 Isoform 1 of Heat shock protein HSP 90-alpha	IPI00784295	96593.6875	4.94	17	962.3700562	100	115.0800018	100	1.469523391	0.734101106	17
FDPS Farnesyl diphosphate synthase	IPI00101405	51970.89063	5.83	4	248.4599915	100	95.16000366	100	1.46149936	7.53E-02	4
- Farnesyl pyrophosphate synthetase like-4 protein (Fragment)	IPI00382869	42840.89844	4.87	4	193.3499908	100	64.5	99.99677535	1.46149936	7.53E-02	4
FAM10A5 Protein FAM10A5	IPI00168839	46431.76172	4.96	2	129.6300049	100	75.08000183	99.99971785	1.461395612	6.15E-02	2

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- RET tyrosine kinase/cAMP protein kinase A subunit RI (Fragment)	IPI00783751	72900.52344	5.87	2	90.06999969	100	56.72000122	99.98065882	1.459964263	0.256432855	2
ATIC Bifunctional purine biosynthesis protein PURH	IPI00289499	70461.78906	6.27	1	68.58999634	99.99874257	68.58999634	99.99874257	1.438550707	0	1
LRP1 Low-density lipoprotein receptor-related protein 1 precursor	IPI00020557	544525	5.16	1	71.43000031	99.99934614	71.43000031	99.99934614	1.438001461	0	1
- CALRETICULIN=CALCIUM binding protein (Fragment)	IPI00383751	26354.40039	4.45	5	336.7299805	100	99.38999939	100	1.43744184	0.19821875	7
PDIA4 Protein disulfide-isomerase A4 precursor	IPI00009904	82667.8125	4.96	13	713.0912476	100	96.79000092	100	1.436581845	0.643184275	15
VDAC2 Isoform 2 of Voltage-dependent anion-selective channel protein 2	IPI00216024	39125.44922	5.87	2	84.83999634	100	51.18000031	99.9307399	1.432002983	0.612792332	2
M6PRBP1 Isoform B of Mannose-6-phosphate receptor-binding protein 1	IPI00303882	50756.28125	5.3	2	118.1600037	100	75.11000061	99.99971979	1.425627801	0.213560741	2
CAPZB Capping protein (Actin filament) muscle Z-line, beta	IPI00642256	32963.14844	6.45	1	66.66999817	99.99804348	66.66999817	99.99804348	1.423427359	0	1
TMED9 transmembrane emp24 protein transport domain containing 9	IPI00023542	29224.41992	7.82	3	109.7099915	100	41.50999832	99.35807647	1.422583049	4.87E-03	3
CCT8 T-complex protein 1 subunit theta	IPI00784090	66090.99219	5.42	3	201.7700043	100	77.19000244	99.99982643	1.422271188	0.225009563	3
RPLP2 60S acidic ribosomal protein P2	IPI00008529	13242.07031	4.42	1	112.5800018	100	112.5800018	100	1.422132858	0	1
EEF2 Elongation factor 2	IPI00186290	105563.6484	6.41	9	569.8599854	100	92.70999908	100	1.4102872	0.26325213	9
DBI Isoform 2 of Acyl-CoA-binding protein	IPI00218836	13802.13965	5.41	4	343.3599854	100	130.8300018	100	1.405868777	0.160507474	4
RPN1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa	IPI00025874	78729.54688	5.87	8	400.3912354	100	73.27999878	99.99957295	1.405252219	0.385162086	8
FLNA Filamin-A	IPI00333541	305957.375	5.7	4	183.8144531	100	78.55000305	99.99987309	0.699398995	0.158874634	4
DDT D-dopachrome decarboxylase	IPI00293867	13515.79004	6.71	4	227.5544586	100	85.11000061	100	0.696049978	0.115019818	5
ASL 50 kDa protein	IPI00514772	52806.57031	5.99	4	213.9500122	100	100.5699997	100	0.69178872	0.473434891	4
MCCC2 Isoform 2 of Methylcrotonoyl-CoA carboxylase beta chain, mitochondria	IPI00789428	61882.76172	7.59	2	93.05999756	100	57.93000031	99.98536195	0.689434694	0.392611367	2
TXNL5 11 kDa protein	IPI00789285	12574.73047	5.18	1	93.70999908	100	93.70999908	100	0.685448616	0	1
AIFM1 Isoform 3 of Apoptosis-inducing factor 1, mitochondrial precursor	IPI00157908	72532.10938	9.03	3	201.6999969	100	84.58000183	100	0.684649078	0.174312807	3
ALDH4A1 Aldehyde dehydrogenase 4 family, member A1	IPI00647328	65056.12109	7.62	11	583.0700073	100	90.26000214	100	0.680127339	9.97E-02	11
HP Haptoglobin precursor	IPI00641737	52573.75	6.28	9	624.9700317	100	123.5400009	100	0.67203124	0.178701202	9
AKR1A1 Alcohol dehydrogenase	IPI00220271	39850.12891	6.32	7	365.5299988	100	75.26000214	99.9997293	0.671375591	0.240575306	7

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SORBS2 sorbin and SH3 domain containing 2 isoform 2	IPI00477577	135030.8438	8.56	2	95.86999512	100	49.09000015	99.88793161	0.64739897	0.102807777	2
PAH Phenylalanine-4-hydroxylase	IPI00017579	56707.82031	6.15	3	108.75	100	42.02999878	99.43051374	0.642642069	2.24E-02	3
ARHGDIB 13 kDa protein	IPI00791712	14875.75977	4.69	1	115.5199966	100	115.5199966	100	0.642058364	0	1
VIM Vimentin	IPI00418471	56977.44141	5.06	19	1256.898926	100	125.4199982	100	0.641902248	0.206891731	20
KRT2 Keratin, type II cytoskeletal 2 epidermal	IPI00021304	71239.86719	8.07	4	220.1000061	100	94.55000305	100	0.635602963	0.563268236	5
MAOA Amine oxidase [flavin-containing] A	IPI00008483	65674.00781	7.94	2	124.6600037	100	76.56999969	99.99979979	0.633912676	2.32E-02	2
ALDH1B1 Aldehyde dehydrogenase X, mitochondrial precursor	IPI00103467	62178.58984	6.36	4	218.4100037	100	85.26000214	100	0.631783746	0.296810081	4
MMAB 19 kDa protein	IPI00789857	20551.83008	8.35	1	79.16000366	99.99988972	79.16000366	99.99988972	0.63010828	0	1
GLUD1 Glutamate dehydrogenase 1, mitochondrial precursor	IPI00016801	66531.63281	7.66	18	1232.970093	100	136.3500061	100	0.627133187	0.104454304	18
ACADVL Isoform 2 of Very-long-chain specific acyl-CoA dehydrogenase, mitoch	IPI00178744	78527.97656	9.06	1	62.61999893	99.99502855	62.61999893	99.99502855	0.619817358	0	1
GBE1 1,4-alpha-glucan-branching enzyme	IPI00296635	85817.03906	5.87	2	116.2600021	100	84.94000244	100	0.618293376	0.10896935	2
ARG1 Isoform 2 of Arginase-1	IPI00398768	39380.19922	6.72	5	296.6099854	100	90.51999664	100	0.617329262	0.192660305	5
AKR1C3 Aldo-keto reductase family 1 member C3	IPI00291483	41031.17969	8.05	8	375.8299866	100	75.91000366	99.99976693	0.616212367	0.17179649	8
ANXA6 Annexin A6	IPI00221226	83734.25	5.42	19	1154.843384	100	125.3199997	100	0.612825679	0.152475461	20
SDHA Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondri	IPI00305166	77793.53125	7.06	5	286.25	100	84.20999908	100	0.61243749	7.93E-02	5
NAPRT1 Nicotinate phosphoribosyltransferase domain-containing protein 1	IPI00465085	61989.39063	5.59	2	118.5999908	100	65.83999634	99.99763144	0.610857743	0.136315684	2
DCI Isoform 2 of 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor	IPI00398758	32932.46875	9.07	2	150.519989	100	102.9199982	100	0.607878019	1.15E-02	2
HADHA Trifunctional enzyme subunit alpha, mitochondrial precursor	IPI00031522	93913.70313	9.16	13	831.9099731	100	136.2899933	100	0.604611258	0.261755907	13
ACAT1 Acetyl-CoA acetyltransferase, mitochondrial precursor	IPI00030363	49865.05859	8.98	12	863.3612061	100	137.1499939	100	0.60265697	0.143350807	12
COX4I1 COX4I1 protein	IPI00645361	10672.90039	8.64	1	86.23999786	100	86.23999786	100	0.602129338	0	1
METTL7A Methyltransferase-like protein 7A precursor	IPI00022300	30730.71094	8.7	1	80.56999969	99.9999203	80.56999969	99.9999203	0.597430611	0	1
ALDOC Fructose-bisphosphate aldolase C	IPI00418262	42921.51172	6.41	4	230.3299866	100	93.37999725	100	0.591407925	1.070476818	5
UGP2 Isoform 1 of UTP--glucose-1-phosphate uridylyltransferase	IPI00329331	63091.28906	8.16	11	732.9788818	100	138	100	0.589549727	0.104834218	11

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IDH2 Isocitrate dehydrogenase [NADP], mitochondrial precursor	IPI00011107	56573.30859	8.88	9	502.694458	100	96.40000153	100	0.589263617	0.175067944	9
PGM1 Phosphoglucomutase 1	IPI00844159	66935.90625	6.2	3	219.4700012	100	99.80999756	100	0.583059496	0.222870736	3
ANXA6 annexin VI isoform 2	IPI00002459	83137.89844	5.46	19	1164.003418	100	125.3199997	100	0.582043817	0.229554722	20
CNDP2 53 kDa protein	IPI00646632	58467.37891	5.66	3	151.1600037	100	80.83999634	99.9999251	0.579371507	0.161196563	4
CGN cingulin	IPI00844508	149111.4844	5.44	1	105.4199982	100	105.4199982	100	0.57828691	0	1
PGLS 6-phosphogluconolactonase	IPI00029997	29055.68945	5.7	2	74.86999512	99.99970387	43.54999924	99.59868702	0.576151804	0.179124685	2
ALDH2 Mitochondrial aldehyde dehydrogenase 2 variant (Fragment)	IPI00792207	61065.96094	6.63	13	856.2000122	100	106.4499969	100	0.574772081	0.230323784	14
SUCLG1 succinate-CoA ligase, GDP-forming, alpha subunit	IPI00759493	39717.12109	9.01	2	201.1100006	100	123.6500015	100	0.573125393	0.29745233	2
CRYZ 32 kDa protein	IPI00647366	34670.82031	8.59	3	265.25	100	146.3999939	100	0.571814032	6.74E-02	3
HADHB Trifunctional enzyme beta subunit, mitochondrial precursor	IPI00022793	56777.03906	9.45	6	315.1699829	100	81.19999695	99.99993106	0.56968467	0.166928956	6
ESD 28 kDa protein	IPI00641040	31266.09961	6.29	2	101.8099976	100	53.38000107	99.95826667	0.566424147	0.142422804	2
ACSL1 Isoform 1 of Long-chain-fatty-acid--CoA ligase 1	IPI00012728	85201.29688	6.81	9	591.6699829	100	121.4400024	100	0.564200237	0.141639832	9
- 105 kDa protein	IPI00794900	115433.2422	7.3	8	417.8933411	100	89.48000336	100	0.56145444	0.204001489	8
NDUFAB1 Acyl carrier protein, mitochondrial precursor	IPI00022442	18696.14063	4.82	2	76.83999634	99.99981186	42.20999908	99.45363456	0.554531494	9.98E-03	2
COMT Isoform Soluble of Catechol O-methyltransferase	IPI00375513	26915.57031	5.15	2	143.4600067	100	84.76000214	100	0.553326228	0.104972487	2
SELENBP1 53 kDa protein	IPI00745729	57664.26953	6.03	3	126.8199921	100	50.59000015	99.92066166	0.54588442	0.289257114	4
LAP3 Isoform 2 of Cytosol aminopeptidase	IPI00789806	58388.32813	6.3	7	411.1499939	100	94.19999695	100	0.544348643	0.336521206	7
LTB4DH NADP-dependent leukotriene B4 12-hydroxydehydrogenase	IPI00292657	40639.17188	8.45	3	185.1399994	100	117.6699982	100	0.535863243	5.67E-02	3
ALDH9A1 aldehyde dehydrogenase 9A1	IPI00479877	61023.67188	6.23	1	94.34999847	100	94.34999847	100	0.53357937	0	1
AKR1C2 Aldo-keto reductase family 1 member C2	IPI00005668	40922.30078	7.13	7	332.8800049	100	67.13999939	99.99824417	0.530903107	0.134311606	7
LOC648517 similar to Aldo-keto reductase family 1 member C1 (20-alpha-hydro	IPI00736657	35442.78906	9.01	8	367.0599976	100	67.13999939	99.99824417	0.528947893	0.130105789	8
ETFA 24 kDa protein	IPI00792673	27117.09961	8.77	3	323.25	100	171.9499969	100	0.528755589	0.114205111	3
SNTB1 Isoform 2 of Beta-1-syntrophin	IPI00216858	44616.67188	9.13	1	75.76000214	99.99975874	75.76000214	99.99975874	0.522803241	0	1

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AKR1C4 Aldo-keto reductase family 1 member C4	IPI00289524	41137.30859	6.71	9	401.6599731	100	58.08000183	99.98585891	0.515276088	0.15069302	9
PC Pyruvate carboxylase, mitochondrial precursor	IPI00299402	138358.0469	6.37	10	617.9589233	100	111.5699997	100	0.510588816	0.155875148	10
KRT6C Keratin, type II cytoskeletal 6E	IPI00299145	64682.71875	8.09	5	238.7044373	100	72.30999756	99.99946607	0.505240398	0.202748378	9
CTSB Cathepsin B precursor	IPI00295741	40882.91016	5.88	3	216.3999939	100	106.6100006	100	0.505002674	8.41E-02	3
IL11RA 13 kDa protein	IPI00167641	14096.79004	7.79	1	71.41000366	99.99934312	71.41000366	99.99934312	0.501627318	0	1
SCP2 sterol carrier protein 2 isoform 2	IPI00433347	61608.94141	6.25	6	310.5844421	100	81.47000122	99.99993521	0.500933381	3.89E-02	6
GOT1 Aspartate aminotransferase, cytoplasmic	IPI00219029	49570.83984	6.52	7	378.1199951	100	119.7099991	100	0.498134227	0.171622573	7
UNQ501 MBC3205	IPI00063130	22277.99023	8.91	1	76.41000366	99.99979228	76.41000366	99.99979228	0.49727244	0	1
ABCD3 ABCD3 protein	IPI00185503	68716.28906	9.31	1	88.08000183	100	88.08000183	100	0.493585779	0	1
KHK Isoform C of Ketohexokinase	IPI00216136	35220.62891	5.91	2	70.70999908	99.99922824	38.38999939	98.68331105	0.491911487	0.61627863	2
ALDH1A1 Retinal dehydrogenase 1	IPI00218914	60949.39063	6.3	12	713.7700195	100	116.6299973	100	0.487870292	9.44E-02	12
BAAT Bile acid CoA:amino acid N-acyltransferase	IPI00017819	48856.32031	6.49	2	116.8099976	100	76.13999939	99.99977895	0.487615183	0.170457772	2
BLVRB Flavin reductase	IPI00783862	23637.61914	7.13	2	88.80000305	100	45.20000076	99.72553748	0.485188997	7.15E-02	2
CPT2 Carnitine O-palmitoyltransferase 2, mitochondrial precursor	IPI00012912	79760.85938	8.38	2	125.5344391	100	90.81999969	100	0.484234609	2.61E-02	2
APOC3 13 kDa protein	IPI00657670	13861.62012	7.9	1	87.90000153	100	87.90000153	100	0.481672593	0	1
H1F0 Histone H1.0	IPI00550239	29058.99023	10.84	1	83.52999878	100	83.52999878	100	0.477712143	0	1
GATM Isoform Cytoplasmic of Glycine amidinotransferase, mitochondrial precu	IPI00216279	48966.78125	6.61	16	1090.650024	100	136.7899933	100	0.468700407	0.149332596	18
HADH Isoform 2 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precu	IPI00298406	47125.23047	9.34	5	257.5	100	93.91999817	100	0.464903885	0.175090438	5
NNMT Nicotinamide N-methyltransferase	IPI00027681	33091.32031	5.56	3	126.7999954	100	49.5	99.89802749	0.462527163	8.75E-02	3
PYGL 97 kDa protein	IPI00783313	107098.9297	6.71	6	311.1499939	100	92.09999847	100	0.451907244	0.107860938	6
DBT Lipoamide acyltransferase component of branched-chain alpha-keto acid d	IPI00003944	59823.44141	8.71	2	128.5700073	100	67.80000305	99.99849172	0.449552631	0.286746756	2
C10orf125 Isoform 2 of Protein fucU homolog	IPI00845372	15786.78027	5.2	1	62.58000183	99.99498255	62.58000183	99.99498255	0.448066906	0	1
HSD17B4 Peroxisomal multifunctional enzyme type 2	IPI00019912	88068.99219	8.96	4	248.4700012	100	111.9300003	100	0.447745596	0.110540327	4

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KRT8 Keratin, type II cytoskeletal 8	IPI00554648	58423.62891	5.52	24	1435.693359	100	100.5199966	100	0.445827867	0.133097741	29
CA2 Carbonic anhydrase 2	IPI00218414	32874.30859	6.87	3	201.8099976	100	84.37000275	100	0.445680397	0.270205552	3
AGL Isoform 6 of Glycogen debranching enzyme	IPI00219066	185998.375	6.26	1	99.05999756	100	99.05999756	100	0.444440641	0	1
MAT1A S-adenosylmethionine synthetase isoform type-1	IPI00021772	47392.28906	5.86	7	343.9044495	100	85.58000183	100	0.439050199	0.195045363	7
GPT Alanine aminotransferase 1	IPI00217458	57510.32813	6.77	3	149.25	100	55.59000015	99.97491101	0.435943075	0.103582451	3
PEBP1 Phosphatidylethanolamine-binding protein 1	IPI00219446	23439.92969	7.01	8	666.8200684	100	204.1799927	100	0.434367991	8.84E-02	10
SUCLG2 Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precurso	IPI00096066	51941.89844	6.15	3	178.3399963	100	82.91999817	100	0.432801275	0.121889446	3
KRT18 Keratin, type I cytoskeletal 18	IPI00784347	51196.89844	5.34	10	499.8800049	100	94.44000244	100	0.431715906	0.133893635	11
ALDH1L1 Formyltetrahydrofolate dehydrogenase isoform a variant	IPI00793673	109020.6328	5.63	3	147.3144379	100	74.08999634	99.99964561	0.412926523	0.094784117	3
KRT79 keratin 6L	IPI00241841	62350.57031	6.75	4	183.3800049	100	53.36999893	99.95817045	0.40933095	9.15E-02	6
COL6A3 alpha 3 type VI collagen isoform 3 precursor	IPI00072917	345457.3438	6.47	5	209.8300018	100	48.81999969	99.8807432	0.406413844	0.384537067	5
DPYS Dihydropyrimidinase	IPI00028910	62048.10938	6.81	5	259.3899841	100	66.80000305	99.99810118	0.402646254	0.129384633	5
SLC27A5 Bile acyl-CoA synthetase	IPI00016827	78658.29688	7.81	2	95.38443756	100	63.79999924	99.99621136	0.399810417	0.388472136	2
AKR7A3 Aflatoxin B1 aldehyde reductase member 3	IPI00293721	39376.69141	6.67	2	120.7200012	100	64.08000183	99.99644792	0.39811272	0.119935505	2
SHMT1 Isoform 2 of Serine hydroxymethyltransferase, cytosolic	IPI00220668	53489.17969	7.59	5	269.2744446	100	91.13999939	100	0.390866489	0.116648651	5
HMGCS2 Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor	IPI00008934	61333.76953	8.4	10	557.3499756	100	85.23999786	100	0.387349251	0.231648823	10
SOD1 Superoxide dismutase	IPI00783680	17838.08984	5.7	5	344.0400085	100	116.3600006	100	0.3833138	0.045341039	5
ECHS1 Enoyl-CoA hydratase, mitochondrial precursor	IPI00024993	35335.42969	8.34	11	716.5599365	100	112.2799988	100	0.376487099	0.140857369	11
ASS1 Argininosuccinate synthase	IPI00020632	56147.66016	8.6	14	891.2999878	100	145.4400024	100	0.375343896	0.123097012	14
AOX1 Hypothetical protein AOX1	IPI00743616	161854.2031	6.78	6	257.3444519	100	61.47000122	99.99352137	0.371782628	0.120071905	6
ETFB Isoform 2 of Electron transfer flavoprotein subunit beta	IPI00556451	41287.32813	6.78	2	97.86999512	100	52.68999863	99.95108036	0.368501417	1.99E-02	2
FMO3 Dimethylaniline monooxygenase [N-oxide-forming] 3	IPI00329033	66260.82813	7.9	2	70.88999939	99.99925957	35.97999954	97.70658222	0.367085506	6.41E-02	2
MUT Methylmalonyl-CoA mutase, mitochondrial precursor	IPI00024934	90636.34375	6.48	3	233.6299896	100	92.87999725	100	0.365205416	7.44E-02	3

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CBR1 Carbonyl reductase [NADPH] 1	IPI00295386	33322.12891	8.55	6	352.3799744	100	92.18000031	100	0.36038392	7.41E-02	7
TST Thiosulfate sulfurtransferase	IPI00216293	35752.05859	6.77	8	607.8144531	100	112.8000031	100	0.35902541	0.15092372	8
SULT1A1 Sulfotransferase 1A1	IPI00300026	47814.69922	8.61	8	371.8500061	100	58.77999878	99.98796397	0.357107125	0.242652162	8
ACADS Short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	IPI00027701	47857.05859	8.13	2	93.52999878	100	52.16999817	99.9448579	0.346054799	0.476820127	2
SORD Sorbitol dehydrogenase	IPI00216057	42378.10938	8.23	4	222.5700073	100	103.6699982	100	0.345159078	7.53E-02	4
ALDH6A1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondria	IPI00024990	63211.07813	8.72	8	555.3644409	100	94.58999634	100	0.339850925	0.190832537	8
EHHADH Peroxisomal bifunctional enzyme	IPI00216164	86466.10156	9.22	4	181.9944458	100	66.52999878	99.99797939	0.337618926	0.186726206	4
AGXT Serine--pyruvate aminotransferase	IPI00009367	46426.73047	8.61	7	477.230011	100	109.4599991	100	0.337345167	8.14E-02	7
DECR1 2,4-dienoyl-CoA reductase, mitochondrial precursor	IPI00003482	40019.14844	9.35	6	406.9900208	100	109.6900024	100	0.336664878	0.207259032	6
FBP1 Fructose-1,6-bisphosphatase 1	IPI00073772	41289.14844	6.54	9	692.1900024	100	123.7600021	100	0.335755355	0.213770552	9
DCXR 26 kDa protein	IPI00797249	27252.58984	8.33	6	300.9799805	100	66.70999908	99.99806142	0.334975455	0.15976316	6
CES2 carboxylesterase 2 isoform 1	IPI00332828	72247.0625	6.03	4	187.6900024	100	61.81999969	99.994023	0.319850996	8.44E-02	4
FAH Fumarylacetoacetase	IPI00031708	49546.46094	6.46	2	102.3799973	100	60.52999878	99.99195579	0.318129831	0.271060947	2
EHHADH 8 kDa protein	IPI00797006	7706.140137	7.98	1	123.75	100	123.75	100	0.316339162	0	1
GRHPR Glyoxylate reductase/hydroxypyruvate reductase	IPI00037448	38271.94141	7.01	9	660.7544556	100	124.4100037	100	0.303983164	0.167879777	9
CES1 carboxylesterase 1 isoform c precursor	IPI00607693	68199.60938	6.15	20	1418.180054	100	199.9900055	100	0.301104655	7.78E-02	21
ABHD14B 22 kDa protein	IPI00747859	23098.53906	5.43	2	132.9299927	100	95.76000214	100	0.297778796	2.11E-02	2
ACADSB Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	IPI00024623	52051.67969	6.53	2	138.4299927	100	98.23999786	100	0.295092282	0.122843934	2
HRSP12 Ribonuclease UK114	IPI00005038	15826.7998	8.74	3	173.8899994	100	66.15000153	99.99779462	0.292460237	8.73E-02	3
CAT Catalase	IPI00465436	64367.17969	6.9	11	824.2300415	100	192.7100067	100	0.28859813	0.226602972	11
HGD Homogentisate 1,2-dioxygenase	IPI00303174	54236.85938	6.54	3	136.5500031	100	52.99000168	99.95434557	0.282075849	6.31E-02	3
ACSM2B Acyl-CoA synthetase medium-chain family member 2	IPI00329444	70450.35938	8.5	4	169.4700012	100	55.27000046	99.97299258	0.281032751	0.116167675	4
ACADM Hypothetical protein DKFZp686M24262	IPI00513827	55018.78906	7.94	4	224.1999969	100	80.98000336	99.99992748	0.280258224	0.131217851	4

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CYP3A4 Cytochrome P450 3A4	IPI00465138	63244.41016	8.27	2	113.3099976	100	81.01999664	99.99992814	0.280087256	9.93E-02	2
HPD 40 kDa protein	IPI00795913	44884.14063	5.93	4	243.9700012	100	99.56999969	100	0.27703497	0.110086831	4
LOC554235 29 kDa protein	IPI00419903	29217.00977	6.5	1	109.6800003	100	109.6800003	100	0.275776873	0	1
PBLD Phenazine biosynthesis-like domain-containing protein	IPI00024896	34011.42969	6.06	2	97.97444153	100	66.58000183	99.99800252	0.272116828	0.254207618	2
EPHX1 Epoxide hydrolase 1	IPI00009896	57419.37891	6.77	6	468	100	112.0899963	100	0.27133733	0.18652572	7
PCK2 mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor	IPI00797038	74784.85938	7.57	14	810.9899902	100	106.5	100	0.267152864	0.237991846	15
GOT2 Aspartate aminotransferase, mitochondrial precursor	IPI00018206	52087.64844	9.14	5	367.2200012	100	119.5299988	100	0.265611313	7.02E-02	5
ABAT 4-aminobutyrate aminotransferase, mitochondrial precursor	IPI00009532	61418.91016	8.17	5	293.1699829	100	83.61000061	100	0.265041348	7.77E-02	5
ACSM2A LOC123876 protein	IPI00644771	70304.24219	8.34	4	186.1400146	100	59.06999969	99.98874143	0.262839856	8.48E-02	4
ACY1 Aminoacylase-1	IPI00009268	48344.23047	5.77	4	189.5	100	56.45000076	99.97941821	0.257161298	0.115417865	4
ACAA2 3-ketoacyl-CoA thiolase, mitochondrial	IPI00001539	46153.96875	8.32	11	707.7799683	100	138.3200073	100	0.249699095	0.133874861	11
CYP3A5 Cytochrome P450 3A5	IPI00025831	63206.64063	8.86	2	116.9899979	100	81.08999634	99.99992929	0.249680553	5.18E-02	2
UGT1A6;UGT1A1 UDP-glucuronosyltransferase 1-1 precursor	IPI00434346	64522.89063	8.19	4	242.1600037	100	71.58000183	99.99936834	0.243836956	0.147123014	4
KRT19 Keratin, type I cytoskeletal 19	IPI00479145	46225.37891	5.04	3	156.2599945	100	74.25	99.99965843	0.243770925	0.228261471	3
COL6A1 Collagen alpha-1(VI) chain precursor	IPI00291136	117302.5391	5.26	3	153.4899902	100	65.18000031	99.99724271	0.230245	0.113140106	3
FMO5 Dimethylaniline monooxygenase [N-oxide-forming] 5	IPI00215760	66454.40625	8.41	1	92.36000061	100	92.36000061	100	0.223316497	0	1
HAGH Hydroxyacylglutathione hydrolase	IPI00745553	32141.91016	6.86	1	99.62999725	100	99.62999725	100	0.212380115	0	1
CPS1 Isoform 1 of Carbamoyl-phosphate synthase [ammonia], mitochondrial pre	IPI00011062	180875.9531	6.3	60	4328.580078	100	149.0200043	100	0.209942627	0.128045938	70
MT1X Metallothionein-1X	IPI00008753	8279.200195	8.38	2	112.3200073	100	69.55000305	99.99899195	0.209333742	7.96E-02	2
BDH1 D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	IPI00025341	41766.75	9.11	3	143.5244446	100	56.22999954	99.97834874	0.207026356	0.191009232	3
ADH1A Alcohol dehydrogenase 1A	IPI00218896	45320.80859	8.26	11	859.1099854	100	121.3399963	100	0.206379645	0.112566428	12
OTC Ornithine carbamoyltransferase, mitochondrial precursor	IPI00295363	43936.05859	8.75	7	420.2844543	100	104.0899963	100	0.204474915	0.146839251	7
FTCD Isoform A of Formimidoyltransferase-cyclodeaminase	IPI00001441	62321.57813	5.58	7	389.1799927	100	74.90000153	99.99970591	0.204108108	0.221065709	7

Poorly Differentiated iTRAQ Individual Patients
Poor Diff 215NT

CYP2C8 45 kDa protein	IPI00843846	49430.42188	8.91	4	229.0500031	100	64.80999756	99.9969975	0.198464796	9.45E-02	4
ADH1B Alcohol dehydrogenase 1B	IPI00473031	45270.91016	8.63	11	826.0499268	100	121.3399963	100	0.191141542	7.27E-02	12
UGT2B7 similar to UDP-glucuronosyltransferase 2B7 precursor	IPI00787584	65314.41016	8.41	4	214.0400085	100	74.30999756	99.99966311	0.188711773	0.094843293	4
CYP2C19 Cytochrome P-450 II C (Fragment)	IPI00657852	44746.01953	6.82	2	118.1800003	100	61.59000015	99.99369793	0.184918014	7.57E-02	2
CYP2C9 Cytochrome P450 2C9	IPI00007219	61374.14063	8.13	3	186.4799957	100	79.30999756	99.99989347	0.18187408	5.34E-02	3
SULT2A1 Bile salt sulfotransferase	IPI00216133	37496.32813	5.71	7	352.8500061	100	83.44000244	100	0.17553379	6.35E-02	7
UGT2B17 UDP-glucuronosyltransferase 2B17 precursor	IPI00026932	67707.59375	8.76	1	66.90000153	99.99814441	66.90000153	99.99814441	0.175422632	0	1
FABP1 FABP1 protein (Fragment)	IPI00010290	18729.4707	9.52	6	401.8299866	100	115.1399994	100	0.168469766	7.66E-02	8
ADH1C Alcohol dehydrogenase 1C	IPI00465343	45428	8.63	7	533.5999756	100	121.3399963	100	0.159375773	3.57E-02	8
CYB5A Isoform 1 of Cytochrome b5	IPI00397860	16616.71094	4.88	6	524.5899658	100	227.2200012	100	0.158753224	8.68E-02	6
BHMT Betaine--homocysteine S-methyltransferase 1	IPI00004101	49946.23828	6.58	14	768.6488647	100	125.2300034	100	0.152224165	0.100297875	16
ACAA1 3-ketoacyl-CoA thiolase, peroxisomal precursor	IPI00012828	47604.07031	8.76	4	349.6000061	100	110.1999969	100	0.151389736	5.50E-02	4
GLYAT Isoform 1 of Glycine N-acyltransferase	IPI00402759	37221.21094	8.38	3	135.8099976	100	57.43000031	99.98357584	0.149251882	0.417065012	3
GSTA2 Glutathione S-transferase A2	IPI00745233	29104	8.51	8	439.5299683	100	84.43000031	100	0.147881253	0.100485918	9
ADH4 Alcohol dehydrogenase 4	IPI00218899	45828.03125	8.25	9	690.5800171	100	116.8899994	100	0.142183921	0.12914088	9
RDH16 Retinol dehydrogenase 16	IPI00289551	38852.73828	8.83	4	219.2744446	100	69.81999969	99.99905271	0.138199711	0.12760772	4
CYP2A6 Cytochrome P450 2A6	IPI00299568	61083.51172	9.24	3	171.6900024	100	90.04000092	100	0.127664078	5.91E-02	3
DAK Dihydroxyacetone kinase	IPI00551024	63392.42188	7.12	5	521.5	100	156.3899994	100	0.122755941	0.130857111	6
ALDOB Fructose-bisphosphate aldolase B	IPI00218407	43462.35156	8	12	865.0800171	100	112.6500015	100	0.121983706	0.13276425	16
CYP1A2 Isoform 1 of Cytochrome P450 1A2	IPI00719591	62467.67188	9.18	1	76.54000092	99.9997984	76.54000092	99.9997984	0.121336795	0	1
EMILIN1 EMILIN-1 precursor	IPI00013079	109415.4531	5.1	1	85.91000366	100	85.91000366	100	0.111415738	0	1
GGTLA1 Isoform 2 of Gamma-glutamyltransferase 5 precursor	IPI00339373	61051.73828	7.67	1	74.33999634	99.99966543	74.33999634	99.99966543	0.108954915	0	1
COL1A1 Collagen alpha-1(I) chain precursor	IPI00297646	148007.1406	5.6	1	95.41999817	100	95.41999817	100	7.49E-02	0	1